

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2003, 13:22:16 ; Search time 14650 Seconds

(without alignments)
17411.025 Million cell updates/sec

Title: US-09-845-020A-5

Perfect score: 6235

Sequence: 1 gatcaacttgagacagtagt.....tgccactcccccacagcct 6235

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl1.*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.yl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.scs:*
28: em.un:*
29: em.yl:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6235	100.0	6235	AR156464	AR156464 Sequence
2	6235	100.0	6235	AX250679	AX250679 Sequence
3	6235	100.0	6679	AR156461	AR156461 Sequence
4	6235	100.0	6679	AX250678	AX250678 Sequence
5	6051.2	97.1	227857	AC090844	AC090844 Homo sapi
6	6032	96.7	122132	AC102799	AC102799 Homo sapi
7	5671.6	91.0	100490	AC007776	AC007776 Homo sapi
8	4368.4	70.1	221484	AC019095	AC019095 Homo sapi
9	2834	45.5	2834	AR156465	AR156465 Sequence
10	1612.4	25.9	5527	AF388025	AF388025 Homo sapi
11	1424.8	22.9	221484	AC019095	AC019095 Homo sapi
12	1252	20.1	1252	AR156466	AR156466 Sequence
13	1189.4	19.1	110779	BX470173	BX470173 Human DNA
14	1187.8	19.1	51015	AL732292	AL732292 Human DNA
15	1129.8	18.1	196806	AC104212	AC104212 Homo sapi
16	1109	17.8	189036	AL645608	AL645608 Homo sapi
17	1108.8	17.8	59925	AC092543	AC092543 Homo sapi
18	1084.8	17.4	93048	AC108148	AC108148 Homo sapi
19	1081.8	17.4	156387	BX537114	BX537114 Homo sapi
20	1081.2	17.3	155334	AC015822	AC015822 Homo sapi
21	1081.2	17.3	162036	AC015773	AC015773 Homo sapi
22	1080.2	17.3	144444	HSJ365119	AL078463 Human DNA
23	1071.2	17.2	142498	AC023980	AC023980 Homo sapi
24	1071.2	17.2	145787	AC099499	AC099499 Homo sapi
25	1051.8	16.9	184920	AC097262	AC097262 Homo sapi
26	1046.6	16.8	166720	AC112180	AC112180 Homo sapi
27	1046.6	16.8	192518	AC027745	AC027745 Homo sapi
28	1046.6	16.8	203831	AC093295	AC093295 Homo sapi
29	1045.4	16.8	110000	AL831785-7	Continuation (8 of
30	1035.4	16.6	107908	AL360155	AL360155 Human DNA
31	1035.4	16.6	157800	AL357074	AL357074 Homo sapi
32	1035.4	16.6	159790	AC013613	AC013613 Homo sapi
33	1029	16.5	169063	AC138126	AC138126 Homo sapi
34	1029	16.5	177299	AC073544	AC073544 Homo sapi
35	1028.4	16.5	202488	AC032041	AC032041 Homo sapi
36	1025.2	16.4	150972	AL512380	AL512380 Human DNA
37	1024	16.4	227430	AC091590	AC091590 Homo sapi
38	1017.6	16.3	42969	AC004197	AC004197 Homo sapi
39	1017.6	16.3	43901	AC004198	AC004198 Homo sapi
40	1017.6	16.3	117327	AL663093	AL663093 Human DNA
41	1016.6	16.3	141980	AL450425	AL450425 Human DNA
42	1016.6	16.3	162299	AC016429	AC016429 Homo sapi
43	1013.8	16.3	177883	AC138471	AC138471 Homo sapi
44	1008.6	16.2	145456	AL513366	AL513366 Human DNA
45	1007.2	16.2	62988	AL731680	AL731680 Human DNA

ALIGNMENTS

RESULT 1
AR156464
LOCUS AR156464
DEFINITION Sequence 5 from patent US 6242218.
ACCESSION AR156464
VERSION AR156464.1 GI:15125168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6235)
AUTHORS Treco,D.A., Heartlein,M.W. and Seiden,R.F.
TITLE Genomic sequences for protein production and delivery
JOURNAL Patent: US 6242218-A 5 05-JUN-2001;
FEATURES Location/Qualifiers

source 1. .6235
/organism="unknown"
BASE COUNT 1586 a 1610 c 1708 g 1331 t
ORIGIN

Query Match 100.0%; Score 6235; DB 6; Length 6235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GATCAGCTTGAGAGACAGTACGTCACAGACAGCCTGGGCGACATAGGAGAGCTGTCTACG 60
Db 1 GATCAGCTTGAGAGACAGTACGTCACAGACAGCCTGGGCGACATAGGAGAGCTGTCTACG 60
QY 61 AAAAATCAAAAATTTATGGCGGGGCGATGGGCTGACCTGTATCCCTTAACCTTTGGG 120
Db 61 AAAAATCAAAAATTTATGGCGGGGCGATGGGCTGACCTGTATCCCTTAACCTTTGGG 120
QY 121 ACATCAAGGCAAGTGGATGATCAGTTCAGAGTTCAGAGTACGCTGGGCAACATGGT 180
Db 121 ACATCAAGGCAAGTGGATGATCAGTTCAGAGTTCAGAGTACGCTGGGCAACATGGT 180
QY 181 GAAACCCATATCTCCACTAAAAAATACAAAATTAAGCCAGCATGGTGGCAGGACCTGT 240
Db 181 GAAACCCATATCTCCACTAAAAAATACAAAATTAAGCCAGCATGGTGGCAGGACCTGT 240
QY 241 ATCCGGCTACTCAGAGGCGTGGAGGAGGAGATCACTGTAACCCAGGAGGCGGAGTTG 300
Db 241 ATCCGGCTACTCAGAGGCGTGGAGGAGGAGATCACTGTAACCCAGGAGGCGGAGTTG 300
QY 301 CAGTGAGCTGAGATCACACACACTGCATCCAGCTGGGTGACAGAGCAAGACTGTATCTC 360
Db 301 CAGTGAGCTGAGATCACACACACTGCATCCAGCTGGGTGACAGAGCAAGACTGTATCTC 360
QY 361 AAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420
Db 361 AAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420
QY 421 CTACTCAGAGGCTGAGGTGGAGGATCACTTGAACCTGGGGCAGTCAAGGCTCAGAGA 480
Db 421 CTACTCAGAGGCTGAGGTGGAGGATCACTTGAACCTGGGGCAGTCAAGGCTCAGAGA 480
QY 481 GCCAAGATCATGCCACTACACTCCAGCCTGGGCAACAGAGAGAGACCCTGTCTAAAA 540
Db 481 GCCAAGATCATGCCACTACACTCCAGCCTGGGCAACAGAGAGAGACCCTGTCTAAAA 540
QY 541 AATATATATATATAAAGAAAAAACAAGCTGTATATGTCTCTCTCATATCACTACT 600
Db 541 AATATATATATATAAAGAAAAAACAAGCTGTATATGTCTCTCTCATATCACTACT 600
QY 601 ATGTATATAGTTGGCAAACTCAAGATCAGATAGTCAATTTTAAAGCTTGTGGGCGT 660
Db 601 ATGTATATAGTTGGCAAACTCAAGATCAGATAGTCAATTTTAAAGCTTGTGGGCGT 660
QY 661 ATGGTCTGTGACATCACTCTGCGCTGTCTTCTAGCACAAAAGCAGTATTAACAT 720
Db 661 ATGGTCTGTGACATCACTCTGCGCTGTCTTCTAGCACAAAAGCAGTATTAACAT 720
QY 721 ACATATATGAATTTTATATAGATCGAGATTTGAATTTGATATATGATTTTACATTTTAT 780
Db 721 ACATATATGAATTTTATATAGATCGAGATTTGAATTTGATATATGATTTTACATTTTAT 780
QY 781 AAAATATATCTTTTAAAAATTTTCCCTTAACCATTTTAAAGTGTAAAAAGCGGCGCAG 840
Db 781 AAAATATATCTTTTAAAAATTTTCCCTTAACCATTTTAAAGTGTAAAAAGCGGCGCAG 840
QY 841 GCCATGCTCAGCGCTGTAAATTCAGACATTTGGAGGCTGAGGTGGGAGATCACTTGAG 900
Db 841 GCCATGCTCAGCGCTGTAAATTCAGACATTTGGAGGCTGAGGTGGGAGATCACTTGAG 900
QY 901 ATCAACAGTTGAGAGACCAAGCCTGGCCAAATAGCAAAAACCCATTTCTACTAAAAATAA 960
Db 901 ATCAACAGTTGAGAGACCAAGCCTGGCCAAATAGCAAAAACCCATTTCTACTAAAAATAA 960
```

```
QY 961 AAAATTAGCTGGGCATATGTTGTCACACACTGTGATCCCACTACTTGGAGGCTGAGGCA 1020
Db 961 AAAATTAGCTGGGCATATGTTGTCACACACTGTGATCCCACTACTTGGAGGCTGAGGCA 1020
QY 1021 GGAGAAATGCTTGAACCTGGGAAAGCGGAGTTGAGTGAAGCCATATCATGCTGATGAC 1080
Db 1021 GGAGAAATGCTTGAACCTGGGAAAGCGGAGTTGAGTGAAGCCATATCATGCTGATGAC 1080
QY 1081 TCCAGCTGGGTGACAGAGTGAAGTGGTCTCAACGAAAAAATAAGTGTAAAAAGCAT 1140
Db 1081 TCCAGCTGGGTGACAGAGTGAAGTGGTCTCAACGAAAAAATAAGTGTAAAAAGCAT 1140
QY 1141 TCTTAATTCAGTGTACATCACTGTATCAATCTAGTTCGCTGCTGAGGCAAT 1200
Db 1141 TCTTAATTCAGTGTACATCACTGTATCAATCTAGTTCGCTGCTGAGGCAAT 1200
QY 1201 ACCTGAGAAATAGATGCTTGGTGCACAGGAGCATACATTTCCATTAATCACTAGACACT 1260
Db 1201 ACCTGAGAAATAGATGCTTGGTGCACAGGAGCATACATTTCCATTAATCACTAGACACT 1260
QY 1261 ACCATGAGAAATAGATGCTTGGTGCACAGGAGCATACATTTCCATTAATCACTAGACACT 1320
Db 1261 ACCATGAGAAATAGATGCTTGGTGCACAGGAGCATACATTTCCATTAATCACTAGACACT 1320
QY 1321 GAGAGTTACTCCAGATCTTTTACAAGAATGCTTAAGCCAGTACAGATGAAACAGAGA 1380
Db 1321 GAGAGTTACTCCAGATCTTTTACAAGAATGCTTAAGCCAGTACAGATGAAACAGAGA 1380
QY 1381 AGTGGAGGAGGAGCTGCAGCCCTTTAATCAATGAAGAAATACCTGGTGGAGCTCTCT 1440
Db 1381 AGTGGAGGAGGAGCTGCAGCCCTTTAATCAATGAAGAAATACCTGGTGGAGCTCTCT 1440
QY 1441 GGATGCTGGAAGATGAATTAACGGGGGTCTGTGAGCCTGCCCTGTCAATCACTGTG 1500
Db 1441 GGATGCTGGAAGATGAATTAACGGGGGTCTGTGAGCCTGCCCTGTCAATCACTGTG 1500
QY 1501 ACTTCTGAGCCTCCAGTCCATCTCAGCCCATGTGTATGCGCAGATATATAGCCCT 1560
Db 1501 ACTTCTGAGCCTCCAGTCCATCTCAGCCCATGTGTATGCGCAGATATATAGCCCT 1560
QY 1561 CACTCTGTTGGTCTTTATTTCCCATATGAGGCTGAGAGTGTGATTAAGCCGTTAT 1620
Db 1561 CACTCTGTTGGTCTTTATTTCCCATATGAGGCTGAGAGTGTGATTAAGCCGTTAT 1620
QY 1621 TCAAGATGTACAGCTTCTTACAGAAAGTATGTCTACAGAAACAGCAGGCGCTTGCA 1680
Db 1621 TCAAGATGTACAGCTTCTTACAGAAAGTATGTCTACAGAAACAGCAGGCGCTTGCA 1680
QY 1681 AGATGATCTAATCGAAATCTTACCTGGCTCAGCAGCAGTATGCTGTATCTGTGAAC 1740
Db 1681 AGATGATCTAATCGAAATCTTACCTGGCTCAGCAGCAGTATGCTGTATCTGTGAAC 1740
QY 1741 AAGTTTTCCTCTCTGAGAGCCATCCCTTGGGCTACAAACACACAGTGTGTTAGAGGA 1800
Db 1741 AAGTTTTCCTCTCTGAGAGCCATCCCTTGGGCTACAAACACACAGTGTGTTAGAGGA 1800
QY 1801 TGAATATGACGAATGCTTACACTGTATATCCAGCACTTTGGAGGCGCAAGGCGGTGG 1860
Db 1801 TGAATATGACGAATGCTTACACTGTATATCCAGCACTTTGGAGGCGCAAGGCGGTGG 1860
QY 1861 ATGGCTGAGGCTGAGAGGTGACAGCATGGCGGAGTCTTCACAGCCCTGTGTGCTTC 1920
Db 1861 ATGGCTGAGGCTGAGAGGTGACAGCATGGCGGAGTCTTCACAGCCCTGTGTGCTTC 1920
QY 1921 GGGCGCTCTCTGCTGGGCTCCACATCTGGTGGCACTTGGAGAGCCCTTACAGCCACG 1980
Db 1921 GGGCGCTCTCTGCTGGGCTCCACATCTGGTGGCACTTGGAGAGCCCTTACAGCCACG 1980
QY 1981 CTGCACGTGTGGAGCCCTTTCTGGGCTGGCCAAAGGCGGCTCCCTCAGCTTGC 2040
Db 1981 CTGCACGTGTGGAGCCCTTTCTGGGCTGGCCAAAGGCGGCTCCCTCAGCTTGC 2040
QY 2041 AGGAGGTGTGAGAGGAGGCTCAACAGCAAGAACCGGGGCTGCGCCACGGGCTTGGCGG 2100
```

|||||
Db 2041 AGGAGGCTGAGAGGAGGCTCAGACAGAACCGGGGCTGCGACGGCGCTGGGGC 2100
Qy 2101 CAGGTGAGTTCGGGGTGGGGTGGGCTTGGCGGGCCCCCGACATCGAGAGCGGGCCAG 2160
Db 2101 CAGGTGAGTTCGGGGTGGGGTGGGCTTGGCGGGCCCCCGACATCGAGAGCGGGCCAG 2160
Qy 2161 CCGTGCAGAGCCCGGGCAATGAGAGGCTTAGCACCGCGGGCCAGCGGCTGGAGAGGTGT 2220
Db 2161 CCGTGCAGAGCCCGGGCAATGAGAGGCTTAGCACCGCGGGCCAGCGGCTGGAGAGGTGT 2220
Qy 2221 ACTGGGTGCCAGCAGTGGCCCGCGCGGCTGTGCTCGATTTCTCACTGGGC 2280
Db 2221 ACTGGGTGCCAGCAGTGGCCCGCGCGGCTGTGCTCGATTTCTCACTGGGC 2280
Qy 2281 CTTAGCAGCCTTCCGGGGGAGAGGCTGGGACCTGAGCCCGCATGCTGAGCCCTCC 2340
Db 2281 CTTAGCAGCCTTCCGGGGGAGAGGCTGGGACCTGAGCCCGCATGCTGAGCCCTCC 2340
Qy 2341 CCTCATGAGGCTCCTGTGCGGGCCGAGCGCTCCCGAGAGCACACCCCTGCTCCACAG 2400
Db 2341 CCTCATGAGGCTCCTGTGCGGGCCGAGCGCTCCCGAGAGCACACCCCTGCTCCACAG 2400
Qy 2401 CGCCGAGTCCCATGACACGCAAGGGCTGAGAAATGCGGGCGCACGGGACCTGG 2460
Db 2401 CGCCGAGTCCCATGACACGCAAGGGCTGAGAAATGCGGGCGCACGGGACCTGG 2460
Qy 2461 CAGGACCTACCCCTGCGACCCCTGTGCGGAATCCTAGTGGGTGAAGCCAGTGGCTCT 2520
Db 2461 CAGGACCTACCCCTGCGACCCCTGTGCGGAATCCTAGTGGGTGAAGCCAGTGGCTCT 2520
Qy 2521 GAGCTGAGTGAAGCTTGAAGACCTTATGTCTAGCTCAGAGGATCGTAATTAACCAAT 2580
Db 2521 GAGCTGAGTGAAGCTTGAAGACCTTATGTCTAGCTCAGAGGATCGTAATTAACCAAT 2580
Qy 2581 CAGCACCCTGTGTAGCTCAGGCTGTGTGAATGCACCAATGCACACTGTATCTAGCT 2640
Db 2581 CAGCACCCTGTGTAGCTCAGGCTGTGTGAATGCACCAATGCACACTGTATCTAGCT 2640
Qy 2641 ACTGTGAGGGGGCTTGGAGAACCTTATGTCTAGCTCAGAGGATGTGTAATTAACCAATC 2700
Db 2641 ACTGTGAGGGGGCTTGGAGAACCTTATGTCTAGCTCAGAGGATGTGTAATTAACCAATC 2700
Qy 2701 GGCACCTGTATCTAGCTCAAGTTTGTAAACACCAATCAGCACCTGTGTCTAGCTC 2760
Db 2701 GGCACCTGTATCTAGCTCAAGTTTGTAAACACCAATCAGCACCTGTGTCTAGCTC 2760
Qy 2761 AGGCTATGTGAATGCACCAATGCACAGTGTGTATCTGCTACTTTCATGGGCATCCGTGT 2820
Db 2761 AGGCTATGTGAATGCACCAATGCACAGTGTGTATCTGCTACTTTCATGGGCATCCGTGT 2820
Qy 2821 GAAACAGACCAACCAAGGCTTGTGTGAGCAATTAAGCTTCTATCCTCTGGGTGACAGT 2880
Db 2821 GAAACAGACCAACCAAGGCTTGTGTGAGCAATTAAGCTTCTATCCTCTGGGTGACAGT 2880
Qy 2881 GGGGTGAGTCCGAAAGAGATGCAGCGAAGGAGATAGGGTGGGGCCGCTTTATAGAT 2940
Db 2881 GGGGTGAGTCCGAAAGAGATGCAGCGAAGGAGATAGGGTGGGGCCGCTTTATAGAT 2940
Qy 2941 TTGGGTAGTAAAGAAATTAACAGTCAAAAGGGGTTGTCTCTGGGGGCGAGAGAGG 3000
Db 2941 TTGGGTAGTAAAGAAATTAACAGTCAAAAGGGGTTGTCTCTGGGGGCGAGAGAGG 3000
Qy 3001 GGGGTGCAAGGTCTCAGTGGGGGCTTTTGTAGCCAGAGATGAGCCAGGAAAAAGACT 3060
Db 3001 GGGGTGCAAGGTCTCAGTGGGGGCTTTTGTAGCCAGAGATGAGCCAGGAAAAAGACT 3060
Qy 3061 TTTCAGAGTAAATCATCAATTAAGGCAAGGACCCGCAATTAACACTCTTTTGTGTG 3120
Db 3061 TTTCAGAGTAAATCATCAATTAAGGCAAGGACCCGCAATTAACACTCTTTTGTGTG 3120
Qy 3121 GAATGTCATCAGTTAAGTTGGGCGAGGCAATTCATCTTTTGTGTGATTTCTAGTTAC 3180
|||||

Db 3121 GAATGTCATCAGTTAAGTTGGGCGAGGCAATTCATCTTTTGTGTGATTTCTAGTTAC 3180
Qy 3181 TTACGGCCATCGGGCGATATATGTCAGTAAACAGGGGATGCGATGCTTGGCTGGGCT 3240
Db 3181 TTACGGCCATCGGGCGATATATGTCAGTAAACAGGGGATGCGATGCTTGGCTGGGCT 3240
Qy 3241 CAGAGGCTTGAACAGTACTGTGTGGGGCTTGGAGAAATGTTGTGTGACACTCTGTAT 3300
Db 3241 CAGAGGCTTGAACAGTACTGTGTGGGGCTTGGAGAAATGTTGTGTGACACTCTGTAT 3300
Qy 3301 CTAGTTAATCTAGTGGGAGCTGGAACCTTGTGTCTAGCTCAGGATGTGAACCA 3360
Db 3301 CTAGTTAATCTAGTGGGAGCTGGAACCTTGTGTCTAGCTCAGGATGTGAACCA 3360
Qy 3361 CCAATCAGCGGCTGTCAAAACAGACCACTGGGCTCTACCAATGAGAGATGTGGGTGG 3420
Db 3361 CCAATCAGCGGCTGTCAAAACAGACCACTGGGCTCTACCAATGAGAGATGTGGGTGG 3420
Qy 3421 GGCAGATTAAGATAAAGAGGCTCCGAGCCAGCAGTGGCCAGCCAGAGTCC 3480
Db 3421 GGCAGATTAAGATAAAGAGGCTCCGAGCCAGCAGTGGCCAGCCAGAGTCC 3480
Qy 3481 CTATCCAAATATGAGCAGCTTGTCTTTGTGCTGTTCCGATTAATCTTGTCTACTGTCG 3540
Db 3481 CTATCCAAATATGAGCAGCTTGTCTTTGTGCTGTTCCGATTAATCTTGTCTACTGTCG 3540
Qy 3541 CTTTGTGGTCCACACTCTTTATGACCTGTAACTACACCAAGGCTCGACGCTTC 3600
Db 3541 CTTTGTGGTCCACACTCTTTATGACCTGTAACTACACCAAGGCTCGACGCTTC 3600
Qy 3601 ACTCCTGAAGCCACTAAAGACACGAGCCCGGAGGAGTAATGAACTCCGGCCGCT 3660
Db 3601 ACTCCTGAAGCCACTAAAGACACGAGCCCGGAGGAGTAATGAACTCCGGCCGCT 3660
Qy 3661 GCTTTAAGAGCTATTAACACTACCGGAGAGTCTGACACTTCTCTAGCCAGAGA 3720
Db 3661 GCTTTAAGAGCTATTAACACTACCGGAGAGTCTGACACTTCTCTAGCCAGAGA 3720
Qy 3721 CCAGGACCCACCAAGGAAGAACTGGAACATCTGAAACATCAGAAAGAACAACT 3780
Db 3721 CCAGGACCCACCAAGGAAGAACTGGAACATCTGAAACATCAGAAAGAACAACT 3780
Qy 3781 CCAGATGACACCACTTAAAGAGCTGTAACTACCTGCGAGGGTCCGGCTCTCTTCTG 3840
Db 3781 CCAGATGACACCACTTAAAGAGCTGTAACTACCTGCGAGGGTCCGGCTCTCTTCTG 3840
Qy 3841 AAGTCAGTGAACCAAGCACTACAGTGTGGACACAAAGCCAGAGTGTGAGTCAAG 3900
Db 3841 AAGTCAGTGAACCAAGCACTACAGTGTGGACACAAAGCCAGAGTGTGAGTCAAG 3900
Qy 3901 CTGGCAACATGATTAATGCCCCTCTGTGCAAAAAAAATTAACAAAAATTTGGGG 3960
Db 3901 CTGGCAACATGATTAATGCCCCTCTGTGCAAAAAAAATTAACAAAAATTTGGGG 3960
Qy 3961 AGCATGGTGCCTGGCTGTGTGCTGCAAGCTACCGGGGAGGCTAAAGTGGAGATGCT 4020
Db 3961 AGCATGGTGCCTGGCTGTGTGCTGCAAGCTACCGGGGAGGCTAAAGTGGAGATGCT 4020
Qy 4021 TGAGCCTGGAGGTAAAGTGAAGTGAAGTGTATTAACACAGCCCTCTAGGCTGG 4080
Db 4021 TGAGCCTGGAGGTAAAGTGAAGTGAAGTGTATTAACACAGCCCTCTAGGCTGG 4080
Qy 4081 GGCAGACTGAGACCTGTTCCCTCGCAAAAAATTAACAAAAATTAAGAGAGT 4140
Db 4081 GGCAGACTGAGACCTGTTCCCTCGCAAAAAATTAACAAAAATTAAGAGAGT 4140
Qy 4141 GCTGTATATGCTAGGCGCATGCTGTATGCTGTAAATCCAGACCTTTGGGAACCCAG 4200
Db 4141 GCTGTATATGCTAGGCGCATGCTGTATGCTGTAAATCCAGACCTTTGGGAACCCAG 4200
Qy 4201 GCGGGCGGCTACCTTAAGGTGAGAGTGTGAGACAGGCTCGCCAACTGAGAAAGGCC 4260
Db 4201 GCGGGCGGCTACCTTAAGGTGAGAGTGTGAGACAGGCTCGCCAACTGAGAAAGGCC 4260

QY	4261	ATCTCTTCTAAAAATACAAAATTTAGCCGGCTGTGTGGGGGCACTGGTGGAGCATGGCTGTAA	4320
Db	4261	ATCTCTTCTAAAAATACAAAATTTAGCCGGCTGTGTGGGGGCACTGGTGGAGCATGGCTGTAA	4320
QY	4321	TCCCGCATCTCAGGAGAGGCTGAGGCGAGAGAAATCACTTGAACCCAGAGAGCGCGGCTTGC	4380
Db	4321	TCCCGCATCTCAGGAGAGGCTGAGGCGAGAGAAATCACTTGAACCCAGAGAGCGCGGCTTGC	4380
QY	4381	AGTAGGCGGAGATCTGTGCATTGTGCCTCCACCACATCCAGGCTGGGGCAACAGAGCCAAA	4440
Db	4381	AGTAGGCGGAGATCTGTGCATTGTGCCTCCACCACATCCAGGCTGGGGCAACAGAGCCAAA	4440
QY	4441	CTCTGTCTTAAAAAAGTGCCTGCATCTAAGAGGTGTGCATCTCAATAG	4500
Db	4441	CTCTGTCTTAAAAAAGTGCCTGCATCTAAGAGGTGTGCATCTCAATAG	4500
QY	4501	TTGCCAGCGAACATGTTTAAAGATGTGGAGCTCCTGCCCTTCATGTCTGTAAAAACC	4560
Db	4501	TTGCCAGCGAACATGTTTAAAGATGTGGAGCTCCTGCCCTTCATGTCTGTAAAAACC	4560
QY	4561	CACCCCTCAAGGCGAGGTGAGTGGCTCATGTGCTTAAATCCAGACATTTGGGAGCCGAG	4620
Db	4561	CACCCCTCAAGGCGAGGTGAGTGGCTCATGTGCTTAAATCCAGACATTTGGGAGCCGAG	4620
QY	4621	GCGGGTGGATCACCTGAGGTGAGAGTTCGAGACAGGCTGACCAACAACTGGTGAAT	4680
Db	4621	GCGGGTGGATCACCTGAGGTGAGAGTTCGAGACAGGCTGACCAACAACTGGTGAAT	4680
QY	4681	CCGACCTTACTAAAAATACAAATTTAGATGACATGGTGTGCATGCTGTAAATCCAC	4740
Db	4681	CCGACCTTACTAAAAATACAAATTTAGATGACATGGTGTGCATGCTGTAAATCCAC	4740
QY	4741	CTACTTGGGAGGTGAGGCGAGGAAAATCACTAGAACCAAGGGAGCGGAGTGTAGTGAAG	4800
Db	4741	CTACTTGGGAGGTGAGGCGAGGAAAATCACTAGAACCAAGGGAGCGGAGTGTAGTGAAG	4800
QY	4801	CCGAGATGTGCATTCGACTTCACGCTGAGACCAATGAGCGAAACTCCATCTCAAAAAAC	4860
Db	4801	CCGAGATGTGCATTCGACTTCACGCTGAGACCAATGAGCGAAACTCCATCTCAAAAAAC	4860
QY	4861	AACAACAACAAACCACTCTCTACTCCAGGAGGCTGGGTACAGAGCTGGGCGACATCAGT	4920
Db	4861	AACAACAACAAACCACTCTCTACTCCAGGAGGCTGGGTACAGAGCTGGGCGACATCAGT	4920
QY	4921	GCAAGTGTCTAGCCACAGACACTTAAGCGGGAGCTGCGAGAGCCGGGACAGATTAACGTG	4980
Db	4921	GCAAGTGTCTAGCCACAGACACTTAAGCGGGAGCTGCGAGAGCCGGGACAGATTAACGTG	4980
QY	4981	TGTGAGATCACTGTGTGTGAGATCAGACGCTCCCTGCCATTGGTGACACAGGGGGCCCCA	5040
Db	4981	TGTGAGATCACTGTGTGTGAGATCAGACGCTCCCTGCCATTGGTGACACAGGGGGCCCCA	5040
QY	5041	AGCACAGAGATGGCCCCCATCCAGTCAACACATCCACTTCATCCAGAGATGTCTGTTT	5100
Db	5041	AGCACAGAGATGGCCCCCATCCAGTCAACACATCCACTTCATCCAGAGATGTCTGTTT	5100
QY	5101	CTTGGCAGCGTGGGGTAAATTAGACAGAGAGTGAACAGTCTTGGGTGTGCTCACTCAAC	5160
Db	5101	CTTGGCAGCGTGGGGTAAATTAGACAGAGAGTGAACAGTCTTGGGTGTGCTCACTCAAC	5160
QY	5161	TGCCCGAGGCAAGGCTTGTGCTCTGTAGAAAACCTCAAGGCTCTAGGCGGGGACAGGAGG	5220
Db	5161	TGCCCGAGGCAAGGCTTGTGCTCTGTAGAAAACCTCAAGGCTCTAGGCGGGGACAGGAGG	5220
QY	5221	TCACGCGCTGTATCCACAGACTTTGGGAGGCGGAGGCGGAGTGAATCAAGAGTCAAGAGA	5280
Db	5221	TCACGCGCTGTATCCACAGACTTTGGGAGGCGGAGGCGGAGTGAATCAAGAGTCAAGAGA	5280
QY	5281	TCGTGACATCTCTGGCTTAACAGCGGTGAACCCCTCTCTACTAAAAATTAACAAAAATTGG	5340
Db	5281	TCGTGACATCTCTGGCTTAACAGCGGTGAACCCCTCTCTACTAAAAATTAACAAAAATTGG	5340

QY	5341	CCGGGCAATGTCGCGGGCACTGTATGTTCCAGCTACTCGGGAGGCTGAGCGAGAAATG	5400
Db	5341	CCGGGCAATGTCGCGGGCACTGTATGTTCCAGCTACTCGGGAGGCTGAGCGAGAAATG	5400
QY	5401	GGGTAAACCCGAGGAGGAGAGTTGGTGCATGTAGCCGAGATGCGCGCACTGCATCCACGCT	5460
Db	5401	GGGTAAACCCGAGGAGGAGAGTTGGTGCATGTAGCCGAGATGCGCGCACTGCATCCACGCT	5460
QY	5461	GGGCGACAGACAGACACTCCATCTGTGAAAAAAGAAAAAGAAAGCTTCAGGTGTGAGCCAGA	5520
Db	5461	GGGCGACAGACAGACACTCCATCTGTGAAAAAAGAAAAAGAAAGCTTCAGGTGTGAGCCAGA	5520
QY	5521	GGCCCAAGGCTGTATTTCTGTCACTTACCATGACCTTGGGCAAGGCACTTCCCTCCCTGGC	5580
Db	5521	GGCCCAAGGCTGTATTTCTGTCACTTACCATGACCTTGGGCAAGGCACTTCCCTCCCTGGC	5580
QY	5581	CCAGTTCAACGGGGTTGGAAATGACTCCAAAGTCCCTTCACAGATTAAAGCTGCATGGTTG	5640
Db	5581	CCAGTTCAACGGGGTTGGAAATGACTCCAAAGTCCCTTCACAGATTAAAGCTGCATGGTTG	5640
QY	5641	TAAATGTAGAAAGATGAGGAGGAGTTTCCCTCTCTCAACCCAGCCGCTGACCTCAAGGT	5700
Db	5641	TAAATGTAGAAAGATGAGGAGGAGTTTCCCTCTCTCAACCCAGCCGCTGACCTCAAGGT	5700
QY	5701	GAATGACACAGGGAAGTCACTGTCGCCAATCCCGAGTTCCAAAGCCCTTGGGAGCCCTAC	5760
Db	5701	GAATGACACAGGGAAGTCACTGTCGCCAATCCCGAGTTCCAAAGCCCTTGGGAGCCCTAC	5760
QY	5761	TGTCAAGGTCCTGCACAGAGAGGTGAAAGTCAAGTGAACCAATGGCTCCGAAGGCTTTG	5820
Db	5761	TGTCAAGGTCCTGCACAGAGAGGTGAAAGTCAAGTGAACCAATGGCTCCGAAGGCTTTG	5820
QY	5821	CCCTATTTGGGGACAGACATCCGGTTCCTCGGGCTCAACGGGAAATTCAGGGGCTTTAGC	5880
Db	5821	CCCTATTTGGGGACAGACATCCGGTTCCTCGGGCTCAACGGGAAATTCAGGGGCTTTAGC	5880
QY	5881	CGAATGAGTCAATGGGGGGCGGGGGGTTCTTGGGGGAGTTCCAGCTAATCAATTTGGGA	5940
Db	5881	CGAATGAGTCAATGGGGGGCGGGGGGTTCTTGGGGGAGTTCCAGCTAATCAATTTGGGA	5940
QY	5941	CAGGACACCTCGGAACCTTCATGGTGCCTATCCAAAGTGTGGGGTGAGCAGACAGCCAA	6000
Db	5941	CAGGACACCTCGGAACCTTCATGGTGCCTATCCAAAGTGTGGGGTGAGCAGACAGCCAA	6000
QY	6001	GACCCAAATGTCCTTATATCAGATGAGGGGCTCAGAGGTCGCCAGACAGCAGCCTCCGG	6060
Db	6001	GACCCAAATGTCCTTATATCAGATGAGGGGCTCAGAGGTCGCCAGACAGCAGCCTCCGG	6060
QY	6061	AGAGTTTGGGGGTAGAAATGGAGCAACACAGAGCTTCTTTTCTCTTAGAATTTGGG	6120
Db	6061	AGAGTTTGGGGGTAGAAATGGAGCAACACAGAGCTTCTTTTCTCTTAGAATTTGGG	6120
QY	6121	GGCTTTGGGGGACAGGCTTGAGATATCCAAAGAGAGGGGCAAGAGACATCCCCACAG	6180
Db	6121	GGCTTTGGGGGACAGGCTTGAGATATCCAAAGAGAGGGGCAAGAGACATCCCCACAG	6180
QY	6181	TCTGCGAAGAGGAGAGAGGGAGACCCCGAGCTCACTGCGCACTTCCCAACAGGCT	6235
Db	6181	TCTGCGAAGAGGAGAGAGGGAGACCCCGAGCTCACTGCGCACTTCCCAACAGGCT	6235
RESULT 2			
LOCUS	AX250679	6235 bp	DNA
DEFINITION	Sequence 6 from Patent WO0168882.	linear	PAT 05-OCT-2001
ACCESSION	AX250679		
VERSION	AX250679.1	GI:15984423	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		
REFERENCE	1		

AUTHORS Ivanov, E.
TITLE Methods for homologous recombination
JOURNAL Patent: WO 0168882-A 6 20-SEP-2001;
TRANSMARKOTIC THERAPIES, INC. (US)
FEATURES Location/Qualifiers
source 1. 6235
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1586 a 1610 c 1708 g 1331 t
ORIGIN
Query Match 100.0%; Score 6235; DB 6; Length 6235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATCACTTGAGACAGTATGTTCAAGACCAAGCTGGGAGCATAGGAGACTGTCTCTACG 60
DB 1 GATCACTTGAGACAGTATGTTCAAGACCAAGCTGGGAGCATAGGAGACTGTCTCTACG 60
QY 61 AAAAATCAAAAAATTTATGGCCGGCATGTGGCTGCTGATTCCTGAACTTTGGG 120
DB 61 AAAAATCAAAAAATTTATGGCCGGCATGTGGCTGCTGATTCCTGAACTTTGGG 120
QY 121 ACATCAAGGCAAGTGATGATCTGAGAGTTCAGAGTACCTGCTGGCCAACTATGT 180
DB 121 ACATCAAGGCAAGTGATGATCTGAGAGTTCAGAGTACCTGCTGGCCAACTATGT 180
QY 181 GAAACCCCTATCTCCACTTAAAAATTTACCAAAATTTACCCAGGCAATGGTGGCAGCCACTGTA 240
DB 181 GAAACCCCTATCTCCACTTAAAAATTTACCAAAATTTACCCAGGCAATGGTGGCAGCCACTGTA 240
QY 241 ATCCGGCTACTCAGAGGAGCTGAGGAGAGAGATGATGAAACCCAGGAGGGAGGTTG 300
DB 241 ATCCGGCTACTCAGAGGAGCTGAGGAGAGAGATGATGAAACCCAGGAGGGAGGTTG 300
QY 301 CAGTGAGCTGAGATCACACCACTGCACCTCAGCCCTGGGTGACAGAGCAAGACTTATCTC 360
DB 301 CAGTGAGCTGAGATCACACCACTGCACCTCAGCCCTGGGTGACAGAGCAAGACTTATCTC 360
QY 361 AAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420
DB 361 AAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420
QY 421 CTACTCAGAGGAGCTGAGGAGAGATGATGAACTGGGGAGTCAAGGCTATAGTGA 480
DB 421 CTACTCAGAGGAGCTGAGGAGAGATGATGAACTGGGGAGTCAAGGCTATAGTGA 480
QY 481 GCCAAGATCATGCCACTACCTCCAGCTGGGCAACAGAGAGAGACCCCTGTCTTAAAA 540
DB 481 GCCAAGATCATGCCACTACCTCCAGCTGGGCAACAGAGAGAGACCCCTGTCTTAAAA 540
QY 541 AATAATATATATAAAGAAAAAAGAGCTGTATTATGCTCTGGTCCATATATATCT 600
DB 541 AATAATATATATAAAGAAAAAAGAGCTGTATTATGCTCTGGTCCATATATATCT 600
QY 601 ATGTATATAGTTTGAACCTCAAGAGATCAGATAGTCAATTTTAAAGCTGTGGCCGT 660
DB 601 ATGTATATAGTTTGAACCTCAAGAGATCAGATAGTCAATTTTAAAGCTGTGGCCGT 660
QY 661 ATGGCTCTGTGCACATCTCTGCCCTGTCTTCTACACAAAAAGCAGCTATAAACAT 720
DB 661 ATGGCTCTGTGCACATCTCTGCCCTGTCTTCTACACAAAAAGCAGCTATAAACAT 720
QY 721 ACATATCATGAATTTTATAGACATCGAGATTGAAATTCATATGATTTTACATTTAT 780
DB 721 ACATATCATGAATTTTATAGACATCGAGATTGAAATTCATATGATTTTACATTTAT 780
QY 781 AAAATTAATCTTTAAAAATTTCCCTTAACCATTTAAAGTGTAAGGCGGCGAGGC 840
DB 781 AAAATTAATCTTTAAAAATTTCCCTTAACCATTTAAAGTGTAAGGCGGCGAGGC 840
QY 841 GCCATGTCACGCCCTGTAAATTCACAGACTTGGAGGCTGAGTGGGAGATCACTTGA 900

DB 841 GCCATGTCACGCCCTGTAAATTCACAGACTTGGAGGCTGAGTGGGAGATCACTTGA 900
QY 901 ATCAACAGTTGAGACACCAAGCTGGCCAACTATGCAAAACCCATTTCTACTAAAAATAAA 960
DB 901 ATCAACAGTTGAGACACCAAGCTGGCCAACTATGCAAAACCCATTTCTACTAAAAATAAA 960
QY 961 AAAATTAAGTGGGCTAGAGTGGTGCACACCTGTGATCCAGACTTTGGAGGCTAGGCA 1020
DB 961 AAAATTAAGTGGGCTAGAGTGGTGCACACCTGTGATCCAGACTTTGGAGGCTAGGCA 1020
QY 1021 GGAGATGCTTGAACCTTGGAGGAGGAGTTCAGTGGAGCCAACTATGCTGAC 1080
DB 1021 GGAGATGCTTGAACCTTGGAGGAGGAGTTCAGTGGAGCCAACTATGCTGAC 1080
QY 1081 TCCAGCTGGGTGACAGAGTGAAGTCTCTCAACGAAAAAAGTGTAAAGCCAT 1140
DB 1081 TCCAGCTGGGTGACAGAGTGAAGTCTCTCTCAACGAAAAAAGTGTAAAGCCAT 1140
QY 1141 TCCTAATTCAGTATCATGATGATCATCTCAGGCTGCTGCTGAGGCA 1200
DB 1141 TCCTAATTCAGTATCATGATGATCATCTCAGGCTGCTGCTGAGGCA 1200
QY 1201 ACCTGAGAGTGAAGTGGTGGTACAGAGATACATACATTTCCATTTACTAGACT 1260
DB 1201 ACCTGAGAGTGAAGTGGTGGTGGTACAGAGATACATACATTTCCATTTACTAGACT 1260
QY 1261 ACCAAGTGGCCATCCAAAGAGTGTGTTTATTAATCTACACTCCCCACCAACAAAT 1320
DB 1261 ACCAAGTGGCCATCCAAAGAGTGTGTTTATTAATCTACACTCCCCACCAACAAAT 1320
QY 1321 GAGAGTACTCCAGATCTTTCAAAAGATGCTTAAGCCAGTACAGTAAACAGGA 1380
DB 1321 GAGAGTACTCCAGATCTTTCAAAAGATGCTTAAGCCAGTACAGTAAACAGGA 1380
QY 1381 AGTGGAGGAGGAGTGGCAGGCCCTTCAACCATGAAGAAATACCTGTTAGGCTTCT 1440
DB 1381 AGTGGAGGAGGAGTGGCAGGCCCTTCAACCATGAAGAAATACCTGTTAGGCTTCT 1440
QY 1441 GGATGCTGAGAGGATGAATACGGGGGTCTGAGAGCTGCCCCCTGTAGATCACTGTG 1500
DB 1441 GGATGCTGAGAGGATGAATACGGGGGTCTGAGAGCTGCCCCCTGTAGATCACTGTG 1500
QY 1501 ACTTGCAGCCCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 1560
DB 1501 ACTTGCAGCCCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 1560
QY 1561 CACTCTGTGTTGATCTTATTTCTCCCATGAGGAGCTGAAGTCTGATTTGAGCCGTTAT 1620
DB 1561 CACTCTGTGTTGATCTTATTTCTCCCATGAGGAGCTGAAGTCTGATTTGAGCCGTTAT 1620
QY 1621 TCAAGATGACAGCTTTCTTGACAGAGAAATGATGTACAGAAACAGCAGGGGCTTGGCA 1680
DB 1621 TCAAGATGACAGCTTTCTTGACAGAGAAATGATGTACAGAAACAGCAGGGGCTTGGCA 1680
QY 1681 AGATGATGATCACTGCAAAATCCATACCTGGCTGACCAAGCTAGTTCTGTATGTAAC 1740
DB 1681 AGATGATGATCACTGCAAAATCCATACCTGGCTGACCAAGCTAGTTCTGTATGTAAC 1740
QY 1741 AAGTTTTCACCTTCTGAGAGCCATCCCTTGGTACAAACACAGGTTGGTGAAGGA 1800
DB 1741 AAGTTTTCACCTTCTGAGAGCCATCCCTTGGTGGTACAAACACAGGTTGGTGAAGGA 1800
QY 1801 TGAATATGAGAGTCCCTTACACCTGTATATCCACACACTTTGGAGGCGCAAGCGGGTGG 1860
DB 1801 TGAATATGAGAGTCCCTTACACCTGTATATCCACACACTTTGGAGGCGCAAGCGGGTGG 1860
QY 1861 ATGGCTTGAAGCTGAGAGTGAACAGATGCGGAGTCTCTCAACAGCCCTGCTTCTCTC 1920
DB 1861 ATGGCTTGAAGCTGAGAGTGAACAGATGCGGAGTCTCTCAACAGCCCTGCTTCTCTC 1920
QY 1921 GCGGCTCTCTGCTGAGGCTCCCACTTCTGAGGAGTGAAGAGCCCTTCAAGCCACCG 1980

Db 1921 GGGGCTCTCTGCTGGGCTCCCACTTCGGGTGGCACTGAGGAGCCCTTCAGCCACCG 1980
QY 1981 CTGACACTGTGGAGACCCCTTTCTGGGCTGGCCAAAGCCAGACCGCGCTCCCTCAAGCTTGC 2040
Db 1981 CTGACACTGTGGAGACCCCTTTCTGGGCTGGCCAAAGCCAGACCGCGCTCCCTCAAGCTTGC 2040
QY 2041 AGGAGAGTGTGGAGGAGAGAGCTCAAGCAGGAGACCGGGGCTGGCAGCGGGCTTGGCGGGC 2100
Db 2041 AGGAGAGTGTGGAGGAGAGAGCTCAAGCAGGAGACCGGGGCTGGCAGCGGGCTTGGCGGGC 2100
QY 2101 CAGCTGAGATTCCGGGTGGGCGGTGGGCTTGGCGGGGCCCGCACTCGAGACGCGGCGAG 2160
Db 2101 CAGCTGAGATTCCGGGTGGGCGGTGGGCTTGGCGGGGCCCGCACTCGAGACGCGGCGAG 2160
QY 2161 CCCCTGGCAGGCCCCGGGCAATGAGAGGCTTAGCACCCGGGCGACCGGCTGGGAGGGGTGT 2220
Db 2161 CCCCTGGCAGGCCCCGGGCAATGAGAGGCTTAGCACCCGGGCGACCGGCTGGGAGGGGTGT 2220
QY 2221 ACTGGGTGCCCAACAGTGGCCAGCGCCGGCGGCTGTGTGCTGCGATTTCTCACTGGGC 2280
Db 2221 ACTGGGTGCCCAACAGTGGCCAGCGCCGGCGGCTGTGTGCTGCGATTTCTCACTGGGC 2280
QY 2281 CTTAGCAGCCTTCCCGGGGAGAGGCTCGGGACCTGGAGCCGCGCATGGCTGAGCCTCC 2340
Db 2281 CTTAGCAGCCTTCCCGGGGAGAGGCTCGGGACCTGGAGCCGCGCATGGCTGAGCCTCC 2340
QY 2341 CCTTCATAGGGGCTCCTGTGCGGCCCCGAGACCTCCCGCAGAGCAGCACCCCTGCTCCAG 2400
Db 2341 CCTTCATAGGGGCTCCTGTGCGGCCCCGAGACCTCCCGCAGAGCAGCACCCCTGCTCCAG 2400
QY 2401 CGCCCACTGCCATGAGCAGCAGAGGGGCTGAGAGTGGGGCGAGCGGACCGGGGACTGG 2460
Db 2401 CGCCCACTGCCATGAGCAGCAGAGGGGCTGAGAGTGGGGCGAGCGGACCGGGGACTGG 2460
QY 2461 CAGGACAGTACCCCTGCGAGCCCTGTGTGCGGATCCACTGGGTGAAGCAGTGGGCTCCT 2520
Db 2461 CAGGACAGTACCCCTGCGAGCCCTGTGTGCGGATCCACTGGGTGAAGCAGTGGGCTCCT 2520
QY 2521 GAGTGTGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAAT 2580
Db 2521 GAGTGTGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAAT 2580
QY 2581 CAGCACCCTGTGCTAGCTCAGGGGTGTGTAATGCACCAATCCACACTGCTATCTAGCT 2640
Db 2581 CAGCACCCTGTGCTAGCTCAGGGGTGTGTAATGCACCAATCCACACTGCTATCTAGCT 2640
QY 2641 ACTCTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAATC 2700
Db 2641 ACTCTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAATC 2700
QY 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGCACCCTGTCTAGCTC 2760
Db 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGCACCCTGTCTAGCTC 2760
QY 2761 AGGATATGTATGACCAATCGACAGTCTGTATCTGCTACTTCAATGGGCAATCCGT 2820
Db 2761 AGGATATGTATGACCAATCGACAGTCTGTATCTGCTACTTCAATGGGCAATCCGT 2820
QY 2821 GAAAGAGCACAACAAGGCTTTGTGTGACCAATTAAGCTTCTATCACTGCGGTGAGGT 2880
Db 2821 GAAAGAGCACAACAAGGCTTTGTGTGACCAATTAAGCTTCTATCACTGCGGTGAGGT 2880
QY 2881 GGGCTGAGTCCGAAAAAGAGTCAAGGAGATTAAGGTGGGCGCTTTTATAGAT 2940
Db 2881 GGGCTGAGTCCGAAAAAGAGTCAAGGAGATTAAGGTGGGCGCTTTTATAGAT 2940
QY 2941 TTGGGTAGGTAAAGAAAATTACAGTCAAGAGGGGTTTGTCTGCGGGGCGAGAGTGG 3000
Db 2941 TTGGGTAGGTAAAGAAAATTACAGTCAAGAGGGGTTTGTCTGCGGGGCGAGAGTGG 3000
QY 3001 GGGGTGCAAGGTGCTCAGTGGGGTGCTTTTGAAGCAGATGAGCAGAAAGAGACT 3060
Db 3001 GGGGTGCAAGGTGCTCAGTGGGGTGCTTTTGAAGCAGATGAGCAGAAAGAGACT 3060

QY 3061 TTCAAGGTAATGTCAATTAAGGCAAGACCCGCAATTACACCTCTTTGTGGTG 3120
Db 3061 TTCAAGGTAATGTCAATTAAGGCAAGACCCGCAATTACACCTCTTTGTGGTG 3120
QY 3121 GAAATGTCAAGTAAAGTGGGCGAGGGCAATTCACCTCTTTGTGTGATCTCTAGTAC 3180
Db 3121 GAAATGTCAAGTAAAGTGGGCGAGGGCAATTCACCTCTTTGTGTGATCTCTAGTAC 3180
QY 3181 TTCAAGGCAATCTGGGCGTATATGTGCAAGTTACAGGGGATCGATGGCTTGGGCT 3240
Db 3181 TTCAAGGCAATCTGGGCGTATATGTGCAAGTTACAGGGGATCGATGGCTTGGGCT 3240
QY 3241 CAGAGCTTGAACAGTACTGTGTGGGCGCTTGGAGAAATGTTGTGTGACACTGTAT 3300
Db 3241 CAGAGCTTGAACAGTACTGTGTGGGCGCTTGGAGAAATGTTGTGTGACACTGTAT 3300
QY 3301 CTAGTTAATCTAAGGGGAGGTGGAGAACCTTTGTGTGCTAGGATTTGAACCA 3360
Db 3301 CTAGTTAATCTAAGGGGAGGTGGAGAACCTTTGTGTGCTAGGATTTGAACCA 3360
QY 3361 CCAATCAGCGCCCTGTCAAAACAGACCACTGCGCTACCAATCAGCAGATGTGGTGG 3420
Db 3361 CCAATCAGCGCCCTGTCAAAACAGACCACTGCGCTACCAATCAGCAGATGTGGTGG 3420
QY 3421 GGCAGATTAAGATAAAGAGAGGCTGCCGAGCCAGCAGTGGCAACGCGCAGAGTCC 3480
Db 3421 GGCAGATTAAGATAAAGAGAGGCTGCCGAGCCAGCAGTGGCAACGCGCAGAGTCC 3480
QY 3481 CTATCCAAATATAGGCGCTTGTCTTTCTGTTCCTTTGCCATTAATCTGTCTACTGCTG 3540
Db 3481 CTATCCAAATATAGGCGCTTGTCTTTCTGTTCCTTTGCCATTAATCTGTCTACTGCTG 3540
QY 3541 CTTTGTGGGTCCACACTGCTTTTATGAGCTGTAACTACACAGCAAGGTTGAGCTTC 3600
Db 3541 CTTTGTGGGTCCACACTGCTTTTATGAGCTGTAACTACACAGCAAGGTTGAGCTTC 3600
QY 3601 ACTCTGAGGCACTTAAGACAGCAGACCCACCGGAGAGATGAACAACCTCCGGCGGCT 3660
Db 3601 ACTCTGAGGCACTTAAGACAGCAGACCCACCGGAGAGATGAACAACCTCCGGCGGCT 3660
QY 3661 GCCTTAAGAGCTATTAACACTACGGGAGGTCGAGGCTTCACTCCAGCCAGCGAGA 3720
Db 3661 GCCTTAAGAGCTATTAACACTACGGGAGGTCGAGGCTTCACTCCAGCCAGCGAGA 3720
QY 3721 CCACGAACCCACAGAGGAAGAACTGCGAACCATCTGTAACATCAGAAAGAAACAACT 3780
Db 3721 CCACGAACCCACAGAGGAAGAACTGCGAACCATCTGTAACATCAGAAAGAAACAACT 3780
QY 3781 CCAGATGCAACCTTAAGAGCTGTAAACACTCACTCGAGGGGTCCGCGCTCTCTTGG 3840
Db 3781 CCAGATGCAACCTTAAGAGCTGTAAACACTCACTCGAGGGGTCCGCGCTCTCTTGG 3840
QY 3841 AAGTCAGTGAAGCAACACATCCAGTTCGAGCACAAGCCCGAGGTTTGAATACG 3900
Db 3841 AAGTCAGTGAAGCAACACATCCAGTTCGAGCACAAGCCCGAGGTTTGAATACG 3900
QY 3901 CTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAAAATTTCAAAAAATTTGGCGG 3960
Db 3901 CTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAAAATTTCAAAAAATTTGGCGG 3960
QY 3961 AGCATGTGTGCTCGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4020
Db 3961 AGCATGTGTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4020
QY 4021 TGAAGCTGGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 4080
Db 4021 TGAAGCTGGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 4080
QY 4081 GGAAGACTGAGACCTGTTTCCCTCCGAAAAAAATTTGAACAAAGTGAATTAAGAGT 4140
Db 4081 GGAAGACTGAGACCTGTTTCCCTCCGAAAAAAATTTGAACAAAGTGAATTAAGAGT 4140

4141 GCCTGATATGCGTAGCGCAGTGGCTCATGCTGTAAATCCAGCACTTTGGGAACCGAG 4200
4141 GCCTGATATGCGTAGCGCAGTGGCTCATGCTGTAAATCCAGCACTTTGGGAACCGAG 4200
4201 GCGGGCGGGTCACTAAGGTCAGAGTGTGAGACCAAGCTGGCCAAACATGAGAAAGCC 4260
4201 GCGGGCGGGTCACTAAGGTCAGAGTGTGAGACCAAGCTGGCCAAACATGAGAAAGCC 4260
4261 ATCTCTCTTAAAAAATACAAAATTAACCGCTGTGGGGCAGAGTGGGAGCAGTGGCTTAA 4320
4261 ATCTCTCTTAAAAAATACAAAATTAACCGCTGTGGGGCAGAGTGGGAGCAGTGGCTTAA 4320
4321 TCCAGCTACTCAGAGGCTGAGGAGAGATCACTTGAACCCAGAGGCGCGGTTGC 4380
4321 TCCAGCTACTCAGAGGCTGAGGAGAGATCACTTGAACCCAGAGGCGCGGTTGC 4380
4381 AGTGAGCCGAGATCGTCCATTGCACTCCACCCTCCAGCTGGGCAACAGAGCCAAA 4440
4441 CTCTGCTTAAAAAATACAAAATTAACCGCTGTGGGGCAGAGTGGGAGCAGTGGCTTAA 4500
4441 CTCTGCTTAAAAAATACAAAATTAACCGCTGTGGGGCAGAGTGGGAGCAGTGGCTTAA 4500
4501 TTGCGAGCAACATGTTTAAAGATGTGAGAGCTCTGCTTCCATGGCTCTTAAAAAC 4560
4501 TTGCGAGCAACATGTTTAAAGATGTGAGAGCTCTGCTTCCATGGCTCTTAAAAAC 4560
4551 CACCTCAAGGCGAGGTCAGTGGCTCATGCTTAAATCCAGCACTTTGGAGGCGGAG 4620
4551 CACCTCAAGGCGAGGTCAGTGGCTCATGCTTAAATCCAGCACTTTGGAGGCGGAG 4620
4621 GCGGGTGTATCACTGAGGTCAGAGTGTGAGAGCAGGCTGAGCAACCAATGGTGAAT 4680
4621 GCGGGTGTATCACTGAGGTCAGAGTGTGAGAGCAGGCTGAGCAACCAATGGTGAAT 4680
4681 CCCACCTCTACTAAAAATACAAAATTAAGTAGAGTGTGAGTGTGCTGTAAATCCAC 4740
4681 CCCACCTCTACTAAAAATACAAAATTAAGTAGAGTGTGAGTGTGCTGTAAATCCAC 4740
4741 CTACTTGGGAGGCTGAGGAGGAAATCACTAAGAACAGGAGGCGGAGTGTGTAGTAG 4800
4741 CTACTTGGGAGGCTGAGGAGGAAATCACTAAGAACAGGAGGCGGAGTGTGTAGTAG 4800
4801 CCGAGATCGTGCATTTGACCTCCAGCTGAGCAATGAGGAGAACTCCATCTAAAAAAC 4860
4801 CCGAGATCGTGCATTTGACCTCCAGCTGAGCAATGAGGAGAACTCCATCTAAAAAAC 4860
4861 AACAAACAAAACCCACTCTTACTTCCAGGAGTGTGGTACAGAGCTGGGCCACATCACT 4920
4861 AACAAACAAAACCCACTCTTACTTCCAGGAGTGTGGTACAGAGCTGGGCCACATCACT 4920
4921 GCAGGTCCTGAGCCACAGAGCTAAAGCGGAGCTCAGAGACCGCGGACAGATTAACAGTG 4980
4921 GCAGGTCCTGAGCCACAGAGCTAAAGCGGAGCTCAGAGACCGCGGACAGATTAACAGTG 4980
4981 TGTGATCAGTGTGATGATCAGAGCTCCCTGCAATGTGTGTACCAACAGAGGCGGCCCA 5040
4981 TGTGATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040
5041 AGCAGCAGAGATGAGCCCATCCAGTCCACATCCACTTCTCATCCAGAGATGTGTTT 5100
5041 AGCAGCAGAGATGAGCCCATCCAGTCCACATCCACTTCTCATCCAGAGATGTGTTT 5100
5101 CTGGCAGGCTGGGGTAAATTAAGAGAGAGTGAAGTCTTGGTGTGTGATGATGATGATG 5160
5101 CTGGCAGGCTGGGGTAAATTAAGAGAGAGTGAAGTCTTGGTGTGTGATGATGATGATG 5160
5161 TGCCCGAGGAGGCTGGGGCTGTAGAAAACGTTACAGGCTTACAGGCGGAGCGTGC 5220
5161 TGCCCGAGGAGGCTGGGGCTGTAGAAAACGTTACAGGCTTACAGGCGGAGCGTGC 5220
5221 TCACGCTGTAAATCCAGCACTTTGGAGGCGGAGGCGGAGTGTGATCAGAGTCAAGAGA 5280

5221 TCACGCTGTAAATCCAGCACTTTGGAGGCGGAGGCGGAGTGTGATCAGAGTCAAGAGA 5280
5281 TGTGACCATCTCTGCTTAACACGTTGAACCCCGTCTCTACTTAAAAATTAACAAAATTTGG 5340
5281 TGTGACCATCTCTGCTTAACACGTTGAACCCCGTCTCTACTTAAAAATTAACAAAATTTGG 5340
5341 CGGGCAGATGAGTGGGGGACCTGTAGTTCACCTACTGAGGAGGCTGAGGAGGAGTATG 5400
5341 CGGGCAGATGAGTGGGGGACCTGTAGTTCACCTACTGAGGAGGCTGAGGAGGAGTATG 5400
5401 GCGTGAACCCGAGAGGAGAGTGTGAGTGAACCCAGATTCGCGCCACTGACATCCAGCT 5460
5401 GCGTGAACCCGAGAGGAGAGTGTGAGTGAACCCAGATTCGCGCCACTGACATCCAGCT 5460
5461 GGGCGACAGACGACATCTCATCTGAGAAAAAAGAAAAACCTTCAGTCTGAGCCAGA 5520
5461 GGGCGACAGACGACATCTCATCTGAGAAAAAAGAAAAACCTTCAGTCTGAGCCAGA 5520
5521 GGGCGAGGCTGTAAATCTGTCACTTACATGACCTTGGGCAAGGCACTTCCTCCCTGGC 5580
5521 GGGCGAGGCTGTAAATCTGTCACTTACATGACCTTGGGCAAGGCACTTCCTCCCTGGC 5580
5581 CCAGTTCACGAGGCTGTGAATTCGACCTCAAGGTCCTTCCAGCATTAACGCTCATGTTC 5640
5581 CCAGTTCACGAGGCTGTGAATTCGACCTCAAGGTCCTTCCAGCATTAACGCTCATGTTC 5640
5641 TAAGATGAGACATGGGCGCATTTCCCTCTCTCACCCAGCCGCTGTCACTCAAGT 5700
5641 TAAGATGAGACATGGGCGCATTTCCCTCTCTCACCCAGCCGCTGTCACTCAAGT 5700
5701 GAATGACGAGGAGAGTCACTGTGCCAATCCCGAGTTCCAAAGCCCTTGGGAGCCCTAC 5760
5701 GAATGACGAGGAGAGTCACTGTGCCAATCCCGAGTTCCAAAGCCCTTGGGAGCCCTAC 5760
5761 TGTCAAGGCTCTGACAGAGAGTGAAGTCAAGTGTGAGGCAATTCGCTTGAAGGCTTTC 5820
5761 TGTCAAGGCTCTGACAGAGAGTGAAGTCAAGTGTGAGGCAATTCGCTTGAAGGCTTTC 5820
5821 CCTCATTCGGGACAGACATCCGCTTCTCTGTGCTTACCGGAGTCTTGAAGGCTTTC 5880
5821 CCTCATTCGGGACAGACATCCGCTTCTCTGTGCTTACCGGAGTCTTGAAGGCTTTC 5880
5881 CGAATGAGTCAATGGGAGGCGGAGGCTTCTGAGGAGTTCAGTCAATCACTTGGGA 5940
5881 CGAATGAGTCAATGGGAGGCGGAGGCTTCTGAGGAGTTCAGTCAATCACTTGGGA 5940
5941 CAGGACAGCCTGGAACCTTTCGATGTGCTTATCCAAAGTGTGGGAGTGGGACAGACCAA 6000
5941 CAGGACAGCCTGGAACCTTTCGATGTGCTTATCCAAAGTGTGGGAGTGGGACAGACCAA 6000
6001 GACCCATGCTCTTATCTCAGTGAAGGCTCAGAGGCTCCAGACAGGAGCTCCCG 6060
6001 GACCCATGCTCTTATCTCAGTGAAGGCTCAGAGGCTCCAGACAGGAGCTCCCG 6060
6061 AGAGTTGGGGGTAGGAATGGAGAACAGGCTCTTTTCTCTCTTAAATTTGGG 6120
6061 AGAGTTGGGGGTAGGAATGGAGAACAGGCTCTTTTCTCTCTTAAATTTGGG 6120
6121 GCGTTGGGAGAGGCTTGAATCCAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6180
6121 GCGTTGGGAGAGGCTTGAATCCAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6180
6181 TCTGCCAGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6235
6181 TCTGCCAGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6235

RESULT 3
ARI56461 6679 bp DNA linear PAT 08-AUG-2001
LOCUS ARI56461
DEFINITION Sequence 1 from patent US 6242218.
ACCESSION ARI56461

VERSION AR156461.1 GI:15125165
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6679)
Trecu,D.A., Heartlein,M.W. and Selden,R.F.
TITLE Genomic sequences for protein production and delivery
JOURNAL Patent: US 6242218-A 1 05-JUN-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 1684 a 1739 c 1830 g 1426 t
ORIGIN
Query Match 100.0%; Score 6235; DB 6; Length 6679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATCACTGAGGACAGTATTCMAAGACACGCTGGGAGCATAGGGAGACTGTCTACG 60
Db |
QY 20 GATCACTGAGGACAGTATTCMAAGACACGCTGGGAGCATAGGGAGACTGTCTACG 79
Db |
QY 61 AAAAATCAAAAAATTATGGCCGGGCGATGTGGCTCAGCTGTATATCCCTGAACCTTTGGG 120
Db |
QY 80 AAAAATCAAAAAATTATGGCCGGGCGATGTGGCTCAGCTGTATATCCCTGAACCTTTGGG 139
Db |
QY 121 ACATCAAGGCAAGTGTATCACTTGTAGGTCAAGAGTTCGAGACTAGCCTGGCCAACTGGT 180
Db |
QY 140 ACATCAAGGCAAGTGTATCACTTGTAGGTCAAGAGTTCGAGACTAGCCTGGCCAACTGGT 199
Db |
QY 181 GAAACCCATCTCCACAAAAAATACAAAAATTAGCCAGCATGTGGTGGGAGGACCTGTGTA 240
Db |
QY 200 GAAACCCATCTCCACAAAAAATACAAAAATTAGCCAGCATGTGGTGGGAGGACCTGTGTA 259
Db |
QY 241 ATCCCGGCTACTAGAGGCTGAGGCGAGGAATCACTTGAACCCAGAGGCGGAGGTTG 300
Db |
QY 260 ATCCCGGCTACTAGAGGCTGAGGCGAGGAATCACTTGAACCCAGAGGCGGAGGTTG 319
Db |
QY 301 CAGTGAAGTATGATCACACCACTGCATCCAGCCTGGGTGACAGAGCAAGACTGTATCTC 360
Db |
QY 320 CAGTGAAGTATGATCACACCACTGCATCCAGCCTGGGTGACAGAGCAAGACTGTATCTC 379
Db |
QY 361 AAAAAAATAAAAAATAAAAAATTAGCCAGCATGTGGTGGGAGGACCTGTGTA 420
Db |
QY 380 AAAAAAATAAAAAATAAAAAATTAGCCAGCATGTGGTGGGAGGACCTGTGTA 439
Db |
QY 421 CTACTCAGAGGCTGAGGTGGAGGATCACTTGAACCTGGGCGAGTAAAGGCTACAGTGA 480
Db |
QY 440 CTACTCAGAGGCTGAGGTGGAGGATCACTTGAACCTGGGCGAGTAAAGGCTACAGTGA 499
Db |
QY 481 GCCAAGATCAATGACCACTCCAGCCTGGGCAACAGAGAGAGACCCCTGTCTAAAAA 540
Db |
QY 500 GCCAAGATCAATGACCACTCCAGCCTGGGCAACAGAGAGAGACCCCTGTCTAAAAA 559
Db |
QY 541 AAAAAAATAAAAAATAAAAAATGAGTGTATGTCTCCGTGGTCAATCACTACTACT 600
Db |
QY 560 AAAAAAATAAAAAATAAAAAATGAGTGTATGTCTCCGTGGTCAATCACTACTACTACT 619
Db |
QY 601 ATGTATATAGTTTGAACCAATCAAGATCCAGATAGTCAATTTTTTTAGGCTTGGGGCGT 660
Db |
QY 620 ATGTATATAGTTTGAACCAATCAAGATCCAGATAGTCAATTTTTTTAGGCTTGGGGCGT 679
Db |
QY 661 ATGGTCTGTGTCAAATCACTGTGCCCTGTCTTTAGACAAAGAGGCTATAAACAAT 720
Db |
QY 680 ATGGTCTGTGTCAAATCACTGTGCCCTGTCTTTAGACAAAGAGGCTATAAACAAT 739
Db |
QY 721 ACATACATGAATTTTTTATAGACATGAGATTTGAATTTATATGATTTTAACTTTAT 780
Db |
QY 740 ACATACATGAATTTTTTATAGACATGAGATTTGAATTTATATGATTTTAACTTTAT 799
Db |
QY 781 AAAATATCTTTTAAAAAATTTCCCTTAACCATTTAAAAAGTAAAAAGCGGCGAGCGC 840
Db |

Db 800 AAAATATCTTTTAAAAAATTTCCCTTAACCATTTAAAAAGTAAAAAGCGGCGAGCGC 859
QY 841 GCCATTCGTACAGCCCTGTAAATTCAGACATTTGGAGGCTGAGTGGGAGATCACTTGAAG 900
Db |
QY 860 GCCATTCGTACAGCCCTGTAAATTCAGACATTTGGAGGCTGAGTGGGAGATCACTTGAAG 919
Db |
QY 901 ATCAACAGTTTGAACCAAGCTGGCCAAACATAGCAAAACCCATTTCTACTAAAAATPAA 960
Db |
QY 920 ATCAACAGTTTGAACCAAGCTGGCCAAACATAGCAAAACCCATTTCTACTAAAAATPAA 979
Db |
QY 961 AAAATTAAGCTGGGATGATGTGTGCACACCTGTGATCCAGCTACTTGGGAGGCTGAGGCA 1020
Db |
QY 980 AAAATTAAGCTGGGATGATGTGTGCACACCTGTGATCCAGCTACTTGGGAGGCTGAGGCA 1039
Db |
QY 1021 GGAGAAATCGCTTGAACCTGGGAAAGGAGTGTGAGAGCAACATCATCCACTGCAC 1080
Db |
QY 1040 GGAGAAATCGCTTGAACCTGGGAAAGGAGTGTGAGAGCAACATCATCCACTGCAC 1099
Db |
QY 1081 TCCAGCCTGGGTGACAGAGTGAACCTTCTGTCAACGAAAAAAGTGTAAAAAGCCAT 1140
Db |
QY 1100 TCCAGCCTGGGTGACAGAGTGAACCTTCTGTCAACGAAAAAAGTGTAAAAAGCCAT 1159
Db |
QY 1141 TCCTAATTCAGTGTACATCAGTGTACATCTCAGTGTGGCTACTCGCTCTGAGGAT 1200
Db |
QY 1160 TCCTAATTCAGTGTACATCAGTGTACATCTCAGTGTGGCTACTCGCTCTGAGGAT 1219
Db |
QY 1201 ACCTGAGAAAGTGAAGTTCCTTGTCTACAGAGCATACACATTTCCATTTAACTAGACACT 1260
Db |
QY 1220 ACCTGAGAAAGTGAAGTTCCTTGTCTACAGAGCATACACATTTCCATTTAACTAGACACT 1279
Db |
QY 1261 ACCAAGTTGCCATCCAAAGAGGTTTTTTTTTACAAATCTACACCTCCCCAGCAACAAAT 1330
Db |
QY 1280 ACCAAGTTGCCATCCAAAGAGGTTTTTTTTTACAAATCTACACCTCCCCAGCAACAAAT 1339
Db |
QY 1321 GAGAGTACTATCCAGATCCTTTTACAAAGATGCTTAAAGCCAGTACAGATGAAAAAGGA 1380
Db |
QY 1340 GAGAGTACTATCCAGATCCTTTTACAAAGATGCTTAAAGCCAGTACAGATGAAAAAGGA 1399
Db |
QY 1381 AGTGGAGGGGAAGCTCCAGACCCCTTCTAAACCATGAAAGAAATCTGTGTAGAGCTTCT 1440
Db |
QY 1400 AGTGGAGGGGAAGCTCCAGACCCCTTCTAAACCATGAAAGAAATCTGTGTAGAGCTTCT 1459
Db |
QY 1441 GAGATGCTGGAAGATGAAATTAACGGGGGTCTCTGGAAGCTGCCCTGTCAATGACTGTG 1500
Db |
QY 1460 GAGATGCTGGAAGATGAAATTAACGGGGGTCTCTGGAAGCTGCCCTGTCAATGACTGTG 1519
Db |
QY 1501 ACTTCTAGGCTCCAGTCCAGTCTCAGCCCATGTGTCATGGCCAGATTAATGAGCCCT 1560
Db |
QY 1520 ACTTCTAGGCTCCAGTCCAGTCTCAGCCCATGTGTCATGGCCAGATTAATGAGCCCT 1579
Db |
QY 1561 CACTCTCTGTTTGGTCTTTATTTCTCCCATGTGGGGCTGAAGTCTGATTGAGCCGTTAT 1620
Db |
QY 1580 CACTCTCTGTTTGGTCTTTATTTCTCCCATGTGGGGCTGAAGTCTGATTGAGCCGTTAT 1639
Db |
QY 1621 TCAAGATGTACAGCTTCTTGTGACAGGAAGTGTGTACAGAAACAGAGGCGCTTGCA 1680
Db |
QY 1640 TCAAGATGTACAGCTTCTTGTGACAGGAAGTGTGTACAGAAACAGAGGCGCTTGCA 1699
Db |
QY 1681 AGATGATCTTAAGTCAAAATCTAACCCTGGCTCAGGCAACACAGCTGTTTGTGATTTGAAC 1740
Db |
QY 1700 AGATGATCTTAAGTCAAAATCTAACCCTGGCTCAGGCAACACAGCTGTTTGTGATTTGAAC 1759
Db |
QY 1741 AAGTTTTTCACTTCTCTGAGGCAATCCCTTGGCTACACACACACAGATTGTTGACAGGA 1800
Db |
QY 1760 AAGTTTTTCACTTCTCTGAGGCAATCCCTTGGCTACACACACAGATTGTTGACAGGA 1819
Db |
QY 1801 TGAATGACAAAGTCCCTTACACCTGTATTTCCAGCACTTTGGAGGCGAAGCGGGTGG 1860
Db |
QY 1820 TGAATGACAAAGTCCCTTACACCTGTATTTCCAGCACTTTGGAGGCGAAGCGGGTGG 1879
Db |
QY 1861 ATGGCTTGAAGCTGAGAGGTGACAGCATGCGGCGAGTCCACAGGCGTCTGCGCTTC 1920
Db |
QY 1880 ATGGCTTGAAGCTGAGAGGTGACAGCATGCGGCGAGTCCACAGGCGCTCTGCGCTTC 1939
Db |

QY 1921 GGGCCCTCTCTGCTGGGCTCCACCTTCGGTGGCATTGAGAGCCCTTACGCCACCG 1980
| | | | |
Db 1940 GGGCCCTCTCTGCTGGGCTCCACCTTCGGTGGCATTGAGAGCCCTTACGCCACCG 1999
| | | | |
QY 1981 CTGACATGTGGAGCCCTTCTGGGCTGGCCAGAGCCAGAGCCGGCTCCCTCAGCTTGC 2040
| | | | |
Db 2000 CTGACATGTGGAGCCCTTCTGGGCTGGCCAGAGCCAGAGCCGGCTCCCTCAGCTTGC 2059
| | | | |
QY 2041 AGGAGGTGTGGAGGAGAGGCTCAAGCAGAACCGGGGCTGCCACAGCGCTTGCGGGC 2100
| | | | |
Db 2060 AGGAGGTGTGGAGGAGAGGCTCAAGCAGAACCGGGGCTGCCACAGCGCTTGCGGGC 2119
| | | | |
QY 2101 CAGTGTAGTCCCGGTGGGCTGGGCTGGCGGGCCCGCAGCTCGAGAGCGGGCAG 2160
| | | | |
Db 2120 CAGTGTAGTCCCGGTGGGCTGGGCTGGCGGGCCCGCAGCTCGAGATTTCTCACTGGGC 2179
| | | | |
QY 2161 CCTGCGAGGCCCCGGGCAATGAGAGGCTTAGCACCCGGGCGAGGGCTGGGAGGGTGT 2220
| | | | |
Db 2180 CCTGCGAGGCCCCGGGCAATGAGAGGCTTAGCACCCGGGCGAGGGCTGGGAGGGTGT 2239
| | | | |
QY 2221 ACTGGGTGCCCCAGCAGTGGCCAGCCCGCGGCTGTGCTCGATTTCTCACTGGGC 2280
| | | | |
Db 2240 ACTGGGTGCCCCAGCAGTGGCCAGCCCGCGGCTGTGCTCGATTTCTCACTGGGC 2299
| | | | |
QY 2281 CTTAGCAGGCTTCCCGGGGGGAGGGCTCGGGGACCTCGAGCCCGCATGGCTGAGCCTTC 2340
| | | | |
Db 2300 CTTAGCAGGCTTCCCGGGGGGAGGGCTCGGGGACCTCGAGCCCGCATGGCTGAGCCTTC 2359
| | | | |
QY 2341 CCTCATAGGGCTCTGTGTGGGCGCCGAGGCTCCCGAGAGCAGCACCCCTGTGTCACAG 2400
| | | | |
Db 2360 CCTCATAGGGCTCTGTGTGGGCGCCGAGGCTCCCGAGAGCAGCACCCCTGTGTCACAG 2419
| | | | |
QY 2401 CGCCCACTCCCATGACACGCAAGGGCTGAGAAAGTGGGGCGAGCGGACCGGAGCTGG 2460
| | | | |
Db 2420 CGCCCACTCCCATGACACGCAAGGGCTGAGAAAGTGGGGCGAGCGGAGCTGG 2479
| | | | |
QY 2461 CAGGAGCTACCCCTGGAGACCCCTGTGTGGGAAATCAGTGGGTGAAGCCAGCTGGGCTCT 2520
| | | | |
Db 2480 CAGGAGCTACCCCTGGAGACCCCTGTGTGGGAAATCAGTGGGTGAAGCCAGCTGGGCTCT 2539
| | | | |
QY 2521 GAGTCTGTGTGAGACTTGGAGAACCTTATGTCTAGCTCAGAGATCGTAAATACACCAAT 2580
| | | | |
Db 2540 GAGTCTGTGTGAGACTTGGAGAACCTTATGTCTAGCTCAGAGATCGTAAATACACCAAT 2599
| | | | |
QY 2581 CAGACCCCTGTGTAGCTCAGGGTCTGTGATGACCAATTCACACTCTGTATCTAGCT 2640
| | | | |
Db 2600 CAGACCCCTGTGTAGCTCAGGGTCTGTGATGACCAATTCACACTCTGTATCTAGCT 2659
| | | | |
QY 2641 ACTGTGATGGGCTTGGAGAACCTTATGTCTAGCTCAGGGATTTGTAATACACCAATCT 2700
| | | | |
Db 2660 ACTGTGATGGGCTTGGAGAACCTTATGTCTAGCTCAGGGATTTGTAATACACCAATCT 2719
| | | | |
QY 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTGTAGCTC 2760
| | | | |
Db 2720 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTGTAGCTC 2779
| | | | |
QY 2761 AGGATGTGTGATGACCAATTCAGACAGTCTGTATCTAGCTACTTTCATGGCCATCCGTGT 2820
| | | | |
Db 2780 AGGATGTGTGATGACCAATTCAGACAGTCTGTATCTAGCTACTTTCATGGCCATCCGTGT 2839
| | | | |
QY 2821 GAAGAGACCAACCAAGGGCTTGTGTAGCAATTAAGGCTCTATACCTCTGGGTGAGAGT 2880
| | | | |
Db 2840 GAAGAGACCAACCAAGGGCTTGTGTAGCAATTAAGGCTCTATACCTCTGGGTGAGAGT 2899
| | | | |
QY 2881 GGGCTGAGTCCGAAAGAGATCAGCGAAGGAGATTAAGGTGGGCGCTTTATYAGAT 2940
| | | | |
Db 2900 GGGCTGAGTCCGAAAGAGATCAGCGAAGGAGATTAAGGTGGGCGCTTTATYAGAT 2959
| | | | |
QY 2941 TTGGGTAGTAAAGAAAAATTACAGTCAAAAGGGGTTTGTCTCTGGGCGGACAGAGTGG 3000
| | | | |
Db 2960 TTGGGTAGTAAAGAAAAATTACAGTCAAAAGGGGTTTGTCTCTGGGCGGACAGAGTGG 3019
| | | | |

QY 3001 GGGGTCGAGAGTGTGCTAGTGGGGTGTCTTTTGAAGCCAGGATGAGCCAGGAAAGAGCT 3060
| | | | |
Db 3020 GGGGTCGAGAGTGTGCTAGTGGGGTGTCTTTTGAAGCCAGGATGAGCCAGGAAAGAGCT 3079
| | | | |
QY 3061 TTCACAAAGTATGATCATCAATTAAGGCAAGGACCCGCAATTTACACCTCTTTTGTGGTG 3120
| | | | |
Db 3080 TTCACAAAGTATGATCATCAATTAAGGCAAGGACCCGCAATTTACACCTCTTTTGTGGTG 3139
| | | | |
QY 3121 GAATGTCAATGATTAAGTGGGGCAGGGCATATTCATCTTCTTGTGTATCTTCACTTAC 3180
| | | | |
Db 3140 GAATGTCAATGATTAAGTGGGGCAGGGCATATTCATCTTCTTGTGTATCTTCACTTAC 3199
| | | | |
QY 3181 TTCAGCCATCTGGGCGGTATATGTGCAATGATACAGGGGATGCGANTGCTTGGCTGGGCT 3240
| | | | |
Db 3200 TTCAGCCATCTGGGCGGTATATGTGCAATGATACAGGGGATGCGANTGCTTGGCTGGGCT 3259
| | | | |
QY 3241 CAGAGGCTTGCAGACTCTGTGTGGGCGCTTGGAGATGTTTGTGTGACACTGTAT 3300
| | | | |
Db 3260 CAGAGGCTTGCAGACTCTGTGTGGGCGCTTGGAGATGTTTGTGTGACACTGTAT 3319
| | | | |
QY 3301 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTGTCTAGCTCAGGGATTTGAAGCA 3360
| | | | |
Db 3320 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTGTCTAGCTCAGGGATTTGAAGCA 3379
| | | | |
QY 3361 CCAATCAGCGCCCTGTCAAAACAGACCACTGGGCTCTCAATCAGCAGAGATGGGGTGG 3420
| | | | |
Db 3380 CCAATCAGCGCCCTGTCAAAACAGACCACTGGGCTCTCAATCAGCAGAGATGGGGTGG 3439
| | | | |
QY 3421 GGCAGATTAAGATTAAGAACAGAGCTCCCGAGCAGCAGATGGCAGCGCAGAGTGC 3480
| | | | |
Db 3440 GGCAGATTAAGATTAAGAACAGAGCTCCCGAGCAGCAGATGGCAGCGCAGAGTGC 3499
| | | | |
QY 3481 CTATCCATATATGGACCTTGTCTTGTGCTGTTGCGATTAATCTTGTACTGCTCG 3540
| | | | |
Db 3500 CTATCCATATATATGACACTTGTCTTGTCTGTTGCGATTAATCTTGTACTGCTCG 3559
| | | | |
QY 3541 CTTTGTGGTCCACACTGCTTTTATGACCTGTATACACTCAGCAGGAAGTGTGACGCTTC 3600
| | | | |
Db 3560 CTTTGTGGTCCACACTGCTTTTATGACCTGTATACACTCAGCAGGAAGTGTGACGCTTC 3619
| | | | |
QY 3601 ACTCTGAGGCACTTAAGACCAAGCCAGCCAGGAGGAGATGAACACTCCGGCGGCT 3660
| | | | |
Db 3620 ACTCTGAGGCACTTAAGACCAAGCCAGGAGGAGATGAACACTCCGGCGGCT 3679
| | | | |
QY 3661 GCCTTAAGAGCTATTAACACTCAGCGGAGAGTCTGACCTTCACTCTCAGCCAGCGAGA 3720
| | | | |
Db 3680 GCCTTAAGAGCTATTAACACTCAGCGGAGAGTCTGACCTTCACTCTCAGCCAGCGAGA 3739
| | | | |
QY 3721 CCAGAACCCAGCAAGGAAGAACTGCAACATCTGAACATCAGAAAGCAACACT 3780
| | | | |
Db 3740 CCAGAACCCAGCAAGGAAGAACTGCAACATCTGAACATCAGAAAGCAACACT 3799
| | | | |
QY 3781 CCAGATGCAACCACTTAAGAGCTGTAAACACTCAGCTCAGAGGGTCCGGCTTCTCTTG 3840
| | | | |
Db 3800 CCAGATGCAACCACTTAAGAGCTGTAAACACTCAGCTCAGAGGGTCCGGCTTCTCTTG 3859
| | | | |
QY 3841 AAGTCACTGAGACCAAGCACTCAGCGATTTGGACACAAAGCCAGAGTGTGATACAGC 3900
| | | | |
Db 3860 AAGTCACTGAGACCAAGCACTCAGCGATTTGGACACAAAGCCAGAGTGTGATACAGC 3919
| | | | |
QY 3901 CTGGGCAACATGATGAATAGCCCTGTGTGCAAAAAAAATTAACAAAAATTTGGCGG 3960
| | | | |
Db 3920 CTGGGCAACATGATGAATAGCCCTGTGTGCAAAAAAAATTAACAAAAATTTGGCGG 3979
| | | | |
QY 3961 AGCATGTGTGCTCGCTGTGTGCTCCAGCTACCGGAGGCTAAAGTGGGAGATTCCT 4020
| | | | |
Db 3980 AGCATGTGTGCTCGCTGTGTGCTCCAGCTACCGGAGGCTAAAGTGGGAGATTCCT 4039
| | | | |
QY 4021 TGAAGCTGGAGGTGAAGACTGCAAGTGAAGTGTGATTTACACAGCCCTTGTAGCTGGG 4080
| | | | |
Db 4040 TGAAGCTGGAGGTGAAGACTGCAAGTGAAGTGTGATTTACACAGCCCTTGTAGCTGGG 4099
| | | | |
QY 4081 GGACAGACTGAGACCTGTCTTCCCTCCGCAAAAAAAATTTGACAAAAAGTGTAAAGAGT 4140
| | | | |

|||||
Db 4100 GGACACACTGAGACCCCTGTTCCCTCCGCAAAAAATGACAAAAGTGAATAAAGGT 4159
QY 4141 GCCTGATATGGTAGGCGCAGTGGCTCATGCCGTATATCCACACTTTGGGAAGCGAG 4200
|||||
Db 4160 GCGTGAATATGGTAGGCGCAGTGGCTCATGCCGTATATCCACACTTTGGGAAGCGAG 4219
QY 4201 GCGGGCGGGTCACCTAAGTCAAGAGTGTGACACAGCCCTGGCCAACTATGAGAAAGCC 4260
Db 4220 GCGGGCGGGTCACCTAAGTCAAGAGTGTGACACAGCCCTGGCCAACTATGAGAAAGCC 4279
QY 4261 ATCTCTTAAAAATCAAAAATTAGCCGGCTGTGGGGGCGAGTGGTGGAGATCCCTGTA 4320
Db 4280 ATCTCTTAAAAATCAAAAATTAGCCGGCTGTGGGGGCGAGTGGTGGAGATCCCTGTA 4339
QY 4321 TCCACACTACTCAGAGGGCTGAGGAGAGAAATCACTTGAAACCCAGAGGGCGGGTTGC 4380
Db 4340 TCCACACTACTCAGAGGGCTGAGGAGAGAAATCACTTGAAACCCAGAGGGCGGGTTGC 4399
QY 4381 AGTGACCCGAGATCGTGCCATTGCACTCCACCACTCCAGCTGGGCAACAGAGCCAAA 4440
Db 4400 AGTGACCCGAGATCGTGCCATTGCACTCCACCACTCCAGCTGGGCAACAGAGCCAAA 4459
QY 4441 CTCTGCTTAAAAAAGTGGCTGACATATTAAGAGTGTGCAATGCAATAG 4500
Db 4460 CTCTGCTTAAAAAAGTGGCTGACATATTAAGAGTGTGCAATGCAATAG 4519
QY 4501 TTGCGACGCAACATGTTTAAAGATGTGAGCTCTGCCCTTCATGGTCTGTTAAAAAC 4560
Db 4520 TTGCGACGCAACATGTTTAAAGATGTGAGCTCTGCCCTTCATGGTCTGTTAAAAAC 4579
QY 4561 CACCCCAAGGCCAGGTGCAGTGGCTCATGCTATATATCCACACTTTGGGAGGCCGAG 4620
Db 4580 CACCCCAAGGCCAGGTGCAGTGGCTCATGCTATATATCCACACTTTGGGAGGCCGAG 4639
QY 4621 GCGGGTGGATCACTAGGTCAAGAGTGTGAGACAGCCGCTGACCAACATGTTGAAT 4680
Db 4640 GCGGGTGGATCACTAGGTCAAGAGTGTGAGACAGCCCTGACCAACATGTTGAAT 4699
QY 4681 CCCACCTCTAATAAATAACAAAATTAGATGAGCATGTGTGTCATGCCCTGTAAATCCAC 4740
Db 4700 CCCACCTCTAATAAATAACAAAATTAGATGAGCATGTGTGTCATGCCCTGTAAATCCAC 4759
QY 4741 CTACTTGGGAGGTGAGGCGAGAAATCACTAGAACCAGGAGCGGAGGTTAGTGA 4800
Db 4760 CTACTTGGGAGGTGAGGCGAGAAATCACTAGAACCAGGAGCGGAGGTTAGTGA 4819
QY 4801 CCGAGATCGTGCATGTGCACTCCAGGCTGAGCAATGAGGAGCAACTGCATCAAAAAAC 4860
Db 4820 CCGAGATCGTGCATGTGCACTCCAGGCTGAGCAATGAGGAGCAACTGCATCAAAAAAC 4879
QY 4861 AACACAAAAACCACACTCTCTACTCCAGGAGCTGGTACAGAGCTGGGCCACATCAGT 4920
Db 4880 AACACAAAAACCACACTCTCTACTCCAGGAGCTGGTACAGAGCTGGGCCACATCAGT 4939
QY 4921 GCAAGTGTGAGCCACAGAGCTAAGCGGAGCTGCAAGACCGCGGACAGATACAGTG 4980
Db 4940 GCAAGTGTGAGCCACAGAGCTAAGCGGAGCTGCAAGACCGCGGACAGATACAGTG 4999
QY 4981 TGTGAGATCAGTGTGAGATCAGAGTCCCTGCTGCTTGGTGAACCAAGGGGGCCCCA 5040
Db 5000 TGTGAGATCAGTGTGAGATCAGAGTCCCTGCTGCTTGGTGAACCAAGGGGGCCCCA 5059
QY 5041 AGCAGCAGAGATGGCCCCATCCAGTCAACACATCACTTCTCATCCAGAGATGTGTTT 5100
Db 5060 AGCAGCAGAGATGGCCCCATCCAGTCAACACATCACTTCTCATCCAGAGATGTGTTT 5119
QY 5101 CTTGCGACGCTGGGGTAAATTAGAGACAGAGGTGACAGTCTTGGGTGTGCTCAGTACAG 5160
Db 5120 CTTGCGACGCTGGGGTAAATTAGAGACAGAGGTGACAGTCTTGGGTGTGCTCAGTACAG 5179
QY 5161 TGGCCAGGCGAGGCTTGTGGCTGTAGAAAAGTTCAAGGCTTAGGCCGGGACGGTGGC 5220
|||||

Db 5180 TGGCCAGGCGAGGCTTGTGGCTGTAGAAAAGTTTACAGGCTTAGGCCGGGACGGTGGC 5239
QY 5221 TCAGGCTGTAAATCCAGCACTTTGGGAGCGGAGCGGGTGGATCAGAGTCAAGAGA 5280
Db 5240 TCAGGCTGTAAATCCAGCACTTTGGGAGCGGAGCGGGTGGATCAGAGTCAAGAGA 5299
QY 5281 TGTGACCATCTGGCTAACACGCGTGAACCCCGTCTTACTAATAAATACAAAAATTGG 5340
Db 5300 TGTGACCATCTGGCTAACACGCGTGAACCCCGTCTTACTAATAAATACAAAAATTGG 5359
QY 5341 CCGGGCATGGTGGCGGGCACTGATAGTCCAGTACTCCGGGAGCGTGAAGCAGAGAAAG 5400
Db 5360 CCGGGCATGGTGGCGGGCACTGATAGTCCAGTACTCCGGGAGCGTGAAGCAGAGAAAG 5419
QY 5401 GCGTGAACCCGAGAGGAGAGATTGAGAGTGGAGCGAGATGCGCCACTGCATCCAGCT 5460
Db 5420 GCGTGAACCCGAGAGGAGAGATTGAGAGTGGAGCGAGATGCGCCACTGCATCCAGCT 5479
QY 5461 GGGCGACAGACAGAGTCCATCTGGAAAAAGAAAAAGAAAGCTTCAAGTCTGAGCCAGA 5520
Db 5480 GGGCGACAGACAGAGTCCATCTGGAAAAAGAAAAAGAAAGCTTCAAGTCTGAGCCAGA 5539
QY 5521 GGGCCAGGCTGTAAATCTGTCACTTACATGACCTTTGGGCAAGCACTTCTCCCTGGC 5580
Db 5540 GGGCCAGGCTGTAAATCTGTCACTTACATGACCTTTGGGCAAGCACTTCTCCCTGGC 5599
QY 5581 CCAGTTCACGGGTTGGAAATGCACTCCAGAGTCCCTTCAGCATTAACGCTGATGGTT 5640
Db 5600 CCAGTTCACGGGTTGGAAATGCACTCCAGAGTCCCTTCAGCATTAACGCTGATGGTT 5659
QY 5641 TAAGATGAGAAATGGGGGCAATTCCCTCTCACCCAGCCCGCTGTCCACTTCAAGT 5700
Db 5660 TAAGATGAGAAATGGGGGCAATTCCCTCTCACCCAGCCCGCTGTCCACTTCAAGT 5719
QY 5701 GAATGACAGAGGAATGACGTGTCCCAATCCCAAGTCCCAAGCCCTTTGGGAGCCCTAC 5760
Db 5720 GAATGACAGAGGAATGACGTGTCCCAATCCCAAGTCCCAAGCCCTTTGGGAGCCCTAC 5779
QY 5761 TGTCAAGGTCGTCAAGAGGAGGTGAAGGTCAAGTGAAGCAATCGCTCGAAGGGTCTTG 5820
Db 5780 TGTCAAGGTCGTCAAGAGGAGGTGAAGGTGAAGGTGAAGCAATCGCTCGAAGGGTCTTG 5839
QY 5821 CCTCATTTGGGAGACAGACATCCGGTTCTCTGTGGCTCTACCGGGATTTCTAGGGGCTTACG 5880
Db 5840 CCTCATTTGGGAGACAGACATCCGGTTCTCTGTGGCTCTACCGGGATTTCTAGGGGCTTACG 5899
QY 5881 CGAATGATCATGGGGGCGGGGGGTTCTGGGGAGTTCCCAAGCTAATCAACTTGGGA 5940
Db 5900 CGAATGATCATGGGGGCGGGGGGTTCTGGGGAGTTCCCAAGCTAATCAACTTGGGA 5959
QY 5941 CAGGACAGCTGGAACCTTTCGATGTGCTATCCAAAGTGTGGGTGGGCAACAGACCAA 6000
Db 5960 CAGGACAGCTGGAACCTTTCGATGTGCTATCCAAAGTGTGGGTGGGCAACAGACCAA 6019
QY 6001 GACCCAATGTCTTATCTCAGGTAGGGGCTCAGGAGGTCTCCAGACAGGCACTTCGG 6060
Db 6020 GACCCAATGTCTTATCTCAGGTAGGGGCTCAGGAGGTCTCCAGACAGGCACTTCGG 6079
QY 6061 AGAGTTTGGGGGTAGGAATGGGAGCAACGAGTTCTTTTCTCTCTTCTAGAAATTTGG 6120
Db 6080 AGAGTTTGGGGGTAGGAATGGGAGCAACGAGTTCTTTTCTCTCTTCTAGAAATTTGG 6139
QY 6121 GCGTTGGGGGACAGGCTTGTGAATTCCAAAGAGAGGGGCAAGAGCACTCCCAACAA 6180
Db 6140 GCGTTGGGGGACAGGCTTGTGAATTCCAAAGAGAGGGGCAAGAGCACTCCCAACAA 6199
QY 6181 TCTGCCAGACGAGAGAGGAGAGCCCGACTCAGTTCGCACTTCCCAAGGCGCT 6235
Db 6200 TCTGCCAGACGAGAGAGGAGAGCCCGACTCAGTTCGCACTTCCCAAGGCGCT 6254
RESULT 4
AX250678

LOCUS	AX250678	6679 bp	DNA	linear	PAT 05-OCT-2001
DEFINITION	Sequence 5 from Patent WO0168882.				
ACCESSION	AX250678				
VERSION	AX250678.1	GI:15984422			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Ivanov, E.				
TITLE	Methods for homologous recombination				
JOURNAL	Patent: WO 0168882 A 5 20-SEP-2001; TRANSCRIPTOTIC THERAPIES, INC. (US)				
FEATURES	Location/Qualifiers				
source	1. 6679				
BASE COUNT	1684 a	1739 c	1830 g	1426 t	
ORIGIN					
Query Match	100.0%;	Score 6235;	DB 6;	Length 6679;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 6235; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1	GATC	ACTTGGAGACAGTAGTTC	CAAGACCAGCCTGGGGCAGCATATGAGCAGCTGTCTCTACG	60
DB	20	GATC	ACTCTTGAGAGCAGTAGTTC	CAAGACCAGCCTGGGGCAGCATATGAGCAGCTGTCTCTACG	79
OY	61	AAAAAT	CAAAAATTAATGCGCGGCGATGTCACGTCGTGTAATCCCTGA	CTTTGGG	120
DB	80	AAAAAT	CAAAAATTAATGCGCGGCGATGTCACGTCGTGTAATCCCTGA	CTTTGGG	139
OY	121	ACATCA	AGGCAAGAGGATCAGCTTGAGGTCAGAGAGTTCAGACTGAGCTGGCCCA	CAATGGT	180
DB	140	ACATCA	AGGCAAGAGGATCAGCTTGAGGTCAGAGAGTTCAGACTGAGCTGGCCCA	CAATGGT	199
OY	181	GAAC	CCCTATCTCCACTAAAAAATACAAAAATTAGCCAGGATGGTGGCAGGACCTGTA	240	
DB	200	GAAC	CCCTATCTCCACTAAAAAATACAAAAATTAGCCAGGATGGTGGCAGGACCTGTA	259	
OY	241	ATCC	CGGTACTCAGAGAGGCTGAGGCGAGAGATATCTTGAACCCAGAGGCGGAGGTTG	300	
DB	260	ATCC	CGGTACTCAGAGAGGCTGAGGCGAGAGATATCTTGAACCCAGAGGCGGAGGTTG	319	
OY	301	CAGT	AGAGCTGAGATCACACCACTGACATCCAGCCTGGGGTGACAGAGCAAGACTATCTC	360	
DB	320	CAGT	AGAGCTGAGATCACACCACTGACATCCAGCCTGGGGTGACAGAGCAAGACTATCTC	379	
OY	361	AAAA	AAAAATTAATAAATAATTAACCGAGGATGGTAGTGACACCTCTAGTCTCAG	420	
DB	380	AAAA	AAAAATTAATAAATAATTAACCGAGGATGGTAGTGACACCTCTAGTCTCAG	439	
OY	421	CTACT	CAGAGAGGCTGAGGTGGGAGGATATCTTGAACCTGGGGCACTCAAGGCTACAGTGA	480	
DB	440	CTACT	CAGAGAGGCTGAGGTGGGAGGATATCTTGAACCTGGGGCACTCAAGGCTACAGTGA	499	
OY	481	GCAA	AGATCATGACCACTACACTCCAGCCTGGGGCAACAGAGAGAGCCTGTCTCTAAAAA	540	
DB	500	GCAA	AGATCATGACCACTACACTCCAGCCTGGGGCAACAGAGAGAGCCTGTCTCTAAAAA	559	
OY	541	AATA	TATATATATATAAGAAAAAAGACGCTCTTTTATGTCTCTGGTCCATACATATCTACT	600	
DB	560	AATA	TATATATATATAAGAAAAAAGACGCTCTTTTATGTCTCTGGTCCATACATATCTACT	619	
OY	601	ATGTA	TATATAGTTTGCAAACTCAAGAGTCAGATAGTCAATTTTATAGGCTGTGGGCGGT	660	
DB	620	ATGTA	TATATAGTTTGCAAACTCAAGAGTCAGATAGTCAATTTTATAGGCTGTGGGCGGT	679	
OY	661	ATGG	CTCTGTGTGCACAAATCATCTGCGCCCTGTCTTTCTTAGCACAAAAAGCAGCTATAACAT	720	
DB	680	ATGG	CTCTGTGTGTGCACAAATCATCTGCGCCCTGTCTTTCTTAGCACAAAAAGCAGCTATAACAT	739	

QY	721	ACATACATGAAATTTTATTAACACATCCGAGATTGAAATTTCAATATGATTTTATACATTTTAT	780
Db	740	ACATACATGAAATTTTATTAACACATCGGATTTGAAATTTCAATATGATTTTATACATTTTAT	799
QY	781	AAATTAATCTTTTAAAAATTTTCCCGTAACCATTTTAAAAAGTGTAAAAAGCCGGCAGCGC	840
Db	800	AAATTAATCTTTTAAAAATTTTCCCGTAACCATTTTAAAAAGTGTAAAAAGCCGGCAGCGC	859
QY	841	GCATTCGTACAGCCCTGTATATTCACAGACTTTGGGAGGCGTAGTGAGTGAGATCATCTTGAG	900
Db	860	GCATTCGTACAGCCCTGTATATTCACAGACTTTGGGAGGCGTAGTGAGTGAGATCATCTTGAG	919
QY	901	ATCAACACTTCGAGACACAGCCTGGCCAAACATAGCAAAAACCCATTCTACTAAAAATPAA	960
Db	920	ATCAACACTTCGAGACACAGCCTGGCCAAACATAGCAAAAACCCATTCTACTAAAAATPAA	979
QY	961	AAATTAATCTTTTAAAAATTTTCCCGTAACCATTTTAAAAAGTGTAAAAAGCCGGCAGCGC	1020
Db	980	AAATTAATCTTTTAAAAATTTTCCCGTAACCATTTTAAAAAGTGTAAAAAGCCGGCAGCGC	1039
QY	1021	GGAGAAATCGCTTGAACCTGGGAAAGCGAGGTGTGAGTAGAGCCAAATCATATCCACTGCAC	1080
Db	1040	GGAGAAATCGCTTGAACCTGGGAAAGCGAGGTGTGAGTAGAGCCAAATCATATCCACTGCAC	1099
QY	1081	TCACAGCTGGGTGACAGAGTAGACATTCGTCTACACGAAAAAAAAGTGTAAAGCCAT	1140
Db	1100	TCACAGCTGGGTGACAGAGTAGACATTCGTCTACACGAAAAAAAAGTGTAAAGCCAT	1159
QY	1141	TCCTAATTCATGTATACATCATGTATATCATATCTCAGGTCTGCCTACTCTCGCTCTGAGCAT	1200
Db	1160	TCCTAATTCATGTATACATCATGTATATCATATCTCAGGTCTGCCTACTCTCGCTCTGAGCAT	1219
QY	1201	ACCTGAGAAGTAGAGTTGCTGTGTGCACAGAGATACACATTTCCACATTACTAGACACT	1260
Db	1220	ACCTGAGAAGTAGAGTTGCTGTGTGCACAGAGATACACATTTCCACATTACTAGACACT	1279
QY	1261	ACCAAGTTGCCATCCACGAGAGGAGTGTTTTTTTTAAATATCTACATCTCCCCCGACAACAAT	1320
Db	1280	ACCAAGTTGCCATCCACGAGAGGAGTGTTTTTTTTAAATATCTACATCTCCCCCGACAACAAT	1339
QY	1321	GAGAGTATCTCCAAATCTCTTAAACAAAGATGCTATGAAGCCGATACAGATGAATAACAGGA	1380
Db	1340	GAGAGTATCTCCAAATCTCTTAAACAAAGATGCTATGAAGCCGATACAGATGAATAACAGGA	1399
QY	1381	AGTGGGAGGGGAAAGCTGCCAGCCCTCTTAACATCAATGAAGAAATACCTGGTAGACCTTCT	1440
Db	1400	AGTGGGAGGGGAAAGCTGCCAGCCCTCTTAACATCAATGAAGAAATACCTGGTAGACCTTCT	1459
QY	1441	GGATTCGTGGAAGATGAATTAACGGGGGGTCTCTGAGAGCTGCCCTGTCAAGTACATCTGTG	1500
Db	1460	GGATTCGTGGAAGATGAATTAACGGGGGGTCTCTGAGAGCTGCCCTGTCAAGTACATCTGTG	1519
QY	1501	ACTTCGTAGCCTCCAGTCCAGTCTCAGGCCCATGTGTATATGGCCAGATATATAGACCTT	1560
Db	1520	ACTTCGTAGCCTCCAGTCCAGTCTCAGGCCCATGTGTATATGGCCAGATATATAGACCTT	1579
QY	1561	CAGTCTCGTTGGCTTATTTTCACCATCTGGGGCTGAAGTCTGGATTTAGCCGTTAT	1620
Db	1580	CAGTCTCGTTGGCTTATTTTCACCATCTGGGGCTGAAGTCTGGATTTAGCCGTTAT	1639
QY	1621	TCAAGATGTACAGCTTTCTTGACAGAAAGTAGTGTACAGAAACAGCAGAGGGGCTTGCA	1680
Db	1640	TCAAGATGTACAGCTTTCTTGACAGAAAGTAGTGTACAGAAACAGCAGAGGGGCTTGCA	1699
QY	1681	AGATGATCTAACTGCAAAATCTCTACCTGGCTCAGCCACACAGCTAGTTCTGTGATCTTGAAC	1740
Db	1700	AGATGATCTAACTGCAAAATCTCTACCTGGCTCAGCCACACAGCTAGTTCTGTGATCTTGAAC	1759
QY	1741	AAGTTTTTTCACCTTCTCTGAGGCCATCCCTGGCTACAAACACACAGTGTGGTTTACACAGA	1800
Db	1760	AAGTTTTTTCACCTTCTCTGAGGCCATCCCTGGCTACAAACACACAGTGTGGTTTACACAGA	1819

OY		1801	TGAATGACGAAGTCCCTTAACACTGTATATCCACGACTTTGGAGGCCAAGCGGGGTGG	1860
Dd		1820	TGAATGACGAAGTCCCTTAACACTGTATATCCACGACTTTGGAGGCCAAGCGGGGTGG	1879
OY		1861	ATGAGTTTAGCCTGAGAGTGACAGCATGCCGGAGTCCTACAGACCCTGGTTCGCCTC	1920
Dd		1880	ATGAGTTTAGCCTGAGAGTGACAGCATGCCGGAGTCCTACAGACCCTGGTTCGCCTC	1939
OY		1921	GCGCGCTCTCTGCGCTGGGCTCCACATTGCGTGCACTTGAGGAGCCCTTCAGCCACCG	1980
Dd		1940	GCGCGCTCTCTGCGCTGGGCTCCACATTGCGTGCACTTGAGGAGCCCTTCAGCCACCG	1999
OY		1981	CTGCACGTGGGAGACCCCTTTCTGAGGCTGGGCCAAGGCCAGCCGCTCCCTACGTTGC	2040
Dd		2000	CTGCACGTGGGAGACCCCTTTCTGAGGCTGGGCCAAGGCCAGCCGCTCCCTACGTTGC	2059
OY		2041	AGGAGGTGTGAGGAGAGAGGCTCAAGCAGAGAACCGGGGCTGGCACAGGGCCCTTAGGGG	2100
Dd		2060	AGGAGGTGTGAGGAGAGAGGCTCAAGCAGAGAACCGGGGCTGGCACAGGGCCCTTAGGGG	2119
OY		2101	CAGCTGAGTTCCGGGTGGGCTGGGCTTGGCGGGCCCCCGCACTCGGAGCAGCGGGCAG	2160
Dd		2120	CAGCTGAGTTCCGGGTGGGCTGGGCTTGGCGGGCCCCCGCACTCGGAGCAGCGGGCAG	2179
OY		2161	CCCTGCCAGGCCCCGGGCAATGAGAAGGTTTACACCCGGGCGCACGGCTCGCGAGGCTGT	2220
Dd		2180	CCCTGCCAGGCCCCGGGCAATGAGAAGGTTTACACCCGGGCGCACGGCTCGCGAGGCTGT	2239
OY		2221	ACTGGGTGCCCCAGCAGTGCACAGGCCCGCGGCGCTGTACTGCTCGATTTTCTACTGGG	2280
Dd		2240	ACTGGGTGCCCCAGCAGTGCACAGGCCCGCGGCGCTGTACTGCTCGATTTTCTACTGGG	2299
OY		2281	CTTAGCAGCCTTCCC CGGGGCAAGGGCTCGGGACCTGCAGCCGCGCATGCCGTGACCTCC	2340
Dd		2300	CTTAGCAGCCTTCCC CGGGGCAAGGGCTCGGGACCTGCAGCCGCGCATGCCGTGACCTCC	2359
OY		2341	CCTCCATGGGGTCCGTGTGGGGCCCCGAGCCTCCCGAGAGACACACCCCTGCTCCACAG	2400
Dd		2360	CCTCCATGGGGTCCGTGTGGGGCCCCGAGCCTCCCGAGAGAGACACCCCTGCTCCACAG	2419
OY		2401	CGCCAGTCCCATGCAACGACGCAAGGGCTGAGAAATGCGGGCGCAGCGCACCGGAGATGG	2460
Dd		2420	CGCCAGTCCCATGCAACGACGCAAGGGCTGAGAAATGCGGGCGCAGCGCACCGGAGATGG	2479
OY		2461	CAGGCAGCTACCCCTGCAGCCCTGGTGGGAATCCACTGGGTGAAGCCAGCTGGGCTCT	2520
Dd		2480	CAGGCAGCTACCCCTGCAGCCCTGGTGGGAATCCACTGGGTGAAGCCAGCTGGGCTCT	2539
OY		2521	GAGTCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGAGTCTGTAATACACAAT	2580
Dd		2540	GAGTCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGAGTCTGTAATACACAAT	2599
OY		2581	CAGACACCCCTGTAGCTCAGGAGTGTGTAATGACCAATCCACACTGTGTATCTAGCT	2640
Dd		2600	CAGACACCCCTGTAGCTCAGGAGTGTGTAATGACCAATCCACACTGTGTATCTAGCT	2659
OY		2641	ACTGTGATGGGCTTGGAGAACCTTTATGTCTAGCTCAGGAGTGTGTAATACACAATC	2700
Dd		2660	ACTGTGATGGGCTTGGAGAACCTTTATGTCTAGCTCAGGAGTGTGTAATACACAATC	2719
OY		2701	GGCACCTGTGATCTAGCTCAAGGTTTTGTAACACACCAATCAGCACCCCTGTGTAGCTC	2760
Dd		2720	GGCACCTGTGATCTAGCTCAAGGTTTTGTAACACACCAATCAGCACCCCTGTGTAGCTC	2779
OY		2761	AGGGTATGTGAATGACCAATCGACAGCTGTATCTGGCTACTTTCAITGGGCATCCCTGT	2820
Dd		2780	AGGGTATGTGAATGACCAATCGACAGCTGTATCTGGCTACTTTCAITGGGCATCCCTGT	2839
OY		2821	GAAAGAGACACCAACAGGCTTTGTGTGAGCAATAAAGCTTCTACACCTGGGGGAGAGT	2880
Dd		2840	GAAAGAGACACCAACAGGCTTTGTGTGAGCAATAAAGCTTCTACACCTGGGGGAGAGT	2899
OY		2881	GCGGTGATCCGAANAAGAGACTCAGCGAAGGGAATTAAGGTTGGGCGCTTTTATAGAT	2940

Db	2900	GGGCTGAGTCCGAAAAAGAGCTCAGCCGAAAGGAGATAAAGGTGGGGCCGTTTATAGAT	2959
QY	2941	TTGGGTAGCTAAAGAAAAATTACAGTCAAAAGGGGGTTGTCTCTGGCGGGCAGAGTGG	3000
Db	2960	TTGGGTAGCTAAAGAAAAATTACAGTCAAAAGGGGGTTGTCTCTGGCGGGCAGAGTGG	3019
QY	3001	GGGGTCGCAAGGTGCTCAGTGGGGTCTTTTGAAGCCAGGATGAGCCAGAAAAAGACT	3060
Db	3020	GGGGTCGCAAGGTGCTCAGTGGGGTCTTTTGAAGCCAGGATGAGCCAGAAAAAGACT	3079
QY	3061	TTTCAACAGTATGTCTATCAATTAAAGCAAGGACCCGCGCATTTACACTCTTTTGTGTG	3120
Db	3080	TTTCAACAGTATGTCTATCAATTAAAGCAAGGACCCGCGCATTTACACTCTTTTGTGTG	3139
QY	3121	GAATGTCAATGTTAAAGTTGGGGCGGGCAATTCACCTCTTTTGTGATTTCTAGTTAC	3180
Db	3140	GAATGTCAATGTTAAAGTTGGGGCGGGCAATTCACCTCTTTTGTGATTTCTAGTTAC	3199
QY	3181	TTTCAAGCCATCTGGGCGTATATGTGCAAGTTACAGGGGATCGATGGCTTGGTGGCT	3240
Db	3200	TTTCAAGCCATCTGGGCGTATATGTGCAAGTTACAGGGGATCGATGGCTTGGTGGCT	3259
QY	3241	CAGAGGCTTGACAGCTACTCTGTGTGGGCTTGGAGAACTTTTGTGTGACACTCTGAT	3300
Db	3260	CAGAGGCTTGACAGCTACTCTGTGTGGGCTTGGAGAACTTTTGTGTGACACTCTGAT	3319
QY	3301	CTAGTTATCTAGTGGGGAGCTGGAGAACTTTTGTGTACTCTAGGGATGTAAAGCA	3360
Db	3320	CTAGTTATCTAGTGGGGAGCTGGAGAACTTTTGTGTACTCTAGGGATGTAAAGCA	3379
QY	3361	CCAACTCAGCGCCCTGTCAAAAACAGACACTGGGCTTACCAATCAGCAGGATGTGGTGG	3420
Db	3380	CCAACTCAGCGCCCTGTCAAAAACAGACACTGGGCTTACCAATCAGCAGGATGTGGTGG	3439
QY	3421	GGCCAGATTAAGAAATAAAGCAGGCTCCGAGCCAGACAGTGGCAACGGCCACAGTCC	3480
Db	3440	GGCCAGATTAAGAAATAAAGCAGGCTCCGAGCCAGACAGTGGCAACGGCCACAGTCC	3499
QY	3481	CTATCACAATATGGCAGCTTGTCTTTTCTGTGTGCGATTAATCTTGTACTGTCTG	3540
Db	3500	CTATCACAATATGGCAGCTTGTCTTTTCTGTGTGCGATTAATCTTGTACTGTCTG	3559
QY	3541	CTTTTGGGCTCCACACTGCTTTTATAGAGCTGTAAACACTCACACAGAAAGTCTGACGTT	3600
Db	3560	CTTTTGGGCTCCACACTGCTTTTATAGAGCTGTAAACACTCACACAGAAAGTCTGACGTT	3619
QY	3601	ACTCTGAAGCCTTAAGACACAGAGCCACCGGGAGGATGAACAACCTCCGGCCGCT	3660
Db	3620	ACTCTGAAGCCTTAAGACACAGAGCCACCGGGAGGATGAACAACCTCCGGCCGCT	3679
QY	3661	GGCTTAAAGGTATTAACACTCACCGCGGAAGGTCTGCAGCTTCACTCCTCAGCCAGCAGA	3720
Db	3680	GGCTTAAAGGTATTAACACTCACCGCGGAAGGTCTGCAGCTTCACTCCTCAGCCAGCAGA	3739
QY	3721	CCACGAACCCACAGAAAGAGAAACTCGAACAACATCTGAACATCGAAGAGAACAACT	3780
Db	3740	CCACGAACCCACAGAAAGAGAAACTCGAACAACATCTGAACATCGAAGAGAACAACT	3799
QY	3781	CCAGATGACACACCTTAAAGAGCTGTAAACACTCACCTGCGAGGGTCCGGGCTTCTTCTG	3840
Db	3800	CCAGATGACACACCTTAAAGAGCTGTAAACACTCACCTGCGAGGGTCCGGGCTTCTTCTG	3859
QY	3841	AAAGTCAGTGAACCAAGCAGCTACACAGTTTGGACACCAAGCCAGAGTTTGAGATAGC	3900
Db	3860	AAAGTCAGTGAACCAAGCAGCTACACAGTTTGGACACCAAGCCAGAGTTTGAGATAGC	3919
QY	3901	CTGGGCAACATGATGAAGTGCCTGTGCAAAAAAATAAATAAATAAATAAATAAATAAATAA	3960
Db	3920	CTGGGCAACATGATGAAGTGCCTGTGCAAAAAAATAAATAAATAAATAAATAAATAAATAA	3979
QY	3961	AGCATGTGTGTCCTGTGTGTCACAGTACACCGGAGGCTAAATGTGAGAGATGCT	4020

Dh 3980 AGATGGTGGTCCGTGCTGTGTCACCGGGAGGCTAAAGTGGAGGATGCGCT 4039
Qy 4021 TGAGCCCTGGAGGTGAAGACTGCGAGTGTATTTGTACCAAGCCCTTAGCTGGG 4080
Dh 4040 TGAGCCCTGGAGGTGAAGACTGCGAGTGTATTTGTACCAAGCCCTTAGCTGGG 4099
Qy 4081 GGACAGACTAGACCCCTGTTCCCTCCGCAAAAAATTTGACAAAGGTATTAAGAGT 4140
Dh 4100 GGACAGACTAGACCCCTGTTCCCTCCGCAAAAAATTTGACAAAGGTATTAAGAGT 4159
Qy 4141 GCGTGAATATGGCTAGGGGCGAGTGGCTATGCTGTAAATCCGACACTTTGGGAACGAG 4200
Dh 4160 GCGTGAATATGGCTAGGGGCGAGTGGCTATGCTGTAAATCCGACACTTTGGGAACGAG 4219
Qy 4201 GCGGGGGGCTACCTAAGTTCAGAGAGTGTGAGACAGCCTGGCCAAATGAGAAAGCC 4260
Dh 4220 GCGGGGGGCTACCTAAGTTCAGAGAGTGTGAGACAGCCTGGCCAAATGAGAAAGCC 4279
Qy 4261 ATCTCTCTAAAAATTAACAAATTAAGCGGGGCTGGGGGCGAGTGGGAGCATGGCTGTAA 4320
Dh 4280 ATCTCTCTAAAAATTAACAAATTAAGCGGGGCTGGGGGCGAGTGGGAGCATGGCTGTAA 4339
Qy 4321 TCCAGCTACTCAGAGAGCTGAGGCGAGAGATCACTTGAACCCAGAGGCGGGGTTCG 4380
Dh 4340 TCCAGCTACTCAGAGAGCTGAGGCGAGAGATCACTTGAACCCAGAGGCGGGGTTCG 4399
Qy 4381 AGTGAAGCGAGATGTGCCATTTGCACTCCACCTCCAGCTGGGCGCAAGAGCCAA 4440
Dh 4400 AGTGAAGCGAGATGTGCCATTTGCACTCCACCTCCAGCTGGGCGCAAGAGCCAA 4459
Qy 4441 CTCTGTCTAAAAATTAACAAATTAAGCGGGGCTGGGGGCGAGTGGGAGCATGGCTGTAA 4500
Dh 4460 CTCTGTCTAAAAATTAACAAATTAAGCGGGGCTGGGGGCGAGTGGGAGCATGGCTGTAA 4519
Qy 4501 TTGGCAGGCAACATGTTTAAGAAATGTGAGAGCTCTGCTTCCATGATGCTGTAAAAAC 4560
Dh 4520 TTGGCAGGCAACATGTTTAAGAAATGTGAGAGCTCTGCTTCCATGATGCTGTAAAAAC 4579
Qy 4561 CACCCTTAAGGCGCAGGTGCACTGCTATGCTTAATCCAGCACTTTGGGAGGCGAG 4620
Dh 4580 CACCCTTAAGGCGCAGGTGCACTGCTATGCTTAATCCAGCACTTTGGGAGGCGAG 4639
Qy 4621 GCGGGTGGATCACCCTGAGGTGAGAGTTCGAGACAGCCTGACCAACCAATGGTGAAT 4680
Dh 4640 GCGGGTGGATCACCCTGAGGTGAGAGTTCGAGACAGCCTGACCAACCAATGGTGAAT 4699
Qy 4681 CCCACCTCTACTAAAAATTAACAAATTAAGATGAGCATGGTGTGATGCCCTGAATCCAC 4740
Dh 4700 CCCACCTCTACTAAAAATTAACAAATTAAGATGAGCATGGTGTGATGCCCTGAATCCAC 4759
Qy 4741 CTACTTTGGAGGCTGAGGCGAGAAATCACTAAGAACAGGAGGCGAGGTTGTATGAG 4800
Dh 4760 CTACTTTGGAGGCTGAGGCGAGAAATCACTAAGAACAGGAGGCGAGGTTGTATGAG 4819
Qy 4801 CCGAGATCGTGCCTATTCAGCTCCAGCCTGAGCAATGAGCAAACTCTCAAAAAAAC 4860
Dh 4820 CCGAGATCGTGCCTATTCAGCTCCAGCCTGAGCAATGAGCAAACTCTCAAAAAAAC 4879
Qy 4861 AACAAACAAAAACCACTCTACTCCAGAGGAGCTGGGTACAGAGCTGGGCCACATCAGT 4920
Dh 4880 AACAAACAAAAACCACTCTACTCCAGAGGAGCTGGGTACAGAGCTGGGCCACATCAGT 4939
Qy 4921 GCAAGGTGCTGAGGCGCAGAGACTTAAGGCGAGCTGCGAGAGCCGGGAGCAATACAGTG 4980
Dh 4940 GCAAGGTGCTGAGGCGCAGAGACTTAAGGCGAGCTGCGAGAGCCGGGAGCAATACAGTG 4999
Qy 4981 TGTAGATCAAGTGTGTGATCAGACGCTCCCTGCATTTGTTGACACACAGGAGGCGCCCA 5040
Dh 5000 TGTAGATCAAGTGTGTGATCAGACGCTCCCTGCATTTGTTGACACACAGGAGGCGCCCA 5059
Qy 5041 AGCACAGAGATGGCCCATTCAGTCAACACATCCACTTCTCATCCAGAGATGTCTGTTT 5100
Dh 5060 AGCACAGAGATGGCCCATTCAGTCAACACATCCACTTCTCATCCAGAGATGTCTGTTT 5119

Qy 5101 CTGGGACAGCGTGGGTAAATTAAGACAGAGGTGACACTTTGGGTGTGCTCAGTCAGAC 5160
Dh 5120 CTGGGACAGCGTGGGTAAATTAAGACAGAGGTGACACTTTGGGTGTGCTCAGTCAGAC 5179
Qy 5161 TGCCCGCAGAGGCTTGTGGCTGTAGAAAAAGCTTCAAGGCTTAGGCGGGCAGGTGGC 5220
Dh 5180 TGCCCGCAGAGGCTTGTGGCTGTAGAAAAAGCTTCAAGGCTTAGGCGGGCAGGTGGC 5239
Qy 5221 TCAGCGCTGTAAATCCACACTTTGGAGGCGCGAGGCGGTGATCAGAGGTCAAGAGA 5280
Dh 5240 TCAGCGCTGTAAATCCACACTTTGGAGGCGCGAGGCGGTGATCAGAGGTCAAGAGA 5299
Qy 5281 TCGTAGCATTCTGGCTTAACAGGTGAAGAACCCCGCTCTACTAAAAATNCAAAAAATTTGG 5340
Dh 5300 TCGTAGCATTCTGGCTTAACAGGTGAAGAACCCCGCTCTACTAAAAATNCAAAAAATTTGG 5359
Qy 5341 CCGGCGATGTTGGGCGGACCTGTAGTTCAGACTCTCGGAGGCTGAGGAGAGAAATG 5400
Dh 5360 CCGGCGATGTTGGGCGGACCTGTAGTTCAGACTCTCGGAGGCTGAGGAGAGAAATG 5419
Qy 5401 GCGTGAACCCGAGAGGCGAGAGTTCAGTGAAGCGAGATCGGCCACTGACCTCCAGCT 5460
Dh 5420 GCGTGAACCCGAGAGGCGAGAGTTCAGTGAAGCGAGATCGGCCACTGACCTCCAGCT 5479
Qy 5461 GCGGCGACAGACAGACTCCATCTGGAAGAAAAAGAAAAAGTTCAAGTGTGAGCCAGA 5520
Dh 5480 GCGGCGACAGACAGACTCCATCTGGAAGAAAAAGAAAAAGTTCAAGTGTGAGCCAGA 5539
Qy 5521 GCGCGAGCTGTAAATTTGTACATTACATGACCTTGGGCAAGGACCTTCCCTGGC 5580
Dh 5540 GCGCGAGCTGTAAATTTGTACATTACATGACCTTGGGCAAGGACCTTCCCTGGC 5599
Qy 5581 CCAGTTCACGGGGTGTGAATGACTCCAAAGTCCCTTCAGACATTAAGCTGCAATGTTTC 5640
Dh 5600 CCAGTTCACGGGGTGTGAATGACTCCAAAGTCCCTTCAGACATTAAGCTGCAATGTTTC 5659
Qy 5641 TAAATGGAAGATGGGCACTTTCCCTCTCTACCCGACCCGCTGTCCACTTCAAGT 5700
Dh 5660 TAAATGGAAGATGGGCACTTTCCCTCTCTACCCGACCCGCTGTCCACTTCAAGT 5719
Qy 5701 GAATGACAGGGAAGTCACTGTCCTCCATCCCGAGTTCCAAAGGCCCTTGGGGACCTTAC 5760
Dh 5720 GAATGACAGGGAAGTCACTGTCCTCCATCCCGAGTTCCAAAGGCCCTTGGGGACCTTAC 5779
Qy 5761 TGTCAAGGTGCTGACAGAGAGTGAAGGTGACAGTCAAGTGCCTTCGAAGGCTTTG 5820
Dh 5780 TGTCAAGGTGCTGACAGAGAGTGAAGGTGACAGTCAAGTGCCTTCGAAGGCTTTG 5839
Qy 5821 CCTCATTTGGGACAGACATCCGGTTCCTCTGCGCTCAACCGGANTCTAAGGGGCTTAGC 5880
Dh 5840 CCTCATTTGGGACAGACATCCGGTTCCTCTGCGCTCAACCGGANTCTAAGGGGCTTAGC 5899
Qy 5881 CGAATGAGTCAATGGGGGCGGGGGGTTCTGGGGGAATTCACAGCTTAATCAACTTGGGA 5940
Dh 5900 CGAATGAGTCAATGGGGGCGGGGGGTTCTGGGGGAATTCACAGCTTAATCAACTTGGGA 5959
Qy 5941 CAGGACAGCTGGAACCTTGTGATGGTGCCTATCCAAATGTGGGGTGGGACAGCCAA 6000
Dh 5960 CAGGACAGCTGGAACCTTGTGATGGTGCCTATCCAAATGTGGGGTGGGACAGCCAA 6019
Qy 6001 GACCCAATGTCTTATCTCAGAGTAGGGCTCAAGAGTCTCCAGACAGGACCTTCGG 6060
Dh 6020 GACCCAATGTCTTATCTCAGAGTAGGGCTCAAGAGTCTCCAGACAGGACCTTCGG 6079
Qy 6061 AGAGTTTGGGGTGAAGTGGAGCAACAGGCTCTTTTCTTCTTGAATTTGGG 6120
Dh 6080 AGAGTTTGGGGTGAAGTGGAGCAACAGGCTCTTTTCTTCTTGAATTTGGG 6139
Qy 6121 GCGTTGGGGGACAGGCTTGAAGATCCAAAGGAGGGGCAAGAGCACTCCCCACAAAG 6180
Dh 6140 GCGTTGGGGGACAGGCTTGAAGATCCAAAGGAGGGGCAAGAGCACTCCCCACAAAG 6199

QY	6181	TCTGCCAGAGCAGAGAGACCCGCTCAGTCCACTTCCGCCACAGGCCT	6235
Db	6200	TCTGCCAGAGCAGAGAGAGACCCGCTCAGTCCACTTCCGCCACAGGCCT	6254
RESULT 5	AC090844/C		
LOCUS	AC090844	227857 bp	DNA
DEFINITION	Homo sapiens chromosome 17, clone RP11-387H17, complete sequence.		
ACCESSION	AC090844		
VERSION	AC090844.7	GI:22539183	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	Bliren,B., Nusbaum,C. and Lander,E.		
TITLE	Homo sapiens chromosome 17, clone RP11-387H17		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 227857)		
AUTHORS	Bliren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barne,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Campoliano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgibbon,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., Larocque,K., Lamazares,R., Landers,T., Lehoccky,J., Levine,R., Liu,G., Maclean,C., McDonald,P., Margulis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrim,J., Menus,L., Mhova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunhngang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,M., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 227857)		
AUTHORS	Bliren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barne,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgibbon,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Graham,L., Grand-pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., McDonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Mhova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunhngang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zalnoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	4 (bases 1 to 227857)		
AUTHORS	Bliren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barne,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgibbon,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Graham,L., Grand-pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., McDonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Mhova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunhngang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zalnoun,J., Zembek,L., Zimmer,A. and Zody,M.		

TITLE	JOURNAL	COMMENT
Direct Submission	Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	On Aug 29, 2002 this sequence version replaced gi:22539183. All repeats were identified using RepeatMasker: http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center	Center: Whitehead Institute/ MIT Center for Genome Research	Center code: WIR
Web site: http://www-seq.wi.mit.edu	Contact: sequence.submissions@genome.wi.mit.edu	Project Information
Center project name: H12018	Center clone name: 387_H_17	
Location/Qualifiers	1..227857	
/organism="Homo sapiens"	/mol_type="genomic DNA"	/db_xref="taxon:9606"
/chromosome="17"	/map="17"	/clone="RP11-387H17"
/clone_lib="RP11-387H17"	/complement(4..40)	
/rpt_family="L1MB8"	41..348	
/rpt_family="AluX"	/complement(349..456)	
/rpt_family="L1MB8"	/complement(514..824)	
/rpt_family="AluX"	3751..3913	
/rpt_family="MIR"	/complement(3961..4285)	
/rpt_family="AluX"	/complement(4288..4570)	
/rpt_family="AluX"	5865..5908	
/rpt_family="AluX"	6880..7112	
/rpt_family="L2"	/complement(9578..9582)	
/note="<30 qual SINGL region"	/complement(9650..9654)	
/note="<30 qual SINGL region"	/complement(10553..10666)	
/rpt_family="MIR3"	/complement(10698..10994)	
/rpt_family="AluY"	/complement(11328..11629)	
/rpt_family="AluX"	/complement(11733..12049)	
/rpt_family="AluX"	/complement(12097..12319)	
/rpt_family="AluX"	/complement(12331..12944)	
/rpt_family="MIR5"	/complement(12764..12773)	

```

repeat_region      /note="<30 qual SNGL region"
12945. .13393
/rpl_family="LTR7"
complement(13154. .13158)
/note="<30 qual SNGL region"
13293. .13339
/note="single clone coverage"
13307. .13311
/note="<30 qual single clone coverage"
13381. .13386
/note="<30 qual SNGL region"
complement(13394. .14319)
/rpl_family="PTR5"
13402. .13407
/note="<30 qual SNGL region"
complement(14320. .14385)
/rpl_family="Aluub"
complement(14396. .14552)
/rpl_family="MIR3"
14855. .15000
/rpl_family="L1ME"
complement(15072. .15371)
/rpl_family="Alusx"
15372. .15581
/rpl_family="MER58B"
complement(15637. .15814)
/rpl_family="Aluub"
complement(15815. .16120)
/rpl_family="Alusx"
complement(16121. .16257)
/rpl_family="Aluub"
16447. .16478
/rpl_family="L2"
16580. .16863
/rpl_family="AluO"
16870. .16896
/rpl_family="(TAAA)n"
16899. .17217
/rpl_family="MSTA"
complement(17244. .17412)
/rpl_family="Aluub"
complement(17413. .17709)
/rpl_family="AlusC"
complement(17711. .18000)
/rpl_family="Aluy"
complement(18001. .18132)
/rpl_family="Aluub"
18219. .18259
/rpl_family="L1MC4"
complement(18360. .18386)
/rpl_family="FLAM_C"
18387. .18526
/rpl_family="L1MC4"
18541. .18845
/rpl_family="Alusx"
18897. .19197
/rpl_family="Alusx"
19637. .20125
/rpl_family="MLT2A2"
complement(20626. .20736)
/rpl_family="Tigger1"

```

Query Match 97.1% Score 6051.2; DB 9; Length 227857;
 Best Local Similarity 99.4% Pred. No. 0;
 Matches 6201; Conservative 0; Mismatches 23; Indels 16; Gaps 12;

```

QY 1 GATCATTGAGACAGTATGATCAAGACGAGCTGGGAGCATAGGAGACTGTCTCTACG 60
DB 16197 GATCATTGAGACAGTATGATCAAGACGAGCTGGGAGCATAGGAGACTGTCTCTACG 16138
QY 61 AAAAAATTAATTAATGAGCGGAGCATGAGGCTCAGCTGTATATCCCTGAACCTTTGGG 120
DB 16137 AAAAAATTAATTAATGAGCGGAGCATGAGGCTCAGCTGTATATCCCTGAACCTTTGGG 16078

```

```

QY 121 ACATCAAGCAAGTGGATCATCTTGGAGTCAGAGTTGCGAGACTAGCTGGGCCACATGTT 180
DB 16077 ACATCAAGCAAGTGGATCATCTTGGAGTCAGAGTTGCGAGACTAGCTGGGCCACATGTT 16018
QY 181 GAAACCTTATCTCCATAAAAAATTAACCAAGCATGCTGGCAGGCACTGTGA 240
DB 16017 GAAACCTTATCTCTACT-AAAAATACAAAAATTAACCAAGCATGCTGGCAGGCACTGTGA 15959
QY 241 ATCCGGCTACTCAGAGGCTGAGGAGAGATACCTTGAACCCAGAGGCGGAGTTG 300
DB 15958 ATCCGGCTACTCAGAGGCTGAGGAGAGATACCTTGAACCCAGAGGCGGAGTTG 15899
QY 301 CAGTGAAGTGAATACACCACTGACCTGACCTGGGAGGAGAGCAAGATCATATC 360
DB 15898 CAGTGAAGTGAATACACCACTGACCTGACCTGGGAGGAGAGCAAGATCATATC 15839
QY 361 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 15838 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15779
QY 421 CTACTCAGAGGCTGAGGAGGAGATCATCTTGAACCTGGGAGGAGGCTCAAGGCTACAGTGA 480
DB 15778 CTACTCAGAGGCTGAGGAGGAGATCATCTTGAACCTGGGAGGAGGCTCAAGGCTACAGTGA 15720
QY 481 GCCAAGATCATGCCACTACCTCCAGCCTGGGAGCAGAGAGAGACCCCTGTCTTAAAAA 540
DB 15719 GCCAAGATCATGCCACTACCTCCAGCCTGGGAGCAGAGAGAGACCCCTGTCTTAAAAA 15660
QY 541 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
DB 15659 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15603
QY 601 ATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
DB 15602 ATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15543
QY 661 ATGCTCTGTGCACAAATCACTCTGCGCTGCTTGTACACAAAGAGCTTAACAT 720
DB 15542 ATGCTCTGTGCACAAATCACTCTGCGCTGCTTGTACACAAAGAGCTTAACAT 15483
QY 721 ACATCAAGCAAGTGGATCATCTTGGAGTCAGAGTTGCGAGACTAGCTGGGCCACAT 780
DB 15482 ACATCAAGCAAGTGGATCATCTTGGAGTCAGAGTTGCGAGACTAGCTGGGCCACAT 15423
QY 781 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 837
DB 15422 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15363
QY 838 CGCGCATCGTCACGCGCTGTAATTCACACACTTGGGAGGCTGAGGAGGAGATCACT 897
DB 15362 CGCGCATCGTCACGCGCTGTAATTCACACACTTGGGAGGCTGAGGAGGAGATCACT 15303
QY 898 GAGATCAACAGTTCGAGACAGCAGCTGGCCAAATAGCAAAACCCATTTCTTAATAAT 957
DB 15302 GAGATCAACAGTTCGAGACAGCAGCTGGCCAAATAGCAAAACCCATTTCTTAATAAT 15243
QY 958 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1017
DB 15242 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15183
QY 1018 GCAGAGAAATGCTTGAACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1077
DB 15182 GCAGAGAAATGCTTGAACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15123
QY 1078 CACTTCACAGCTGGGAGAGAGTGAAGTTCGTCACAG-AAAAAATTAATTAATTAATTAAT 1136
DB 15122 CACTTCACAGCTGGGAGAGAGTGAAGTTCGTCACAG-AAAAAATTAATTAATTAATTAAT 15063
QY 1137 CCATTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1196
DB 15062 CCATTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15003

```

QY 1197 GCATACCTGAGAGTGTGCTGTGTCACAGACATACACTTCCATTTAACTAGA 1256
|||||
Db 15002 GCATACCTGAGAGTGTGCTGTGTCACAGACATACACTTCCATTTAACTAGA 14943
QY 1257 CACTACCAAGTTCACATCCAGAGAGGTTTTTTTTTACAAATCTACACTCCCCAGCAAC 1316
|||||
Db 14942 CACTACCAAGTTCACATCCAGAGAGGTTTTTTTTTACAAATCTACACTCCCCAGCAAC 14883
QY 1317 AATGAGAGTTACTCCAGATCTTTACAAAGATGCTTAAAGCCAGTACAGATGAAAC 1376
|||||
Db 14882 AATGAGAGTTACTCCAGATCTTTACAAAGATGCTTAAAGCCAGTACAGATGAAAC 14823
QY 1377 AGAATGGAGGAGGAGAGCTGCCAGGCCCTTTACCACTTGAATAAATTAAGTGAAGCC 1436
|||||
Db 14822 AGAATGGAGGAGGAGAGCTGCCAGGCCCTTTACCACTTGAATAAATTAAGTGAAGCC 14763
QY 1437 TTCTGATCTGGAGAGATGATTAAGAGGAGGCTCTGAGAGCTGCCCTGTAGATCAC 1496
|||||
Db 14762 TTCTGATCTGGAGAGATGATTAAGAGGAGGCTCTGAGAGCTGCCCTGTAGATCAC 14703
QY 1497 TGTGACTTGTGAGCTTCACAGTCCAGTCTCAGCCCATGTGTCAATGGCCAGTAAATGAG 1556
|||||
Db 14702 TGTGACTTGTGAGCTTCACAGTCCAGTCTCAGCCCATGTGTCAATGGCCAGTAAATGAG 14644
QY 1557 CCTCAGCTCTGTTGGTCTTATTTCT-CCCCATGAGGAGGCTGAGTGGATTGAGCC 1615
|||||
Db 14643 CCTCAGCTCTGTTGGTCTTATTTCTCCCATGAGGAGGCTGAGTGGATTGAGCC 14584
QY 1616 GTTATTCAGAGATGTACAGCTTTCTTACAGAGAAATAGTGTCAAGAAACAGCAGGAGCT 1675
|||||
Db 14583 GTTATTCAGAGATGTACAGCTTTCTTACAGAGAAATAGTGTCAAGAAACAGCAGGAGCT 14524
QY 1676 TGGCAAGATGATTAACATGCAAAATCCTACCTGGCTCAGCCACCAAGTATGTTGTGATCT 1735
|||||
Db 14523 TGGCAAGATGATTAACATGCAAAATCCTACCTGGCTCAGCCACCAAGTATGTTGTGATCT 14464
QY 1736 TGAACAAGTTTTTCTACTTCTGTGAGGCCATCCCTGGCTACAAACACAGTGGTTGA 1795
|||||
Db 14463 TGAACAAGTTTTTCTACTTCTGTGAGGCCATCCCTGGCTACAAACACAGTGGTTGA 14404
QY 1796 CAGGATGAATGACG-AACTCCCTTACACTGTATATCCAGCACTTTGGAGGCCAAGGC 1854
|||||
Db 14403 CAGGATGAATGACGAAAGTGCCTTACACTGTATATCCAGCACTTTGGAGGCCAAGGC 14344
QY 1855 GGGTGGATGGCTTGAGACCTGAGAGGTGACAGCATGGCGGACATGCTCAGAGCCCTGTTTC 1914
|||||
Db 14343 GGGTGGATGGCTTGAGACCTGAGAGGTGACAGCATGGCGGACATGCTCAGAGCCCTGTTTC 14284
QY 1915 GCTCTGGGCGCTCTCTGCTGGGCTCCCACTTGGGTGAGCATTGAGAGCCCTTACG 1974
|||||
Db 14283 GCTCTGGGCGCTCTCTGCTGGGCTCCCACTTGGGTGAGCATTGAGAGCCCTTACG 14224
QY 1975 CCACGCTGCACTGTGGAGAGCCCTTTCTGGGCTGGCCAAAGGCAGAGCCGCTCCCTCA 2034
|||||
Db 14223 CCACGCTGCACTGTGGAGAGCCCTTTCTGGGCTGGCCAAAGGCAGAGCCGCTCCCTCA 14164
QY 2035 GCTTGGAGAGAGGTGTGAGAGGAGAGGCTTAACAGAGAAACCGGGGCTGCCAGAGGCTT 2094
|||||
Db 14163 GCTTGGAGAGAGGTGTGAGAGGAGAGGCTTAACAGAGAAACCGGGGCTGCCAGAGGCTT 14104
QY 2095 GCGGCGCAGCTGAGATTCCGGGTGGGCGTGGGCTTGGCGGCGCCGCACTCGGAGAGCG 2154
|||||
Db 14103 GCGGCGCAGCTGAGATTCCGGGTGGGCGTGGGCTTGGCGGCGCCGCACTCGGAGAGCG 14044
QY 2155 GGCACACCTGACAGGCGCCCGGGCAATGAGAGGCTTAAGCAACCCGGGCGACAGGCTCGGA 2214
|||||
Db 14043 GGCACACCTGACAGGCGCCCGGGCAATGAGAGGCTTAAGCAACCCGGGCGACAGGCTCGGA 13984
QY 2215 GGGTGTACTGTGGTGGCCCAAGAGTGCAGCCCGCGGCTGTGTGCTCGATTTCTCA 2274
|||||
Db 13983 GGGTGTACTGTGGTGGCCCAAGAGTGCAGCCCGCGGCTGTGTGCTCGATTTCTCA 13924
QY 2275 CTGGGCTTACAGAGCTTCCCGGGGCGAGGCTCGGGACCTCAGAGCCCGCATGCTCA 2334

Db 13923 CTGGGCTTACAGAGCTTCCCGGGGCGAGGCTCGGAGCTCAGAGCCCGCATGCTCA 13864
QY 2335 GCTCCCTCCATAGGAGCTCTGTGGGCGCCGAGACCTCCCGAGAGACACACCCCTGTCT 2394
|||||
Db 13863 GCTCCCTCCATAGGAGCTCTGTGGGCGCCGAGAGCTCCCGAGAGAGACACACCCCTGTCT 13804
QY 2395 CCACAGCGCCAGTCCCATGACACAGCAAGGCTGAGAAATGCGGGGCGACGAGCCGG 2454
|||||
Db 13803 CCACAGCGCCAGTCCCATGACACAGCAAGGCTGAGAAATGCGGGGCGACGAGCCGG 13744
QY 2455 GACTGGAGGACGCTACCCCTGAGAGCCCTGGTGGGAATCAGTGGGTGAAGCAGCTGG 2514
|||||
Db 13743 GACTGGAGGACGCTACCCCTGAGAGCCCTGGTGGGAATCAGTGGGTGAAGCAGCTGG 13684
QY 2515 GCTCTGAGTCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGAGATTCGTAATAC 2574
|||||
Db 13683 GCTCTGAGTCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGAGATTCGTAATAC 13624
QY 2575 ACCAATCAGACCTGTGTCTAGCTCAGGCTGTGTGAATGACCAATCCACTCTGTAT 2634
|||||
Db 13623 ACCAATCAGACCTGTGTCTAGCTCAGGTTCTGTGAATGACCAATCCACTCTGTAT 13564
QY 2635 CTAAGTACTGTGAATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGAGATTCGTAATAC 2694
|||||
Db 13563 CTAAGTACTGTGAATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGAGATTCGTAATAC 13504
QY 2695 CCAATCGGCACTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTCT 2754
|||||
Db 13503 CCAATCGGCACTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTCT 13444
QY 2755 TACCTAGGCTATGTGAATGACCAATCAGACCTGTATCTAGCTCAGGATTTCAATGGCAT 2814
|||||
Db 13443 TACCTAGGCTATGTGAATGACCAATCAGACCTGTATCTAGCTCAGGATTTCAATGGCAT 13384
QY 2815 CCGTGTGAAGAGACCAACAAAGGCTTTGTGAGCAATAAAGCTTCATACCTGGGT 2874
|||||
Db 13383 CCGTGTGAAGAGACCAACAAAGGCTTTGTGAGCAATAAAGCTTTCACTGTGGGT 13324
QY 2875 GCAAGTGGGCTGAGTCCGAAAGAGAGTCAAGCAAGGAGATGAAGGTGGGCGCTTTA 2934
|||||
Db 13323 GCAAGTGGGCTGAGTCCGAAAGAGAGTCAAGCAAGGAGATGAAGGTGGGCGCTTTA 13264
QY 2935 TAGGATTTGGGTAGTAAAGAAATTAACAGTCAAAAGGGGTTTCTCTGCGGGCAG 2994
|||||
Db 13263 TAGGATTTGGGTAGTAAAGAAATTAACAGTCAAAAGGGGTTTCTCTGCGGGCAG 13204
QY 2995 GAGTGGGGGTCCCAAGGTGCTCAGTGGGGGTCTTTTGAAGCAGAGATGAGCAGAGAA 3054
|||||
Db 13203 GAGTGGGGGTCCCAAGGTGCTCAGTGGGGGTCTTTTGAAGCAGAGATGAGCAGAGAA 13144
QY 3055 AGGACTTTCAGAAAGTAAATGATCAATTAAGCAAGAGACCCGCATTTACACTCTTTT 3114
|||||
Db 13143 AGGACTTTCAGAAAGTAAATGATCAATTAAGCAAGAGACCCGCATTTACACTCTTTT 13084
QY 3115 GTGGTGAATGATCAATTAAGTGGGAGGAGGCAATTCATCTCTTTGTATTTTC 3174
|||||
Db 13083 GTGGTGAATGATCAATTAAGTGGGAGGAGGCAATTCATCTCTTTGTATTTTC 13024
QY 3175 AGTTACTTACAGGCATCTGGGCGTAAATGTGCAAGTTTACAGGGGATTCAGTGGCT 3234
|||||
Db 13023 AGTTACTTACAGGCATCTGGGCGTAAATGTGCAAGTTTACAGGGGATTCAGTGGCT 12964
QY 3235 TGGGCTCAGAGGCTTGCACAGCTACTGTGTGGGGCTTTGGAGATGTTTGTGCAGACT 3294
|||||
Db 12963 TGGGCTCAGAGGCTTGCACAGCTACTGTGTGGGGCTTTGGAGATGTTTGTGCAGACT 12904
QY 3295 CTGTATCTAGTAAATCTAGTGGGAGGTGAGAACTTTGTGTAGCTCAGGAGATTTGA 3354
|||||
Db 12903 CTGTATCTAGTAAATCTAGTGGGAGGTGAGAACTTTGTGTAGCTCAGGAGATTTGA 12844
QY 3355 AAGCAACATTCAGGCGCCCTGTCAAAAACAGACACTCGGCTCAACCAATCAGAGATGT 3414
|||||

Db	12845	AAGCAGACCAATTCAGACGCCCTGTGTAAAAACAGACCACTGGCTTACCAATTCAGAGATGT	12784
QY	3415	GGGTGGGGCCAGATTAAGAGAAATAAAAAGCAGGCTGCCGAGCCAGCAGTGGCAACGCGAC	3474
Db	12783	GGGGGGGGCCAGATTAAGAGAAATAAAAAGCAGGCTGCCGAGCCAGCAGTGGCAACGCGAC	12724
QY	3475	AGGTCCCTATTCACCAATATGGCAGCTTGTGTTCTTTGCTGTTGGGATTAATCTTGCTAC	3534
Db	12723	AGGTCCCAATTCACCAATATGGCAGCTTGTGTTCTTTGCTGTTGGGATTAATCTTGCTAC	12664
QY	3535	TGCTCGCTTTTGGGTCACACAGCTTTATGAGCGTAAACATCAACCAAGAGGTGTC	3594
Db	12663	TGCTCGCTTTTGGGTCACACAGCTTTATGAGCGTAAACATCAACCAAGAGGTGTC	12604
QY	3595	AGCTTCACCTCCTAAGCCATAAGACACAGAGCCACCGGAGGAATGAACAATCCGCG	3654
Db	12603	AGCTTCACCTCCTAAGCCATAAGACACAGAGCCACCGGAGGAATGAACAATCCGCG	12544
QY	3655	CGCGCTCCCTTAAAGCTATTAACATTCACCGGAAAGTTGCAAGCTTCACTCCTCAGCA	3714
Db	12543	CGCGCTCCCTTAAAGCTATTAACATTCACCGGAAAGTTGCAAGCTTCACTCCTCAGCA	12484
QY	3715	GGCAGACCAAGAACCCACCAAGAAAGAACTCGGACACATCTGAACATTAAGAGAA	3774
Db	12483	GGCAGACCAAGAACCCACCAAGAAAGAACTCGGACACATCTGAACATTAAGAGAA	12424
QY	3775	CAAACTCAGATGCACACACCTTAAAGAGCTTAACATCTACGAGAGGTCGCGGCTTC	3834
Db	12423	CAAACTCAGATGCACACACCTTAAAGAGCTTAACTCATCTGAGAGGTCGCGGCTTC	12364
QY	3835	TTCTTGAAGTCACTGAGACCAAGACACTCAAGTTTCGGACACAAGCCAGAGTTTGAG	3894
Db	12363	TTCTTGAAGTCACTGAGACCAAGACACTCAAGTTTCGGACACAAGCCAGAGTTTGAG	12304
QY	3895	ATCAGCTGGGGCAACATGATGAATCCCTCTCTGCAAAAAAATTTACAAAAT	3954
Db	12303	ATCAGCTGGGGCAACATGATGAATCCCTCTCTGCG-AAAAAATTTACAAAAT	12245
QY	3955	TGCGCGAGCAATGGTGGCCGCTGCTGGTCCAGCTACGGGGAGGCTAAAGTGGAGG	4014
Db	12244	TGCGCGAGCAATGGTGGCTCGTGGTCCAGCTACGGGGAGGCTAAAGTGGAGG	12185
QY	4015	ATCGCTTGAGCCTGGGAGGTGAAGACTGCAGTGAAGCTGATTTGTACCAACAGCCCTCAG	4074
Db	12184	ATCGCTTGAGCCTGGGAGGTGAAGACTGCAGTGAAGCTGATTTGTACCAACAGCCCTCAG	12125
QY	4075	GCTGGGGGACACACTAGACCTGTTTCCCTCCGAAAAAATTTACAAAATGTAAATA	4134
Db	12124	GCTGGGGGACACACTAGACCTGTTTCCCTCCGAAAAAATTTACAAAATGTAAATA	12065
QY	4135	AGAGGTGCCGATATGGGCTAAGGGCGAGTGGCTCATAGCCGTAAATCCAGACCTTTGGGA	4194
Db	12064	AGAGGTGCCGATATGGGCTAAGGGCGAGTGGCTCATAGCCGTAAATCCAGACCTTTGGGA	12005
QY	4195	GGCGAGGCGGGCGGGTCACTAAAGTCAGAGATGTGAGACACAGCCTGGGCAACATGAGGA	4254
Db	12004	GGCGAGGCGGGCGGGTCACTAAAGTCAGAGATGTGAGACACAGCCTGGGCAACATGAGGA	11945
QY	4255	AAGCCATCTCTTAAAAAATACAAAATTTAGCCGGCTGTGGGGGAGTGTGGACATGC	4314
Db	11944	AAGCCATCTCTTAAAAAATACAAAATTTAGCCGGCTGTGGGGGAGTGTGGACATGC	11885
QY	4315	CTGTAAATCCAGTACTCAGAGAGCGGAGGCAAGAAATCACTTGAACCCAGAGGCGGC	4374
Db	11884	CTGTAAATCCAGTACTCAGAGAGCGGAGGCAAGAAATCACTTGAACCCAGAGGCGGC	11825
QY	4375	GGTTGCAGTGAGCCGAGATCTGGCATTTGCATCCACCCATCTCAGACCTGGGCAACAAGA	4434
Db	11824	GGTTGCAGTGAGCCGAGATCTGGCATTTGCATCCACCCATCTCAGACCTGGGCAACAAGA	11765
QY	4435	GCCAAACTCTGTTTAAAAAATTTAAAAAATGGCTGCTGACATATTAAGAGTGTGCAATG	4494
Db	11764	GCCAAACTCTGTTTAAAAAATTTAAAAAATGGCTGCTGACATATTAAGAGTGTGCAATG	11705

QY	4495	CAATAGTTGCCAGGCAACATGTTTAAGAAATGTGGAGCTCTCGCTTCATGTCCTGTTA	4554
Db	11704	CAATAGTTGCCAGGCAACATGTTTAAGAAATGTGGAGCTCTCGCTTCATGTCCTGTTA	11645
QY	4555	AAAACCAACCCCTCAAGGCGAAGGTGCAGTGGCTCATGCTCTAATCCAGACTTGGGAG	4614
Db	11644	AAAACCAACCCCTCAAGGCGAAGGTGCAGTGGCTCATGCTCTAATCCAGACTTGGGAG	11585
QY	4615	GCCGAGCGGGGTGATACCTGAGTGCAGAGTGTCCAGACCACTGACCACCATCATGG	4674
Db	11584	GCCGAGCGGGGTGATACCTGAGTGCAGAGTGTCCAGACCACTGACCACCATCATGG	11525
QY	4675	TGAATCCACCTCTACTAAAAATACAAATTAAGATGAGCATGGTGTGCATCCCTGTA	4734
Db	11524	TGAATCCACCTCTACTAAAAATACAAATTAAGATGAGCATGGTGTGCATCCCTGTA	11465
QY	4735	TCCCACTACTTGGGAGGCTGAGGCAAGAAAATCCTAGAACCAAGGAGCGGAGGTTGT	4794
Db	11464	TCCCACTACTTGGGAGGCTGAGGCAAGAAAATCCTAGAACCAAGGAGCGGAGGTTGT	11405
QY	4795	AGTAGCGCGAATGTGCGCAATTGCATCCAGCCCTGAGCAATGAGCAAACTCCATCTCA	4854
Db	11404	AGTAGCGCGAATGTGCGCAATTGCATCCAGCCCTGAGCAATGAGCAAACTCCATCTCA	11345
QY	4855	AAAAACAACAACAAAAACCACTCTCTACTCCCAAGGAGCTGGGTACAGAGCTGGGCCAC	4914
Db	11344	AAAAACAACAACAAAAACCACTCTCTACTCCCAAGGAGCTGGGTACAGAGCTGGGCCAC	11285
QY	4915	ATCAGTGCMAAGTGTCTGAGCCACAGAGCTAAGGCGGAGCTGCAGGACCGCGGACAGATA	4974
Db	11284	ATCAGTGCMAAGTGTCTGAGCCACAGAGCTAAGGCGGAGCTGCAGGACCGCGGACAGATA	11225
QY	4975	ACACTGTGTGATGATCACTGTGTGAGATCAACACCTCCCTGCATTTGGTGTACACACAGGGG	5034
Db	11224	ACACTGTGTGATGATCACTGTGTGAGATCAACACCTCCCTGCATTTGGTGTACACACAGGGG	11165
QY	5035	CCCCCAAGACACAGATAGTGGCCCCCATCACTGACACATCCATCTTCTACCCAGAGATGT	5094
Db	11164	CCCCCAAGACACAGATAGTGGCCCCCATCACTGACACATCCATCTTCTACCCAGAGATGT	11105
QY	5095	CTGTTTCTTGCGACGCTGGGGTAAATTTAGGACAGAAAGTGCACAGTCTTGGGTGGTACAG	5154
Db	11104	CTGTTTCTTGCGACGCTGGGGTAAATTTAGGACAGAAAGTGCACAGTCTTGGGTGGTACAG	11045
QY	5155	TCACACGTGCCCCCAAGGAGGCTTGTGGCTGTGTAGAAAACGTTTAGGCGCTTAGGCGGGCAC	5214
Db	11044	TCACACGTGCCCCCAAGGAGGCTTGTGGCTGTGTAGAAAACGTTTAGGCGCTTAGGCGGGCAC	10985
QY	5215	GGTGGCTCACGCCCTGTAAATCCACAGCACATTTGGAGAGGCGGAGGGGTGATCAGCAGGAC	5274
Db	10984	GGTGGCTCACGCCCTGTAAATCCACAGCACATTTGGAGAGGCGGAGGGGTGATCAGCAGGAC	10925
QY	5275	AGGAGATCTGTGACCATCTGGCTTAACACGGGTGAAAACCCGGTCTCTACTAAAAATACAAAA	5334
Db	10924	AGGAGATCTGTGACCATCTGGCTTAACACGGGTGAAAACCCGGTCTCTACTAAAAATACAAAA	10865
QY	5335	AATTGGCCGGGCGATGTGTGGCGGCGACCTGTAGTTCCAGCTACTCGGGAGCTGTAGGCAAG	5394
Db	10864	AATTGGCCGGGCGATGTGTGGCGGCGACCTGTAGTTCCAGCTACTCGGGAGCTGTAGGCAAG	10805
QY	5395	AGATATGCGGTGAACCCGAGAGGGAAGATTGGCAGTGAAGCGAGATGGGCGCACTGCATGAC	5454
Db	10804	AGATATGCGGTGAACCCGAGAGGGAAGATTGGCAGTGAAGCGAGATGGGCGCACTGCATGAC	10745
QY	5455	CAGCCTGGGCGACAGACCAAGACTCATCTGTGAAAAAGAAAAGAAAACCTTAGAGTCTGA	5514
Db	10744	CAGCCTGGGCGACAGACCAAGACTCATCTGTGAAAAAGAAAAGAAAACCTTAGAGTCTGA	10685
QY	5515	GCCAGAGGCCAGGCTGTAAATTTGTGCACTTACCATGACCTTGGGCAAGGCACTTCTTC	5574
Db	10684	GCCAGAGGCCAGGCTGTAAATTTGTGCACTTACCATGACCTTGGGCAAGGCACTTCTTC	10625

OY 5575 CTTGGCCCAAGTTTACAGGGGTTTGAATCGACTCCAGAGTCCCTTCCAGATTAAAGCTGCA 5634
 |||||||
 DB 10624 CTTGGCCCAAGTTTACAGGGGTTTGAATCGACTCCAGAGTCCCTTCCAGATTAAAGCTGCA 10555
 |||||||
 OY 5635 TGGTTCTAAGTGAAGAGATGGGGCAAGTTTCCCTCTCTCACCCAGCCCGCTGTCCACTT 5694
 |||||||
 DB 10564 TGGTTCTAAGTGAAGAGATGGGGCAAGTTTCCCTCTCTCACCCAGCCCGCTGTCCACTT 10505
 |||||||
 OY 5695 CAAGGTGAATGACCGGGAAGTACAGTCTCCCAATCCCGCACTTCCAAAGCCCTTGGGGA 5754
 |||||||
 DB 10504 CAAGGTGAATGACCGGGAAGTACAGTCTCCCAATCCCGCACTTCCAAAGCCCTTGGGGA 10445
 |||||||
 OY 5755 CCTACTGTCAAGGGTCTGACAGAGAGAGTGAAGTCAAGTGAAGCAATCCGCTCGAAG 5814
 |||||||
 DB 10444 CCTACTGTCAAGGGTCTGACAGAGAGAGTGAAGTCAAGTGAAGCAATCCGCTCGAAG 10385
 |||||||
 OY 5815 GTCTTGCTCATTTGCGGACAGACATCCGGTTTCTCTGCTTACCGGGATTCTAAGGGC 5874
 |||||||
 DB 10384 GTCTTGCTCATTTGCGGACAGACATCCGGTTTCTCTGCTTACCGGGATTCTAAGGGC 10325
 |||||||
 OY 5875 TTTAGCCGAATGAGTCAATGGGGGGGGGGGTTTCTGGGGAGTTCCTCCAGCTAATCAAC 5934
 |||||||
 DB 10324 TTTAGCCGAATGAGTCAATGGGGGGGGGGGTTTCTGGGGAGTTCCTCCAGCTAATCAAC 10265
 |||||||
 OY 5935 TTTGGACAGAGACAGCTTGAACCTTTCATGCTGCTATCAAGTGTGGGGTGGGACAGC 5994
 |||||||
 DB 10264 TTTGGACAGAGACAGCTTGAACCTTTCATGCTGCTATCAAGTGTGGGGTGGGACAGC 10205
 |||||||
 OY 5995 AGCCAAAGCCCAATGCTCTTATCTCAGTACAGGGCTCAGAGGTTCTCCACAGAGCAGC 6054
 |||||||
 DB 10204 AGCCAAAGCCCAATGCTCTTATCTCAGTACAGGGCTCAGAGGTTCTCCACAGAGCAGC 10145
 |||||||
 OY 6055 CTCCGAGAGATTTGGGGGTAGGAATGGGAGACACAGGCTTTTCTCTCTTGA 6114
 |||||||
 DB 10144 CTCCGAGAGATTTGGGGGTAGGAATGGGAGACACACCA-CTTCTTTTCTCTCTTGA 10086
 |||||||
 OY 6115 TTTGGGGGCTTTGGGGAGAGGCTTTCAGAAATCCCAAGAGAGAGGGGCAAGAGCACT-CC 6173
 |||||||
 DB 10085 TTTGGGGGCTTTGGGGAGAGGCTTTCAGAAATCCCAAGAGAGAGGGGCAAGAGCACTGCC 10026
 |||||||
 OY 6174 CCACAGTCTCCAGAGAGAGAGAGAGGAGACCCGAGCTGACACTGCTCCACAGAGC 6233
 |||||||
 DB 10025 CCGCAAGTCTGCGAGAGC-AGAGAGGAGAGCCCGGAGCTGACACTGCTCCACAGAGC 9967
 |||||||

RESULT 6
 AC102799/c 122132 bp DNA linear PRI 01-APR-2003
 LOCUS Homo sapiens chromosome 17, clone CTD-2248B4, complete sequence.
 AC102799
 AC102799.9 GI:29423944
 VERSION HTG.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 122132)
 AUTHORS Birren,B., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 17, clone CTD-2248B4
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 122132)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Hearford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,
 Lamasares,R., Landers,T., Lehoczký,J., Levine,R., Liu,G.,
 Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., Mopheeters,R., Meldrim,J.,

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Menes,L., Mhova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,M.J., Young,G.,
 Zainoun,J., Zemek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 122132)
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrim,J., Menes,L., Mhova,T., Mlenga,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Rieback,M., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zemek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (23-JAN-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 122132)
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrim,J., Menes,L., Mhova,T., Mlenga,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Rieback,M., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zemek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (01-APR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 1, 2003 this sequence version replaced gi:27877372.
 All repeats were identified using RepeatMasker:
 Smith,A.F.A. & Green,P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WtBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

 Project Information
 Center project name: L19697

 Center clone name: 2248_E_4

Location/Qualifiers
1. .122132

	repeat_region	/rpt_family="GC_rich"	18191..18211	
	repeat_region	/rpt_family="GC_rich"	18357..18458	
	repeat_region	/rpt_family="(CCCCG)n"	18651..18810	
	repeat_region	/rpt_family="MIR3"	19403..19442	
	repeat_region	/rpt_family="(TG)n"	complement(20426..20751)	
	repeat_region	/rpt_family="Alusx"	21241..21279	
	repeat_region	/rpt_family="(TCCC)n"	21752..21960	
	repeat_region	/rpt_family="AluJo"	complement(22195..22501)	
	repeat_region	/rpt_family="Aluy"	complement(23668..23962)	
	repeat_region	/rpt_family="Alusp"	24954..25095	
	repeat_region	/rpt_family="MERL15"	25126..25422	
	repeat_region	/rpt_family="Alusx"	complement(25496..25604)	
	repeat_region	/rpt_family="FLAN_A"	25809..25834	
	repeat_region	/rpt_family="(CNA)n"	complement(25851..26165)	
Query Match	Best Local Similarity	96.7%; Score 6032; DB 9; Length 122132;		
	Matches 6190; Conservativity	99.28; Pred. No. 0;	Mismatches 35; Indels 17; Gaps 12;	
Dy	1	GATCACTGGAGGACGTAGTTCAAGACCACCGTCGGGACGATAGGGAGACTGTCCTAGG	60	
Dd	72289	GATCACTGGAGGACGTAGTTCAAGACCACCGTCGGGACGATAGGGAGACTGTCCTAGG	72230	
Oy	61	AAAAATCAAAAATTATAGCCGGGCACTGTGCTCAACGTCGTAAATCCCTGAACCTTTGGG	120	
Dd	72229	AAAAATCAAAAATTATAGCCGGGCACTGTGCTCAACGTCGTAAATCCCTGAACCTTTGGG	72170	
Oy	121	ACATCANAGCAAGTGTATCATCTTGAGGTGAGGATTCGAGACTAGCCTGAGCAACATGGT	180	
Dd	72169	ACATCANAGCAAGTGTATCATCTTGAGGTGAGGATTCGAGACTAGCCTGAGCAACATGGT	72110	
Oy	181	GAAACCCCTATCTCCACATAAATAATTAACAATAATTAAGCCAGGATGTGGGAGGACCTGT	240	
Dd	72109	GAAACCCCTATCTCTACT-AAAAATATACAAAATTATAGCCAGGATGTGGGAGGACCTGT	72051	
Oy	241	ATCCGGGCTACTCAGGAGGCTGAGGCAAGGAATCACTTGAACCCAGAGGGGAGGTTG	300	
Dd	72050	ATCCGGGCTACTCAGGAGGCTGAGGCAAGGAATCACTTGAACCCAGAGGGGAGGTTG	71992	
Oy	301	CAGTAGCTGAGATCACACCACCTGCACCTCGGCTGGGTACAGAGCAAGACTTATCTC	360	
Dd	71990	CAGTAGCTGAGATCACACCACCTGCACCTCGGCTGGGTACAGAGCAAGACTTATCTC	71931	
Oy	361	AAAAAAAAATATAAATAATTAAGCCAGGATGTATGTACACACTCTATGTCTAG	420	
Dd	71930	AAAAAAAAAAAAAAAAAACAAAATAATTAAGCCAGGATGTATGTACACACTCTATGTCTAG	71871	
Oy	421	CTACTCGAGGCGTGGAGGTGGGAGGATCACTTGAACCTGGGGAGTCAAGGGCTACAGTA	480	
Dd	71870	CTACTCGAGGCGTGGAGGTGGGAGGATCACTTGAACCTGGGGAGTCAAGGGCTACAGTA	71812	
Oy	481	GCCAAGATCATGCCACTACACTCCAGCCTGGGGCAGAGAGAGACCTGTCTTAATAA	540	
Dd	71811	GCCAAGATCATGCCACTACACTCCAGCCTGGGGCAGAGAGAGACCTGTCTTAATAA	71752	
Oy	541	AATATATATATATAAGAAAAAACAGCTCTGTTATGTCTCCTGGTCAATCATACTACT	600	
Dd	71751	AATATATATATATAAGAAAAAACAGCTCTGTTATGTCTCCTGGTCAATCATACTACT	71695	

QY	601	ATGATATATAGTTGGCAAACTCCAAAGATCCAGATAGTCAATTTTTTATAGGCTTGCGGCGCT	660
Db	71694	ATGATATATAGTTGGCAAACTCCAAAGATCCAGATAGTCAATTTTTTATAGGCTTGCGGCGCT	716359
QY	661	ATGGTCTCTGCAAACTCACTCGGCGCTGCTTCTAGACACAAACACACTCTPAAACAT	720
Db	71634	ATGGTCTCTGCAAACTCACTCGGCGCTGCTTCTAGACACAAACACACTCTPAAACAT	71575
QY	721	ACATACATGAAATTTTTTATAGATCATCGAGATTTGAATTTTCATTTGATTTTTCATTTTAT	780
Db	71574	ACATACATGAAATTTTTTATAGATCATCGAGATTTGAATTTTCATTTGATTTTTCATTTTAT	71515
QY	781	AAAAATATCTTTTTAAAAATTTTTCCCTTAACATTTTAAAAAGTAAAGCCGCGCA--G	837
Db	71514	AAAAATATCTTTTTAAAAATTTTTCCCTTAACATTTTAAAAAGTAAAGCCGCGCGC	714553
QY	838	CGGGCCATTCGTACAGCGCTGTAAATTTCCAGACTTTTGGGAGGCTGAGAGGTGGGCGAGTCACTT	897
Db	71454	CGGGCCATTCGTACAGCGCTGTAAATTTCCAGACTTTTGGGAGGCTGAGAGGTGGGCGAGTCACTT	713959
QY	898	GAGATCAACAGTTTCGAGACAGCGCTGGCCAACTATACAAACCCCATTTCTACTATAAAT	957
Db	71394	GAGATCAACAGTTTCGAGACAGCGCTGGCCAACTATACAAACCCCATTTCTACTATAAAT	713359
QY	958	AAAAAATTTATGCTGGGCATATGCTGGTACACCTGTATCCAGCTACTTGGGAGGCTGAG	1017
Db	71334	AAAAAATTTATGCTGGGCATATGCTGGTACACCTGTATCCAGCTACTTGGGAGGCTGAG	712759
QY	1018	GCAGGAAATTCGCTTGAACCTGGGAAAGCGGAGGTTGTCAGTACAGCCAACTAATGTCACAG	1077
Db	71274	GCAGGAAATTCGCTTGAACCTGGGAAAGCGGAGGTTGTCAGTACAGCCAACTAATGTCACAG	71215
QY	1078	CACATCAAGCCTGGGTGACAGATGAGACTTCTGCTCAAGGAAAAAAGTGTAAAC	1137
Db	71214	CACATCAAGCCTGGGTGACAGATGAGACTTCTGCTCAAGGAAAAAAGTGTAAATGC	711555
QY	1138	CATTCTTAATTCAGTGTACATTCAGTGTACATCTCAGTGTGCGTACTCTGCTGAGG	1197
Db	71154	CATTCTTAATTCAGTGTGTACATTCAGTGTACATCTCAGTGTGCGTACTCTGCTGAGG	710959
QY	1198	CATTCCTGAGAGAGAGTGGCTGGGACAGAGACATPACATTTCCACTTAACATGAGAC	1257
Db	71094	CATTCCTGAGAGAGAGTGGCTGGGACAGAGACATPACATTTCCACTTAACATGAGAC	71035
QY	1358	ACTACCAAGTTGCCATCCAAAGAGAGTTTTTTTTTACAAATCTPACACTCCGCCAGCAAC	1317
Db	71034	ACTACCAAGTTGCCATCCAAAGAGAGTTTTTTTTTACAAATCTPACACTCCGCCAGCAAC	70975
QY	1318	AATGAGATTAATCTCCAGATCTCTTTCACAAAGATCTCTAAGCCAGTACAGATGAAACA	1377
Db	70974	AATGAGATTAATCTCCAGATCTCTTTCACAAAGATCTCTAAGCCAGTACAGATGAAACA	70915
QY	1378	GGAAGTGGAGGGGAGAACTGACAGCCCTCTPACCATGAGAAATACCTGGTAGAGCCT	1437
Db	70914	GGAAGTGGAGGGGAGAACTGACAGCCCTCTPACCATGAGAAATACCTGGTAGAGCCT	708555
QY	1438	TCTGGATGCTGGAAGATGTAATAACGGGGGCTCTCTGGAGGCTGCCCTGTGAGATCACT	1497
Db	70854	TCTGGATGCTGGAAGATGTAATAACGGGGGCTCTCTGGAGGCTGCCCTGTGAGATCACT	70795
QY	1498	GTCACCTTCGAGGCTCCAGTCCAGTCCAGGCCCCATGTGCATAGGCAAGTAAATGAGC	1557
Db	70794	GTCACCTTCGAGGCTCCAGTCCAG-CTCAGCCCCATGTGCATAGGCAAGTAAATGAGC	70738
QY	1558	CTTCACCTCTCTGTTTGGTCTTTTATCT-CCCCATGTGGGGCTTAAATCTTGATTAAGCGG	1616
Db	70735	CTTCACCTCTCTGTTTGGTCTTTTATCTCCCCCATGTGGGGCTTAAATCTTGATTAAGCGG	70678
QY	1617	TTATTCAGAGATGTACACCTTCTTTCGACAGGAAAGTGTGCACAGAAACAGCAGGGGCTT	1676
Db	70675	TTATTCAGAGATGTACACCTTCTTTCGACAGGAAAGTGTGCACAGAAACAGCAGGGGCTT	70616
QY	1677	GGCAAGATGATCTAATGCAAACTCTACCTCGGCTGAGCCACAGCTAGTCTGTGATCTT	1736

Db	70615	GGCAAGATGATCTAATGCAAAATCTTACCTGGCTCAGCCACACAGCTAAGTTCTTGATCTT	7055
OY	1737	GAACAAGTTTTTCACTTCTCTGAGGCAATCCCTTGGCTCAACAACACAGTTGGTTGAC	1796
Db	70555	GAACAAGTTTTTCCACTTCTCTGAGGCCATCCCTGGCTCAACAACACAGTTGGTTGAC	7049
OY	1797	AGATGAAATGAGC - AAGTCCCTTACACCTGTAAATCCACACACTTTGGAGGCCAAGGC	1855
Db	70495	AGATGAAATGAGCAAAAGTGCTTACACCTGTAAATCCACAGACTTTGGAGGCCAAGGC	7043
OY	1856	GGTGGATGGCTTGAGCCTGAGAGGTGACAGCATGCCGGCAGTCTCACAGCCTCGTTGC	1915
Db	70435	GGTGGATGGCTTGAGCCCTGAGAGGTGACAGCATGCCGGCAGTCTCTCACAGCCTCGTTGC	7037
OY	1916	CTCTCGGGGCGCTCTCTGCTGGGCTCCACTTGGGTGGAGACTTGAAGAGCCCTTCAGGC	1975
Db	70375	CTCTCGGGGCGCTCTCTGCTGGGCTCCACTTGGGTGGAGACTTGAAGAGCCCTTCAGGC	7031
OY	1976	CACCGCTGCACTGTGGAGGCCCTTTCTTGGGCTGGCCAGAGCCAGACCGGCTCCCTCAG	2035
Db	70315	CACCGCTGCACTGTGGAGGCCCTTTCTTGGGCTGGCCAGAGCCAGACCGGCTCCCTCAG	7025
OY	2036	CTTTCAGGGAGGTGTGAGGGAGAGGCTCAAGCAGGAACCGGGGCTTCGCACGGCGCTTG	2095
Db	70255	CTTTCAGGGAGGTGTGAGGGAGAGGCTCAAGCAGGAACCGGGGCTTCGCAGGGCGCTTG	7019
OY	2096	CGGGCCAGCTGGAATTCGGGTGGGCGGTGGGCTTGGGGGGCCCGCACTGSGAGACAGCG	2155
Db	70195	CGGGCCAGCTGGAATTCGGGTGGGCGGTGGGCTTGGGGGGCCCGCACTGSGAGACAGCG	7013
OY	2156	GCCAGCCCTGCGCAGAGCCCGGGGCAATGAGAGGCTTAGCACCCCGGGCCAGCGGCTGCGAG	2215
Db	70135	GCCAGCCCTGCGCAGAGCCCGGGGCAATGAGAGGCTTAGCACCCCGGGCCAGCGGCTGCGAG	7007
OY	2216	GGTGTACTGGGTGCCCCAGCAGTCCAGCCCGCGGGCGTGTGCTGGCTGATTTCTCAC	2275
Db	70075	GGTGTACTGGGTGCCCCAGCAGTCCAGCCCGCGGGCGTGTGCTGGCTGATTTCTCAC	7001
OY	2276	TGGGCTTTAGGAGGCTTCCCGCGGGGGAGGGCTGGGAGCTGCAGCCGCGCATGCTCGAG	2335
Db	70015	TGGGCTTTAGGAGGCTTCCCGCGGGGGAGGGCTGGGAGCTGCAGCCGCGCATGCTCGAG	6995
OY	2336	CCCTCCCTTCATGGGGCTCTGTGTGGGGCCGAGCCCTCCCGCAGAGCACAACCCCTGCTC	2395
Db	69955	CCCTCCCTTCATGGGGCTCTGTGTGGGGCCGAGCCCTCCCGCAGAGCACAACCCCTGCTC	6989
OY	2396	CACAGCGCCCACTGCCATTCGACACACGCAAGGGCTGAGAAATGGCGGGCCACAGCCGGG	2455
Db	69895	CACAGCGCCCACTGCCATTCGACACACGCAAGGGCTGAGAAATGGCGGGCCACAGCCGGG	6983
OY	2456	ACTGGCAGGGCAGTAAACCCCTGCACACCCCTGGGGCGGAATCCACTGTGGTGAAGCCAGTGGG	2515
Db	69835	ACTGGCAGGGCAGTAAACCCCTGCACACCCCTGGGGCGGAATCCCGTGGTGAAGCCAGTGGG	6977
OY	2516	CTCTGTAGTCTGTGTGAGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCGTAAATACA	2575
Db	69775	CTCTGTAGTCTGTGTGAGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCGTAAATACA	6971
OY	2576	CCAATCAGACACCTGTGTCTAAGCTCAGGGTCTGGAATGCACCAATCCACACTCTGTATC	2635
Db	69715	CCAATCAGACACCTGTGTCTAAGCTCAGGGTCTGGAATGCACCAATCCACACTCTGTATC	6965
OY	2636	TAGTACTCTGTATGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACAC	2695
Db	69655	TAGTACTCTGTATGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACAC	6959
OY	2696	CAATCGGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGACCCCTGTCTC	2755
Db	69595	CAATCGGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGACCCCTGTCTC	6953
OY	2756	AGCTCAGGGTATGTAATGACCACAATGACAGTCTGTATCTGGCTACTTTCATGGGCATC	2815

Dh 69535 AGCTCAGGGTATGTGAATGACCAACATCGACTGTATCTGGCTACTTTCATGGGCATC 69476
Oy 2816 CGTGTGAAGAGACCAACAGAGCTTGTGTGACCATTAAGCTTCTATCACTCGGGTG 2875
Db 69475 CGTGTGAAGAGACCAACAGAGCTTGTGTGACCAATTAAGCTTCTATCACTCGGGTG 69416
Oy 2876 CAGGTGGGCTGAGTCCGAAAAGAGAGTCCAGGAAAGGAGATTAAGGGTGGGCGCTTTAT 2935
Db 69415 CAGGTGGGCTGAGTCCGAAAAGAGAGTCCAGGAAAGGAGATTAAGGGTGGGCGCTTTAT 69356
Oy 2936 AGAATTTGGGTAGTAAAGAAAATTTACAGTCAAAAGGGGGTGTGTCTGTGGCGGCAGG 2995
Db 69355 AGAATTTGGGTAGTAAAGAAAATTTACAGTCAAAAGGGGGTGTGTCTGTGGCGGCAGG 69296
Oy 2996 AG-TGGGGGGTCCGAAAGGTGCTCAGTGGGGGTGCTTTTGAAGCCAGATTAAGCCGAGAA 3054
Db 69295 AGTTGGGGGGTCCGAAAGGTGCTCAGTGGGGGTGCTTTTGAAGCCAGGATGAGCCGAGAA 69236
Oy 3055 AGGACTTTCACAAAGGTAAATGTCAATTAAGGCAAGGACCCGCAATTTACACCTTTT 3114
Db 69235 AGGACTTTCACAAAGGTAAATGTCAATTAAGGCAAGGACCCGCAATTTACACCTTTT 69176
Oy 3115 GTGGTGAATGTCACTCACTTAAGTTGGGGCAGGGCATAATCACTTCTTTGTGATTTCTC 3174
Db 69175 GTGGTGAATGTCACTCACTTAAGTTGGGGCAGGGCATAATCACTTCTTTGTGATTTCTC 69116
Oy 3175 AGTACTTCAGGSCATCGGGCGTATATGTCAAGTTTACAGGGATTTGGATTCGCTGCT 3234
Db 69115 AGTACTTCAGGSCATCGGGCGTATATGTCAAGTTTACAGGGATTTGGATTCGCTGCT 69056
Oy 3235 TGGGCTCAGAGGCTTGACAGTACTCTGTGGGGCTTGAGAAATGTTTGTGTGCACACT 3294
Db 69055 TGGGCTCAGAGGCTTGACAGTACTCTGTGGGGCTTGAGAAATGTTTGTGTGCACACT 68996
Oy 3295 CTGTATCTAGTTAATCTAAGTGGGGAAGTGGAACCTTTGTGTCTAGTCTCAGGATTTGTA 3354
Db 68995 CTGTATCTAGTTAATCTAAGTGGGGAAGTGGAACCTTTGTGTCTAGTCTCAGGATTTGTA 68936
Oy 3355 AACGACCAATCAGGGCGCTTCGAAAACAGACCACTCGGCTCTACCATTCAGAGAGAT 3414
Db 68935 AACGACCAATCAGGGCGCTTCGAAAACAGACCACTCGGCTCTACCATTCAGAGAGAT 68876
Oy 3415 GGGTGGGGCAGATTAAGAAATTAAGAGCAGGCTGCCAGCAGCAGAGTGGCAACCGCAC 3474
Db 68875 GGGTGGGGCAGATTAAGAAATTAAGAGCAGGCTGCCAGCAGCAGAGTGGCAACCGCAC 68816
Oy 3475 AGGTCCCTATCCACAATATGGCAGCTTTGTTCTTGTGTGTGGATTAATCTTGTCTAC 3534
Db 68815 AGGTCCCTATCCACAATATGGCAGCTTTGTTCTTGTGTGTGGATTAATCTTGTCTAC 68756
Oy 3535 TGTCTGCTTTTGGGTCCACACTGCTTTTATGAGCTGTAACTACACGAGAGTCTGC 3594
Db 68755 TGTCTGCTTTTGGGTCCACACTGCTTTTATGAGCTGTAACTACACGAGAGTCTGC 68696
Oy 3595 AGCTTCACTCTGGAAGCCATTAAGACCAAGCAGCCAGCGGAGGAATGAACCACTCCGGC 3654
Db 68695 AGCTTCACTCTGGAAGCCATTAAGACCAAGCAGCCAGCGGAGGAATGAACCACTCCGGC 68636
Oy 3655 CGGCTGCTTAAGAGCTATAACACTCCGCGAAGTCTGTGAGCTTCACTCTTCAGCA 3714
Db 68635 CGGCTGCTTAAGAGCTATAACACTCCGCGAAGTCTGTGAGCTTCACTCTTCAGCA 68576
Oy 3715 GCGAGACCAAGACCCACAGAGAGAGAACTGCGAATCTGAACATTCAGAGAA 3774
Db 68575 GCGAGACCAAGACCCACAGAGAGAGAACTGCGAATCTGAACATTCAGAGAA 68516
Oy 3775 CAAACTCCAGATGACCACTTAAGAGCTTAACACTACAGCGAGGGTCCGGGCTTCC 3834
Db 68515 CAAACTCCAGATGACCACTTAAGAGCTTAACACTACAGCGAGGGTCCGGGCTTCC 68456
Oy 3835 TTCTTGAAGTCAAGTGAAGCAAGCACTCACCAGTTTCGAGACACAAGCCAGAGTTTGA 3894
Db 68455 TTCTTGAAGTCAAGTGAAGCAAGCACTCACCAGTTTCGAGACACAAGCCAGAGTTTGA 68396

Oy 3895 ATTCAGCTGGGCAACATGATGAATGCCCTGCTGCAAAAAAAAAAAAAAAAAATTACAAAT 3954
Db 68395 ATTCAGCTGGGCAACATGATGAATGCCCTGCTGCAAAAAAAAAAAAAAAAAATTACAAAT 68336
Oy 3955 TGGCGAGACATGATGGTCCGTGCTGCTGTGGTCCAGCTACGCGGAGAGGCTAAAGTGGAG 4014
Db 68335 TGGCGAGACATGATGGTCCGTGCTGCTGTGGTCCAGCTACGCGGAGAGGCTAAAGTGGAG 68276
Oy 4015 ATTCCTTGAACCTGGAGGTGAAGACTGACCTGTGATTTGAACACAGCCCTTGA 4074
Db 68275 ATTCCTTGAACCTGGAGGTGAAGACTGACCTGTGATTTGAACACAGCCCTTGA 68216
Oy 4075 GCTGGGGGACAGTGAAGACCTGTTTCCCTCCGCAAAAAAAAAATTGACAAAAGTGAATA 4134
Db 68215 GCTGGGGGACAGTGAAGACCTGTTTCCCTCCGCAAAAAAAAAATTGACAAAAGTGAATA 68156
Oy 4135 AGAGTGCCTGATATAGGTAGAGCGAGTGCATAGCTGTAAATCCAGCACTTTGGGA 4194
Db 68155 AGAGTGCCTGATATAGGTAGAGCGAGTGCATAGCTGTAAATCCAGCACTTTGGGA 68096
Oy 4195 GCCGAGCGGGCGGCTCACCTAAGTCAAGAGTGTGAACACAGCCTGGCAACATGGAGA 4254
Db 68095 GCCGAGCGGGCGGCTCACCTAAGTCAAGAGTGTGAACACAGCCTGGCAACATGGAGA 68036
Oy 4255 AAGCCATCTCTTCAAAAAATCAAAATTAAGCGGCTGTGGGGGAGTGTGGAGCATGC 4314
Db 68035 AAGCCATCTCTTCAAAAAATCAAAATTAAGCGGCTGTGGGGGAGTGTGGAGCATGC 67976
Oy 4315 CTGTATCCACAGCTACTCAGAGGCTGAGGCGAGAAATCACTTGAACCCAGAGAGCGGC 4374
Db 67975 CTGTATCCACAGCTACTCAGAGGCTGAGGCGAGAAATCACTTGAACCCAGAGAGCGGC 67916
Oy 4375 GGTTCAGTGAAGCCAGATCGTCCATTTGACTCCACCCACTCCAGCTGGCAACAAGA 4434
Db 67915 GGTTCAGTGAAGCCAGATCGTCCATTTGACTCCACCCACTCCAGCTGGCAACAAGA 67856
Oy 4435 GCCAAACCTGCTCT - AAAAAAAAAAAAAAAAAAGCTGCAATTAAGAGTGTGCA 4492
Db 67855 GCCAAACCTGCTCTTAAAAAAAAAAAAAAAAAGCTGCAATTAAGAGTGTGCA 67796
Oy 4493 TGCAATAGTTCAGAGCAACATGTTTAAGAAATGTGAGACTCGCTTCCTCATAGTCTGT 4552
Db 67795 TGCAATAGTTCAGAGCAACATGTTTAAGAAATGTGAGACTCGCTTCCTCATAGTCTGT 67736
Oy 4553 TAAAAACCCACCTCAAGGCCAGGTGCAAGTGGCTCATGCTTAATCCAGCACTTGGG 4612
Db 67735 TAAAAACCCACCTCAAGGCCAGGTGCAAGTGGCTCATGCTTAATCCAGCACTTGGG 67676
Oy 4613 AGCGGAGGCGGGTGGATCAGTGAAGTCAAGAGTTCAGAGACCACTGACCAACAT 4672
Db 67675 AGCGGAGGCGGGTGGATCAGTGAAGTCAAGAGTTCAGAGACCACTGACCAACAT 67616
Oy 4673 GGTGAATCCCACTCTACTTAAATTAACAAATTAAGATGAGCATGGTGTGATCGTGT 4732
Db 67615 GGTGAATCCCACTCTACTTAAATTAACAAATTAAGATGAGCATGGTGTGATCGTGT 67556
Oy 4733 AATCCACCTACTTGGAGGCTGAGCAGGAAATCACTAGAACCAAGGAGCGGAGTT 4792
Db 67555 AATCCACCTACTTGGAGGCTGAGCAGGAAATCACTAGAACCAAGGAGCGGAGTT 67496
Oy 4793 GTAAGTGAAGTGAAGTGTGCACTTGCACCTGACCTGAGCAATGAGCAATCTCATCTC 4852
Db 67495 GTAAGTGAAGTGAAGTGTGCACTTGCACCTGAGCAATGAGCAATCTCATCTC 67436
Oy 4853 AAAAAAACCAACAAAAAACCAACCTGACTCCAGGAGGCTGGGTACAGAGTGGGGC 4912
Db 67435 AAAAAAACCAACAAAAAACCAACCTGACTCCAGGAGGCTGGGTACAGAGTGGGGC 67376
Oy 4913 ACATAGTGAAGTGTGAGCACAAGAGCTTAAGCGGAGGCTGACAGACCGGAGCAGA 4972
Db 67375 ACATAGTGAAGTGTGAGCACAAGAGCTTAAGCGGAGGCTGACAGACCGGAGCAGA 67316

QY	4973	TAACAGTGTGAGATTCAGTGTGTGAGATTCAGACGTCCTCCATCTTGGTGACACACAGG	5032
Db	67315	TTAACAGTGTGTGAGATTCAGTGTGTGAGATTCAGACGTCCTCCATCTTGGTGACACACAGG	67256
QY	5033	GGCCCCCAAGACACAGAGATGGCCCCCATCCAGTACACATCCACTTCTCATCCAGAGAT	5092
Db	67255	GGCCCCCAAGACACAGAGATGGCCCCCATCCAGTACACATCCACTTCTCATCCAGAGAT	67196
QY	5093	GTCGTGTTCTTGGACACGCTGGGGGTAAATTAGACAGAAAGTGACAGTCTTGGGTGTGTC	5152
Db	67195	GTCGTGTTCTTGGACACGCTGGGGGTAAATTAGACAGAAAGTGACAGTCTTGGGTGTGTC	67136
QY	5153	AGTCAGACTGCCCCAGGACGCGCTTGTGGCTGTAGAAAAGCTTCAGGCGTCCGCGG	5212
Db	67135	AGTCAGACTGCCCCAGGACGCGCTTGTGGCTGTAGAAAAGCTTCAGGCGTCCGCGG	67076
QY	5213	ACGGTGGCTACGCGCTGTATCCACGACTTTGGGAGGCGGAGCGGGTGGATACAGAG	5272
Db	67075	ACGGTGGCTACGCGCTGTATCCACGACTTTGGGAGGCGGAGCGGGTGGATACAGAG	67016
QY	5273	TCAGGAGATCTGTACACATCTCGGCTTAACACGGTGAACCCCGTCTTACTTAATAATACAA	5332
Db	67015	TCAGGAGATCTGTACACATCTCGGCTTAACACGGTGAACCCCGTCTTACTTAATAATACAA	66556
QY	5333	AAAAATGGCGGGGATGGTGGCGGACCTGTAGTTCACAGTACTCGGAGAGCTGAGACA	5392
Db	66955	AAAAATGGCGGGGATGGTGGCGGACCTGTAGTTCACAGTACTCGGAGAGCTGAGACA	66896
QY	5393	GGAGAAATGGCTGAACCCGAGAGGACAGAGTTGAGTGAAGCCGAGATCGCGCCACTCTCAC	5452
Db	66895	GGAGAAATGGCTGAACCCGAGAGGACAGAGTTGAGTGAAGCCGAGATCGCGCCACTCTCAC	66836
QY	5453	TCCAGCCTGGGCGACAGACAAAGTCCATCTGAAAAAAGAAAGAAAGCTTAAAGGCT	5512
Db	66835	TCCAGCCTGGGCGACAGACAAAGTCCATCTGAAAAAAGAAAGAAAGCTTAAAGGCT	66776
QY	5513	GAGCCAGAGGCCAGGCTGTATTTCTGTCTACTTACATGACCTTGGGCAAGGCACTTCTCT	5572
Db	66775	GAGCCAGAGGCCAGGCTGTATTTCTGTCTACTTACATGACCTTGGGCAAGGCACTTCTCT	66716
QY	5573	TCCCTGGGCGGCTTACAGGGGTGGAAATCGACACTCCAAAGTCCCTTCCAGCATTAAGCTG	5632
Db	66715	TCCCTGGGCGGCTTACAGGGGTGGAAATCGACACTCCAAAGTCCCTTCCAGCATTAAGCTG	66656
QY	5633	CATGGTTCATAGATGAGAAAGATGGGGGAGTTCCCTCTCTCACCCAGCCCGTGTCCAC	5692
Db	66655	CATGGTTCATAGATGAGAAAGATGGGGGAGTTCCCTCTCTCACCCAGCCCGTGTGTCCAC	66596
QY	5693	TTCAAGGTGAATGACACAGGAGATGACGTGCCAATCCGCGAGTTCCAAAGCCCTTGGG	5752
Db	66595	TTCAAGGTGAATGACACAGGAGATGACGTGCCAATCCGCGAGTTCCAAAGCCCTTGGG	66536
QY	5753	GACCCCTACTGTACAGGTCGTGCACAGAGAGTGAAGTCAAGTGAAGCCATCGCTTCGAA	5812
Db	66535	GACCCCTACTGTGTACAGGTCGTGCACAGAGAGTGAAGTCAAGTGAAGCCATCGCTTCGAA	66476
QY	5813	GGGTCTTGGCTCATCTGGGACAGACATCCGTTCTCTGTGACTTACCGGGATTCAGAGG	5872
Db	66475	GGGTCTTGGCTCATCTGGGACAGACATCCGTTCTCTGTGACTTACCGGGATTCAGAGG	66416
QY	5873	GCTTTAGCCGATAGTCAATGGGGGGGGGGGTTCTGGGGAGTTTCCACAGCTAATCA	5932
Db	66415	GCTTTAGCCGATAGTCAATGGGGGGGGGGGTTCTGGGGAGTTTCCACAGCTAATCA	66356
QY	5933	ACTTGGGACAGAGACGCTTGAATTTTCGATGTGCTATTCAGATGTGGGGTGGGACACA	5992
Db	66355	ACTTGGGACAGAGACGCTTGAATTTTCGATGTGCTATTCAGATGTGGGGTGGGACACA	66296
QY	5993	GCAGCCAAAGACCAATGCTTATCTCAGGTAGGGGCTCAAGAGGTCTCCACAGACAGCA	6052
Db	66295	GCAGCCAAAGACCAATGCTTATCTCAGGTAGGGGCTCAAGAGGTCTCCACAGACAGCA	66236
QY	6053	GCTTCGAGAGATTGGGGGTAGGAATGGGACCAACGAGGCTTTTCTTCTCTCTTAG	6112

Db	66235	GCCTCCGAGAGATTGGGGGTAGAGATGGGAGACACA-GCTTCTTTTCTCTCTTAG	66177
QY	6113	AAATTGGGGGCTTGGGGGACAGGCTTGAGAAATCCCAAAGAGAGGGGGCAAGACACT-C	6171
Db	66176	AAATTGGGGGCTTGGGGGACAGGCTTGAGAAATCCCAAAGAGAGGGGGCAAGACACTTC	66117
QY	6172	CCCCACAAGTCTCCAG	6231
Db	66116	CCCCACAAGTCTCCAG	66058
QY	6232	GC 6233	
Db	66057	GC 66056	

RESULT 7

AC007776

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 100490)

Bliren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckely,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Depaeye,E., Devon,K., Dewar,R., Donegan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funk,R., Gage,D., Galagan,J., Gardys,S., Gilbert,D., Grant,G., Hagos,B., Heath,A., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lebecky,J., Lien,C., Locke,K., MacDonald,P., Margulis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Melidim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Naylor,J., Nijoff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P., Strange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Toruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.

Submitted (10-JUN-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker: Smtl, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1

2868: contig of 2868 bp in length

2869

gap of unknown length

6849: contig of 3981 bp in length

6850

gap of unknown length

11677: contig of 4828 bp in length

11678

gap of unknown length

16813: contig of 5136 bp in length

16814

gap of unknown length

23727: contig of 6914 bp in length

23728

gap of unknown length

37142: contig of 13415 bp in length

OY	2	ATGCCTTGAGAGACAGTAGTTCAGACACAGCCTGGGACATATAGGAGACTGTCTCTACGA	61
Db	63208	ATCATCTTGAGAGACAGTAGTTCAGACACAGCCTGGGACATATAGGAGACTGTCTCTACGA	63267
OY	62	AAATCAAAAAATTATGGCCGGGCGATATGGGGCTCACGCTGTATACCTTGAACTTTGGGA	121
Db	63268	AAATCAAAAAATTATGGCCGGGCGATATGGGGCTCACGCTGTATACCTTGAACTTTGGGA	63327
OY	122	CATCAAGGCAATGAGTCACTTGAGGTCAGAGTTGCAGACTAGACCTGGCCAAATGGTG	181
Db	63328	CATCAAGGCAATGAGTCACTTGAGGTCAGAGTTGCAGACTAGACCTGGCCAAATGGTG	63387
OY	182	AAACCCATATCCACATATAAAATATCAAAAAATTATGCCAGGCAATGGTGGGACGACCTGTAA	241
Db	63388	AAACCCATATCTACTT - AAAAATATCAAAAAATTATGCCAGGCAATGGTGGGACGACCTGTAA	63446
OY	242	TCCCGGCTACTCAGAGAGGCTGAGGACAGAGAAATCATTGTGAACCCAGAGGCGGAGTTGC	301
Db	63447	TCCCGGCTACTCAGAGAGGCTGAGGACAGAGAAATCATTGTGAACCCAGAGGCGGAGTTGC	63506
OY	302	AGTAGCTGAGATCACACACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCTATCTCA	361
Db	63507	AGTAGCTGAGATCACACACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCTATCTCA	63566
OY	362	AAAAAAATATAAAAAATTTATAGCAGAGGCAATGTAGTGCACACTCTATGTCTACG	421
Db	63567	AAAAAAATATAAAAAATTTATAGCAGAGGCAATGTAGTGCACACTCTATGTCTACG	63626
OY	422	TACTCAGAGAGCGAGGTGGGAGATCACTTGAACCTGGGCGCATAAAGCTTACAGTGA	481
Db	63627	TACTCAGAGAGCGAGGTGGGAGATCACTTGAACCT - GGCGAGTCAAGGCTGCAGTGA	63685
OY	482	CCAAGATCATGCCACTACACTCCAGGCTGGGCAACGAGAGAGAACCCCTGTCTGTAAAA	540
Db	63686	CCAAGATCATGCCACTACACTCCAGGCTGGGCAACGAGAGAGAACCCCTGTCTGTAAAA	63745
OY	541	AATATATATATATAAGAAAAAAACACCTCTGTTATGTCTCGTGCTATACATATCTACT	600
Db	63746	AATATATATATATAAGAAAAAAACACCTCTGTTATGTCTCTCGTGCTATACATATCTACT	63802
OY	601	ATGTATATATATTTGCAAACTCAAAAGATCAGATAGTCAATTTTATAGCTTGGGCGGT	660
Db	63803	ATGTATATATATTTGCAAACTCAAAAGATCAGATAGTCAATTTTATAGCTTGGGCGGT	63862
OY	661	ATGGTCTCTGTCAATCACTCTGCCCTGTCTTTTACGACAAAGACACTTAAAC - CAA	719
Db	63863	ATGGTCTCTGTCAATCACTCTGCCCTGTCTTTTACGACAAAGACACTTAAANCA	63922

QY	720	TACATACATGAATTTTATATAGACATCGAGATTTGAATTTCAATATGATTTTATACATTTTA	719
Db	63923	TACATATACATGAATTTTATATAGACATCGAGATTTGAATTTCAATATGATTTTATACATTTTA	6398
QY	780	TAAATATATCTTTTAAATAATTTTCCCTAACCATTTTAAAGTGTAAAGCCGCCCA ---	836
Db	63983	TAAATATATCTTTTAAATAATTTTCCCTAACCATTTTAAAGTGTAAAGCCGCCCAN	6404
QY	837	-----GCGCGCATCGTCACGCGCTGTAAATTCACGACATTTGGGAGGCTGAGTGGGCGAG	890
Db	64043	GCGNGCGCNCATGGGCTCACGCGCTGTAAATTTCCAGCACTTTGGGAGGCTGAGTGGGCGAG	6410
QY	891	ATCACTTGAATCAACAGTTTGGAGACACGCTGGCCCAACATAGCAAAACCCATTTCTAC	950
Db	64103	ATCACTTGAATCAACAGTTTGGAGACACGCTGGCCCAACATAGCAAAACCCCATTTCTAC	6416
QY	951	TAAAAATTAATAAATTTAGCTGGGATATGTGTGACACCTGTATTCACGACTACTTGGGA	1010
Db	64183	TAAAAATTAATAAATTTAGCTGGGATATGTGTGACACCTGTGTATTCACGACTACTTGGGA	6422
QY	1011	GGCTGAGGACAGAGAAATGCTTTGAACCTGGGAAACGGAGGTTGCAGTGAACCAATCAT	1070
Db	64223	GGCTGAGGACAGAGAAATGCTTTGAACCTGGGAAACGGAGGTTGCAGTGAACCAATCAT	6428
QY	1071	GCCACTGCATTCACAGCTTGGGTGACA -GAGTGAAGCTTGGTCTACAG -AAAAAAAAAG	1128
Db	64283	GCCACTGCATTCACAGCTTGGGTGACANAGAGACATTCGCTCTACAGAAAAAAAAAG	6434
QY	1129	TGTAATAACCATTCCTATTTAGTATCATAGTATCATATCATAGGCTGCGATCTCT	1188
Db	64343	TGTAATAACCATTCCTATTTAGTATCATAGTATCATATCATAGGCTGCGATCTCT	6440
QY	1189	GCTCTGAGGACATACCTGAGAGTAGAGTGTGGTGTACACAGACATACATTTTCCACAT	1248
Db	64403	GCTCTGAGGACATACCTGAGAGTAGAGTGTGGTGTACACAGACATACATTTTCCACAT	6446
QY	1249	TAACTAGACACTACCAAGTGGCCATCCAGAGAG -TTTTTTTTTAAACATCTACACTGCC	1307
Db	64463	TAACTAGACACTACCAAGTGGCCATCCAGAGAGTTTTTTTTTAAACATCTACACTGCC	6452
QY	1308	CCACAGCACAATGAGAGTACTGCACAGTCTTTTACAAAGATGCTTAAGCCCGATACCA	1367
Db	64523	CCACAGCACAATGAGAGTACTGCACAGTCTTTTACAAAGATGCTTAAGCCCGATACCA	6458
QY	1368	GATGAAACAGAGAAAGTGGAGGGAGAGCTGCCAGC -CTTCTAACCATGAAAGAAATACC	1426
Db	64583	GATGAAACAGAGAAAGTGGAGGGAGAGCTGCCAGCNCCTTCAACCATGAAAGAAATACC	6464
QY	1427	TGCTTAGACCTTTCTGATGCTGTGAAGATGAATTAACGGGGTCTCTGAGGCTGCCCCCT	1486
Db	64643	TGCTTAGACCTTTCTGATGCTGTGAAGATGAATTAACGGGGTCTCTGAGGCTGCCCCCT	6470
QY	1487	GTCAGATACGTGATCTTGAGGCTGCAGTCCAGTGTCAAGCCCATGTGCATGGGCGAG	1546
Db	64703	GTCAGATACGTGATCTTGAGGCTGCAGTCCAGTGTCAAG -CTCAAGCCCATGTGTGCATGGGCGAG	6476
QY	1547	TGATAAATGAGCCCTCACCTCTGTTGGTCTTTATTCGCC - -ATGTGGGGCTGAAGTCT	1604
Db	64782	TGATAAATGAGCCCTCACCTCTGTTGGTCTTTATTCGCCCATGTGTGGGGCTGAAGTCT	6482
QY	1605	TGATATGAGCCGTATTCAAGATGTACAGCTTTCTTGACAGGAAGTATGTGCACAGAAA	1664
Db	64822	TGATATGAGCCGTATTCAAGATGTACAGCTTTCTTGACAGGAAGTATGTGCACAGAAA	6488
QY	1665	CAGCAGGGGCTTGGCAAGATGATCTAACTGCAAACTCTACCTGGCTCAGCCACCAGCTAG	1724
Db	64882	CAGCAGGGGCTTGGCAAGATGATCTAACTGCAAACTCTACCTGGCTCAGCCACCAGCTAG	6494
QY	1725	TTTCTGTATCTTGAACAAGTTTTTTCACCTCTGAGAGGCAATCCCTGGCTTACAACAACAC	1784
Db	64942	TTTCTGTATCTTGAACAAGTTTTTTCACCTCTCTGAGAGGCAATCCCTGGCTTACAACAACAC	6500
QY	1785	CAGTTTG - GTTGACACAGATGGAATATGAC - AAGTCCCTTACACCTGTATCTCCACAGCTTGG	1842

QY	398	CACCTACGGGAGAGGCTAAAGTGGAGATTCCTGTAGCCTGGGAGGTAAACATGCACT	4046
Db	67222	CACCTACGGCGGAGGCTAAAGTGGAGATTCCTGTAGCCTGGGAGGTAAACATGCACT	67281
QY	4047	GAGCTGTGATTTACACACAGCCCTTAGCCTGGGGACAGACTGAGACCCCTGTTCCCT	4106
Db	67282	GAGCTGTGATTTACACACAGCCCTTAGCCTGGGGACAGACTGAGACCCCTGTTCCCT	67341
QY	4107	CCGCAAAAAAATTGACAAAAGTGTAAATAGAGTGCCTGATATGCTAGGCGCAGTGGCT	4166
Db	67342	CCGCAAAAAAATTGACAAAAGTGTAAATAGAGTGCCTGATATGCTAGGCGCAGTGGCT	67401
QY	4167	CAGGCCGTGATATCCCAAGCACTTTGGGAGCCGCGGGGGGGGTACCTAAAGCTAGAG	4226
Db	67402	CATGCTGTATATCCCAAGCACTTTGGGAGCCGCGGGGGGGGTACCTAAAGCTAGAG	67461
QY	4227	TGTGAGACAGCCTGGCCAAATGAGAAAGCCATCTTCTTAAATAATACAAATTAGC	4286
Db	67462	TGTGAGACAGCCTGGCCAAATGAGAAAGCCATCTTCTTAAATAATACAAATTAGC	67521
QY	4287	CGGCTGTGGGGGAGTGGTGGAGCAAGCCTGTAAATCCGATACACAGAGAGCTAGGCA	4346
Db	67522	CGGCTGTGGGGGAGTGGTGGAGCAAGCCTGTAAATCCGATACACAGAGAGCTAGGCA	67581
QY	4347	GGAGAAATCACTTGAACCCAGAGAGCGCGGCTTGACAGTGAAGCCAGATCTGCATTTGAC	4406
Db	67582	GGAGAAATCACTTGAACCCAGAGAGCGCGGCTTGACAGTGAAGCCAGATCTGCATTTGAC	67641
QY	4407	TCCACCCACTCTCAAGCCTGGGCAACAAGACCCTCTCTTAAAAAATTTTTAAAAA	4466
Db	67642	TCCACCCACTCTCAAGCCTGGGCAACAAGACCCTCTCTTAAAAAATTTTTAAAAA	67700
QY	4467	GTCCTGTACATTAATAAGAGTGTGCATGCAATGTAATGTGGCAGCAATGTTTAAGAAAT	4526
Db	67701	GTCCTGTACATTAATAAGAGTGTGTGCATGCAATGTAATGTGGCAGCAATGTTTAAGAAAT	67760
QY	4527	GGAAGCTCTGCTTCCATGATGCTCTGTTAAAAAACCACCCCTCAAGGCGAGTGCAGTGGCT	4586
Db	67761	GGAAGCTCTGCTTCCATGATGCTCTGTTAAAAAACCACCCCTCAAGGCGAGTGCAGTGGCT	67820
QY	4587	CATGCCATTAATCCCAAGCACTTTGGGAGGCGCGGGGGGTGATACCTGTAGCTAGAG	4646
Db	67821	CATGCCATTAATCCCAAGCACTTTGGGAGGCGCGGGGGGTGATACCTGTAGCTAGAG	67880
QY	4647	TTGCGAGCAGCCTGACCAACAATGATGAAATCCACCTCTACTAAAAAATACAAATT	4706
Db	67881	TTGCGAGCAGCCTGACCAACAATGATGAAATCCACCTCTACTAAAAAATACAAATT	67940
QY	4707	AGATAGACATGATGTGTGCATGCTGTATATCCCACTACTTTGGGAGGCTAGGCAAGAAA	4766
Db	67941	AGATAGACATGATGTGTGCATGCTGTATATCCCACTACTTTGGGAGGCTAGGCAAGAAA	68000
QY	4767	TCACCTAAGAACAGAGGAGGGGAGAGTGTAGTGAAGCCAGATAGTGGCATTTGAGT -CCAG	4825
Db	68001	TCACCTAAGAACAGAGGAGGGGAGAGTGTAGTGAAGCCAGATAGTGGCATTTGAGT -CCAG	68060
QY	4826	CCTGAGCA -ATGAGCGAAATCCATCTCAAAAAAACACACAAAAAACCACCTCTACT	4884
Db	68061	CCTGAGCAANTGAGCGAAATCCATCTCAAAAAAACACACAAAAAACCACCTCTACT	68120
QY	4885	CCGAGGAGAGTGGGTACA -GAGTGGGCGCAATCAATGCAAGGTGCTGAGCCACAGAGCT	4943
Db	68121	CCGAGGAGAGTGGGTACANGAGTGGGCGCAATCAATGCAAGGTGCTGAGCCACAGAGCT	68180
QY	4944	AAGGCGGAGCTG - -CAGGACCGGCGACAGATTAACAGTGTGTGAGATCAGTGTGAGAT	5001
Db	68181	AAGGCGGAGCTGTNNCAAGAACCGGGGACAGATTAACAGTGTGTGAGATCAGTGTGAGAT	68240
QY	5002	CAGACGCTCCCTGCTATTGTTGACACACAGGGGGGCCCAAGCACAGAGATGGCCCATC	5061
Db	68241	CAGACGCTCCCTGCTATTGTTGACACACAGGGGGGCCCAAGCACAGAGATGGCCCATC	68300

QY	5062	CAGCACACCAATCCACTTCCTGCATCCAGAGATGTCGTCTTTCTTGGACAGCGTGGGGTAAT	5121
Dp	68301	CAGTCACACCAATCCACTTCCTGCATCCAGAGATGTCGTCTTTCTTGGACAGCGTGGGGTAAT	68360
QY	5122	AGCAGACAGAGATCAAGTCTTGGGTGTGGCTAGCTAGACTGTGCCACAGCA---GAGCTT	5177
Dp	68361	AGCAGACAGAGATCAAGTCTTGGGTGTGGCTAGCTAGACTGTGCCACAGCANNKAGNCTTT	68420
QY	5178	GTGGCCCTGT--AGAAAAAGTTCAAGGCGCTTAGGCCGAGCGTGGC--TCAGCGCTGTATTC	5234
Dp	68421	GTGGCCCTGT--AGAAAAAGTTCAAGGCGCTTAGGCCGAGCGTGGCTAGCGCTGTATTC	68480
QY	5235	CCAGCACTTTGGGAGGCGGAGGGGGGTGGATCAGCAGAGTCCAGAGATCTGTACACTCTCG	5294
Dp	68481	CCAGCACTTTGGGAGGCGGAGGGGGGTGGATCAGCAGAGTCCAGAGATCTGTACACTCTCG	68540
QY	5295	GCTTAACAGGGTGAACCCCGCTCTCTACTAATAAATAAATAATTTGGCCGGGATAGTGGC	5354
Dp	68541	GCTTAACAGGGTGAACCCCGCTCTCTACTAATAAATAAATAATTTGGCCGGGATAGTGGC	68600
QY	5355	GGGCACTGTAGTTCCAGCTACTTCGGGAGGCTGAGGCGAGAGATGGCGTAACCCGAGA	5414
Dp	68601	GGGCACTGTAGTTCCAGCTACTTCGGGAGGCTGAGGCGAGAGATGGCGTAACCCGAGA	68660
QY	5415	GGCAGATTTTGCAGTGGAGCGCGAATAGCGCCACTGTGACATCCAGACCTCGGGCGACAGACA	5474
Dp	68661	GGCAGATTTTGCAGTGGAGCGCGAATAGCGCCACTGTGACATCCAGACCTCGGGCGACAGACA	68720
QY	5475	GACATCAATCTGAGAA--AGAAAAAGAAAAAGTTTAGGTCTGAGCCAGACGCCAGCGCTGA	5533
Dp	68721	GACATCAATCTGAGAAAGAAAAAGAAAAAGTTTAGGTCTGAGCCAGACGCCAGCGCTGA	68780
QY	5534	ATTCTGTCACTTACCATGACCTTGGGCAAGGCACTTCCTCCCTGGCCAGTTCAAGGGG	5593
Dp	68781	ATTCTGTCACTTACCATGACCTTGGGCAAGGCACTTCCTCCCTGGCCAGTTCAAGGGG	68840
QY	5594	TTGGAATCGACTCCAGAGTCCCTTCCAGCAATTAAAGCTGCATGTGTTCT--AAATGAGAAG	5652
Dp	68841	TTGGAATCGACTCCAGAGTCCCTTCCAGCAATTAAAGCTGCATGTGTTCTAAAGTGAAG	68900
QY	5653	ATGGGGAGATTCCCGCTCTCTCTCAACCCAGCCGCTGTCCATTCAAAGTGAATGACAGAG	5712
Dp	68901	ATGGGGAGATTCCCGCTCTCTCTCTCAACCCAGCCGCTGTCCATTCAAAGTGAATGACAGAG	68960
QY	5713	AAGTCAGGTGCCAATCCCGCAGTTCCAAAGCCCTTGGGAGCCCTACTGTCAAGGTCGT	5772
Dp	68961	AAGTCAGGTGCCAATCCCGCAGTTCCAAAGCCCTTGGGAGCCCTACTGTCAAGGTCGT	69020
QY	5773	GCACGAGAGAGTGAAGTCAAGTGAAGCAATGCCCTTCGAAAGGTCCTTCGCTCATTTGGGA	5832
Dp	69021	GCACGAGAGAGTGAAGTCAAGTGAAGCAATGCCCTTCGAAAGGTCCTTCGCTCATTTGGGA	69080
QY	5833	CAGACATCCGGTTTCCCTGAGCTTACCGGGAGATTCAAGGGGCTTTCAGCGC--AATGAGTC	5890
Dp	69081	CAGACATCCGGTTTCCCTGAGCTTACCGGGAGATTCAAGGGGCTTTCAGCGCTTTCAGCGCTT	69140
QY	5891	ATGGGGGCGGGGGGGTTCCTGGGGGAGTTTCCAGCTTAATCAACTTTGGGACAGGACAGCC	5950
Dp	69141	ATGGGGGCGGGGGGGTTCCTGGGGGAGTTTCCAGCTTAATCAACTTTGGGACAGGACAGCC	69200
QY	5951	TGGAATCTTGCATGTGTCCTATTCAGATGTGGGGTGGGCAAGCAGACCCAAATGT	6010
Dp	69201	TGGAATCTTGCATGTGTCCTATTCAGATGTGGGGTGGGCAAGCAGACCCAAATGT	69260
QY	6011	CTTATATTCAGAGTAGGGGCTCAGGAGTCTCCACAGCAGGACCTTCGGAGAGTTTGGG	6070
Dp	69261	CTTATATTCAGAGTAGGGGCTCAGGAGTCTCCACAGCAGGACCTTCGGAGAGTTTGGG	69320
QY	6071	GGTAGGAATGGGAGCAACAGGCTTTTCTTTTCTCTTAGAATTTGGGGCTTGGGGG	6130
Dp	69321	GGTAGGAATGGGAGCAACCA--GCTTCTTTTCTCTCTTAGAATTTGGGGCTTGGGGG	69379
QY	6131	ACAGGCTTGAATCCCAAGAGGAGGGGCAAGGACATCCCCCAAGTCT--GCCA	6187


```
/chromosome="17"
/clone="RP11-387H17"
1.1523
misc_feature
/note="assembly_name:Contig17"
1624..2830
misc_feature
/note="assembly_name:Contig18"
2931..4445
misc_feature
/note="assembly_name:Contig19"
4546..5643
misc_feature
/note="assembly_name:Contig20"
5744..7022
misc_feature
/note="assembly_name:Contig21"
7123..8983
misc_feature
/note="assembly_name:Contig22"
9084..11092
misc_feature
/note="assembly_name:Contig23"
11193..12752
misc_feature
/note="assembly_name:Contig24"
12853..14247
misc_feature
/note="assembly_name:Contig25"
14348..16451
misc_feature
/note="assembly_name:Contig26"
16552..18402
misc_feature
/note="assembly_name:Contig27"
18503..21089
misc_feature
/note="assembly_name:Contig28"
21190..24337
misc_feature
/note="assembly_name:Contig29"
24438..27881
misc_feature
/note="assembly_name:Contig30"
27982..30256
misc_feature
/note="assembly_name:Contig31
vector_end:SP6
vector_side:left"
30357..32983
misc_feature
/note="assembly_name:Contig32"
33084..35459
misc_feature
/note="assembly_name:Contig33"
35560..39128
misc_feature
/note="assembly_name:Contig34"
39229..42608
misc_feature
/note="assembly_name:Contig35"
42709..47067
misc_feature
/note="assembly_name:Contig36"
47168..50792
misc_feature
/note="assembly_name:Contig37"
50893..55282
misc_feature
/note="assembly_name:Contig38"
55383..59386
misc_feature
/note="assembly_name:Contig39"
59487..64208
misc_feature
/note="assembly_name:Contig40"
64309..68973
misc_feature
/note="assembly_name:Contig41"
69074..73514
misc_feature
/note="assembly_name:Contig42"
73615..79235
misc_feature
/note="assembly_name:Contig43"
79356..84273
misc_feature
/note="assembly_name:Contig44"
84374..89567
misc_feature
/note="assembly_name:Contig45"
89668..95452
/note="assembly_name:Contig46"
```

Query Match 70.1%; Score 4368.4; DB 2; Length 221484;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 4878; Conservative 0; Mismatches 621; Indels 37; Gaps 16;

QY 1 GATCACTTGAGGAAAGTAGTTCAAGACCAAGCCTGGGACGATTAAGGAGACTGTCTTACG 60
Db 68738 GATCACTTGAGGAAAGTAGTTCAAGACCAAGCCTGGGACGATTAAGGAGACTGTCTTACG 68679

```
QY 61 AAAAATCAAAAAATATGCGCGGCGATGCTGCTCAGCTCTGTAATCCCTGAACTTGGG 120
|||||
Db 68678 AAAAATCAAAAAATATGCGCGGCGATGCTGCTCAGCTCTGTAATCCCTGAACTTGGG 68619
QY 121 ACATCAAGCAAGTAGATGATCATTGAGTGCAGAGATTGCAGACTGACCTGGCCAAATAGT 180
|||||
Db 68618 ACATCAAGCAAGTAGATGATCATTGAGTGCAGAGATTGCAGACTGACCTGGCCAAATAGT 68559
QY 181 GAAACCTATATCCACTCAAAAAATACAAAAATTTAGCCAGGATGGTGGCAGGCACTGTA 240
|||||
Db 68558 GAAACCTATATCTCACT-AAAAATACAAAAATTTAGCCAGGATGGTGGCAGGCACTGTA 68500
QY 241 ATCCCGGCTACTCGAGAGGCTGAGGCGAGAGAAATCACTTGAACCCAGAGGCGGAGTTG 300
|||||
Db 68499 ATCCCGGCTACTCGAGAGGCTGAGGCGAGAGAAATCACTTGAACCCAGAGGCGGAGTTG 68440
QY 301 CAGTGAAGCTGAGATCACACCACTGACACTCCAGCCTGGGTGACAGAGCAAGACTATCTC 360
|||||
Db 68439 CAGTGAAGCTGAGATCACACCACTGACACTCCAGCCTGGGTGACAGAGCAAGACTATCTC 68380
QY 361 AAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420
|||||
Db 68379 AAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 68320
QY 421 CTACTCAGAGGCTGAGGTGGAGGATGATCACTTGAACCTGGGGCAGTCAAGGCTACAGTGA 480
|||||
Db 68319 CTACTCAGAGGCTGAGGTGGAGGATGATCACTTGAACCTGGGGCAGTCAAGGCTACAGTGA 68261
QY 481 GCCAAGATCATGCCACTGACACTCCAGCCTGGGCAACAGAGAGAGAACCCCTGTCTATAAAA 540
|||||
Db 68260 GCCAAGATCATGCCACTGACACTCCAGCCTGGGCAACAGAGAGAGAACCCCTGTCTATAAAA 68201
QY 541 AATATATATATTAAGAAAAAACAAGCTCTGTTATGCTCTGCTGCTGCTCATATATATCT 600
|||||
Db 68200 AATATATATATTAAGAAAAAACAAGCTCTGTTATGCTCTGCTGCTGCTCATATATATCT 68144
QY 601 ATGTATATAGTTTGCACAACTCAAGATGCAGATGTCAATTTTAAAGCTGTGGGCGGT 660
|||||
Db 68143 ATGTATATAGTTTGCACAACTCAAGATGCAGATGTCAATTTTAAAGCTGTGGGCGGT 68084
QY 661 ATGGTCTCTGTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
|||||
Db 68083 ATGGTCTCTGTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 68024
QY 721 ACATCAATGAATTTTATATACATCCAGATTTGAATTTCAATATATATTTTACATTTTAT 780
|||||
Db 68023 ACATCAATGAATTTTATATACATCCAGATTTGAATTTCAATATATATTTTACATTTTAT 67964
QY 781 AAAATATATCTTTTAAAAATTTTCCCTAACATTTTAAAAATGTAAGCCGGCA--G 837
|||||
Db 67963 AAAATATATCTTTTAAAAATTTTCCCTAACATTTTAAAAATGTAAGCCGGCAAGCGC 67904
QY 838 CGCGCATGCTGACGCTGTGTAATTCACAGACTTTGGAGGCTGAGTGGGCGAGATCACTT 897
|||||
Db 67903 CGCGCATGCTGACGCTGTGTAATTCACAGACTTTGGAGGCTGAGTGGGCGAGATCACTT 67844
QY 898 GAGATCAACAGTTTGAGACCGCCTGGCCAAATATGCAAAAAATCCCATTTTCTACTTAAAT 957
|||||
Db 67843 GAGATCAACAGTTTGAGACCGCCTGGCCAAATATGCAAAAAATCCCATTTTCTACTTAAAT 67784
QY 958 AAAAAAATTTACTGGGCTATGATGGGCAACACTGATGATCCAGATCTTGGGAGGCTGAG 1017
|||||
Db 67783 AAAAAAATTTACTGGGCTATGATGGGCAACACTGATGATCCAGATCTTGGGAGGCTGAG 67724
QY 1018 GCAGGAGATGCTTGAACCTGGGAAGGAGGTTGAGAGTGAAGCAATGATCCACTG 1077
|||||
Db 67723 GCAGGAGATGCTTGAACCTGGGAAGGAGGTTGAGAGTGAAGCAATGATGATCCACTG 67664
QY 1078 CACTTCAGCGCTGGGTGACAGAGTAGACTTGTCTCAAG-AAAAAATAAAGTATAAAG 1136
|||||
Db 67663 CACTTCAGCGCTGGGTGACAGAGTAGACTTGTCTCAAGCAAAAAAATAAAGTATAAAG 67604
QY 1137 CCATTCTTAATTCAGTGTACTGATGATCACTCAAGGTGTGGCTACTCTGCTGAG 1196
|||||
```

|||||
Db 67603 CCATTCCTAATTCAGTGTACATATGATACATCTAGGCTCGTACCTCTCTGAG 67544
QY 1197 GCATACCTGAGAGTAGAGTTGCTGTCCAGAGACATACATTTCCACATTAACTAGA 1256
|||||
Db 67543 GCATACCTGAGAGTAGAGTTGCTGTCCAGAGACATACATTTCCACATTAACTAGA 67484
QY 1257 CACTACCAAGTTCACATCCAGAGAGGTTTTTTTTTACAAATCTACACTCCCGCAGCAAC 1316
|||||
Db 67483 CACTACCAAGTTCACATCCAGAGAGGTTTTTTTTTACAAATCTACACTCCCGCAGCAAC 67424
QY 1317 AATGAGAGTTACTCCAGATCCCTTTTACAAAGATGCTCTAAGCCCACTAGCAAGTGAAGAAC 1376
|||||
Db 67423 AATGAGAGTTACTCCAGATCCCTTTTACAAAGATGCTCTAAGCCCACTAGCAAGTGAAGAAC 67364
QY 1377 AGGAATGGGAGGGAGAGCTGCAGGCCCTTTCTAACCATGAGAGAAATACCTGGTAGAGCC 1436
|||||
Db 67363 AGGAATGGGAGGGAGAGCTGCAGGCCCTTTCTAACCATGAGAGAAATACCTGGTAGAGCC 67304
QY 1437 TTCTGGATGCTGGAAGAGTAGAATACGGGGGCTCTGAGAGCTGCCCCCTGTAGATCAC 1496
|||||
Db 67303 TTCTGGATGCTGGAAGAGTAGAATACGGGGGCTCTGAGAGCTGCCCCCTGTAGATCAC 67244
QY 1497 TTGAGCTTCTGAGACCTCCAGTCCAGTCTCAGCCCAATGTCATGGCCAGTGAATAGAG 1556
|||||
Db 67243 TTGAGCTTCTGAGACCTCCAGTCCAG-CTCAGCCCATGTCATGGCCAGTGAATAGAG 67185
QY 1557 CCCTCACTCTCTTTTGGCTTTATTTCT-CCCATGAGGGGCTGAAAGTCTGATTAAGCC 1615
|||||
Db 67184 CCCTCACTCTCTTTTGGCTTTATTTCTCCCATGAGGGGCTGAAAGTCTGATTAAGCC 67125
QY 1616 GTTATTCAGAGATGTACAGCTTTCTTGACAGAAAGTAGTCAACAGAAACAGAGGGCT 1675
67124 GTTATTCAGAGATGTACAGCTTTCTTGACAGAAAGTAGTCAACAGAAACAGAGGGCT 67065
Db 1676 TGSCAAGATGATCTAACTGCAAAATCCATCGGCTCAGCCACAGGCTGTGTATCT 1735
|||||
Db 67064 TGSCAAGATGATCTAACTGCAAAATCCATCGGCTCAGCCACAGGCTGTGTATCT 67005
QY 1736 TGAACAAGTTTTTTTCACTTCTCTGAGGCCATCCCTTGCTACAAACACACAGTGTGTGA 1795
|||||
Db 67004 TGAACAAGTTTTTTTCACTTCTCTGAGGCCATCCCTTGCTACAAACACACAGTGTGTGA 66945
QY 1796 CAGAGTAAATGACG-AGTCCCTTACCTGTAACTCCAGCACTTTGGAGGCCAAGGC 1854
|||||
Db 66944 CAGAGTAAATGACGAAAGTGCCTTACACTGTAACTCCAGCACTTTGGAGGCCAAGGC 66885
QY 1855 GGGTGGATGGCTTGAGGCTGAGGCTGAGAGGTGACAGCATGCCGCGACATCCACAGCCCTGTTTC 1914
|||||
Db 66884 GGGTGGATGGCTTGAGGCTGAGAGGTGAGAGCATGCCGCGACATCCACAGCCCTGTTTC 66825
QY 1915 GCTCTGGGGGCTCTCTCTGCTGGGCTCCACTTGGTGGCACTTTGAGAGCCCTTACAG 1974
|||||
Db 66824 GCTCTGGGGGCTCTCTCTGCTGGGCTCCACTTGGTGGCACTTTGAGAGCCCTTACAGC 66765
QY 1975 CCACGCTGCACTGTGGGAGCCCTTTCTGGGCTGGCCAGAGGCCGCGCTCCCTCA 2034
66764 CCACGCTGCACTGTGGGAGCCCTTTCTGGGCTGGCCAGAGGCCGCGCTCCCTCA 66705
QY 2035 GCTTGGAGGAGGTGTGGAGGGAGAGGCTCAACACAGGAACCGGGGCTGGCCAGCGGCTT 2094
|||||
Db 66704 GCTTGGAGGAGGTGTGGAGGGAGAGGCTCAACACAGGAACCGGGGCTGGCCAGCGGCTT 66645
QY 2095 GCGGGCCAGCTGAGTTCGGGGTGGGGCTGGGGCTGGGGGCCCGCACTCGAGAGAGCG 2154
|||||
Db 66644 GCGGGCCAGCTGAGTTCGGGGTGGGGCTGGGGCTGGGGGCCCGCACTCGAGAGAGCG 66585
QY 2155 GCGCAGCCCTGCGAGGCCCGCGGCAATGAGAGGCTTAGCAACCGGGCCAGCGGCTCGGA 2214
66584 GCGCAGCCCTGCGAGGCCCGCGGCAATGAGAGGCTTAGCAACCGGGCCAGCGGCTCGGA 66525
QY 2215 GGGTGTACTGGGTGCCCGCAGCACTGCCAGCCCGCGGCTGTGTGCTGCATTTCTCA 2274
|||||

Db 66524 GGGTGTACTGGGTGCCCGCAGCACTGCCAGCCCGCGGCTGTGTGCTGCATTTCTCA 66465
QY 2275 CTGGGCTTTAGCAGCCTTCCCGGGGAGGGCTCGGGACCTTCAGCCCGCATGTGCTGA 2334
|||||
Db 66464 CTGGGCTTTAGCAGCCTTCCCGGGGAGGGCTCGGGACCTTCAGCCCGCATGTGCTGA 66405
QY 2335 GCGTCCCTTCATAGGGCTCTGTGGGCCCGGAGCCTTCCCGAGCACCACCCCTGCT 2394
66404 GCGTCCCTTCATAGGGCTCTGTGGGCCCGGAGCCTTCCCGAGCACCACCCCTGCT 66345
QY 2395 CCAAGGGCCCATCCCATCGACACAGCAAGGGCTGAGAAAGTGGGGCGAGGGCACCGG 2454
66344 CCAAGGGCCCATCCCATCGACACAGCAAGGGCTGAGAAAGTGGGGCGAGGGCACCGG 66285
Db 2455 GACTGGAGGAGCAGTACCCCTGCGAGCCCTGTGTCGGAATTCACCTGGGTGAAGCAGCTGG 2514
66284 GACTGGAGGAGCAGTACCCCTGCGAGCCCTGTGTCGGAATTCACCTGGGTGAAGCAGCTGG 66225
QY 2515 GCTCTGAGTCTGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCTAAATAC 2574
66224 GCTCTGAGTCTGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCTAAATAC 66165
QY 2575 ACCAATCAGACCCCTGTGTAGCTCAGGGCTGTGTAATCAGCAATCCACACTGTAT 2634
66164 ACCAATCAGACCCCTGTGTAGCTCAGGGCTGTGTAATCAGCAATCCACACTGTAT 66105
Db 2635 CTAGCTACTGTATGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACA 2694
66104 CTAGCTACTGTATGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACA 66045
QY 2695 CCAATGGGCACTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGACCCCTGTTC 2754
66044 CCAATGGGCACTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGACCCCTGTTC 65985
Db 2755 TACTCAGGGTATGTGAATCAGCAATCGACATCTGTATCTGGCTACTTTCAGGGCAT 2814
65984 TACTCAGGGTATGTGAATCAGCAATCGACATCTGTATCTGGCTACTTTCAGGGCAT 65925
QY 2815 CCGTGTGAAGAGACACCAACAGGCTTGTGTGAGCAATTAAGCTTCTATCACTGGGT 2874
65924 CCGTGTGAAGAGACACCAACAGGCTTGTGTGAGCAATTAAGCTTCTATCACTGGGT 65865
Db 2875 GCAAGTGGGCTGAGTCCGAAAGAGACTCAGCAAGGGAGATAAAGGTGGGCGCTTTTA 2934
65864 GCAAGTGGGCTGAGTCCGAAAGAGACTCAGCAAGGGAGATAAAGGTGGGCGCTTTTA 65805
QY 2935 TAGGATTTGGGTAGTAAAGAAATTTACAGTCAAAAGGGGCTTGTCTCTGGCGGGCAG 2994
65804 TAGGATTTGGGTAGTAAAGAAATTTACAGTCAAAAGGGGCTTGTCTCTGGCGGGCAG 65745
Db 2995 GAGTGGGGGCTGCGAAGGTGCTCAGTGGGGGCTTTTGTGAGCCAGATGAGCCAGGAAA 3054
65744 GAGTGGGGGCTGCGAAGGTGCTCAGTGGGGGCTTTTGTGAGCCAGATGAGCCAGGAAA 65685
QY 3055 AGGACTTTCAAGAGTAAATGTATCAATTAAGGCAAGAGCCGCCATTTACACTCTTTT 3114
65684 AGGACTTTCAAGAGTAAATGTATCAATTAAGGCAAGAGCCGCCATTTACACTCTTTT 65625
Db 3115 GTGGTGAATGTATAGTAAAGTGGGGCAGGGCATTTCACTTTTGTGTATCTTC 3174
65624 GTGGTGAATGTATAGTAAAGTGGGGCAGGGCATTTCACTTTTGTGTATCTTC 65565
Db 3175 AGTTACTTTCAGGCACTGGGCTATATGTGCAAGTTACAGGGAGTGCATGGCTTGGCT 3234
65564 AGTTACTTTCAGGCACTGGGCTATATGTGCAAGTTACAGGGAGTGCATGGCTTGGCT 65505
QY 3235 TGGGCTCAAGGCTTGAACAGTACTGTGTGGGGCTTGGAGAAATGTTGTGCACT 3294
65504 TGGGCTCAAGGCTTGAACAGTACTGTGTGGGGCTTGGAGAAATGTTGTGCACT 65445
Db 3295 CTGTATCTAGTTAATCTAGTGGGAGCTGGAAGAACTTTGTGTAGCTCAGGGATTTGA 3354
65444 CTGTATCTAGTTAATCTAGTGGGAGCTGGAAGAACTTTGTGTAGCTCAGGGATTTGA 65385

QY 3355 AAGCACCAATGAGCGCCCTGTCAAAAACAGACCACTGGCTCTACCAATCAGCAGATGT 3414
DB 65384 AAGCACCAATGAGCGCCCTGTCAAAAACAGACCACTGGCTCTACCAATCAGCAGATGT 65325
QY 3415 GGGTGGGGCCAGATTAAGAGATTAAGAGCAGGCTGCCCGAGCAGCAGTGGCAACGCGCAC 3474
DB 65324 GGGTGGGGCCAGATTAAGAGATTAAGAGCAGGCTGCCCGAGCAGCAGTGGCAACGCGCAC 65265
QY 3475 AGGTCCCTATCCACAAATATGAGCAGCTTTGTCTTTTGTGCTGTTGGATTAATCTTGCTAC 3534
DB 65264 AGGTCCCTATCCACAAATATGAGCAGCTTTGTCTTTTGTGCTGTTGGATTAATCTTGCTAC 65205
QY 3535 TGGTCGCTTTTGGGTCCACAGCTGTTTATGAGCTGTATACCTACACAGAGAGTGTGC 3594
DB 65204 TGGTCGCTTTTGGGTCCACAGCTGTTTATGAGCTGTATACCTACACAGAGAGTGTGC 65145
QY 3595 AGCTTCACTCCCTAAGGCACTAAGACACGACCCACCGGAGAGATGAACAACCTCCGCG 3654
DB 65144 AGCTTCACTCCCTAAGGCACTAAGACACGACCCACCGGAGAGATGAACAACCTCCGCG 65085
QY 3655 CGGCTGCTTTAAGAGCTATTAACACTACCGGAGGTCTGACGTTCTACTCTCAGCCA 3714
DB 65084 CGGCTGCTTTAAGAGCTATTAACACTACCGGAGGTCTGACGTTCTACTCTCAGCCA 65025
QY 3715 GCGAGACCAAGAACCCACGAAAGAAAGTGCAGAACATCTGAACATGAGAGAA 3774
DB 65024 GCGAGACCAAGAACCCACGAAAGAAAGTGCAGAACATCTGAACATGAGAGAA 64965
QY 3775 CAACCTCCAGATCCACACCTTAAGAGCTGTAACTACCTACCTGAGAGGTCCGCGCTCC 3834
DB 64964 CAACCTCCAGATCCACACCTTAAGAGCTGTAACTACCTACCTGAGAGGTCCGCGCTCC 64905
QY 3835 TTCTTGAAGTCACTGAGACCAAGCACTCACAGTTTGGACACAAAGCCAGAGTTTGAG 3894
DB 64904 TTCTTGAAGTCACTGAGACCAAGCACTCACAGTTTGGACACAAAGCCAGAGTTTGAG 64845
QY 3895 ATCAGCCTGGGCAACATGATGAATGCCCTCTGCAAAAAAATTTCAAAAAT 3954
DB 64844 ATCAGCCTGGGCAACATGATGAATGCCCTCTCTGCG-AAAAAATAAATAATTTCAAAAAT 64786
QY 3955 TGGCGAGCATGGTGTGCTGCTGTGTGCCAGCTACGCGGAGGCTAAAGTGGAGG 4014
DB 64785 TGGCGAGCATGGTGTGCTGCTGTGTGCCAGCTACGCGGAGGCTAAAGTGGAGG 64726
QY 4015 ATGCGTTGAGCCTGGGAGGTGAAGACTGCACTGCTGTATTTACCAAGCCCTTAG 4074
DB 64725 ATGCGTTGAGCCTGGGAGGTGAAGACTGCACTGCTGTATTTACCAAGCCCTTAG 64666
QY 4075 GCTGGGGAGACAGACTGAGACCTGTTCCCTCGCAAAAAAATTTGCAAAAGTGTATA 4134
DB 64665 GCTGGGGAGACAGACTGAGACCTGTTCCCTCGCAAAAAAATTTGCAAAAGTGTATA 64606
QY 4135 AGAGGTGCTGATATGCTAGGCGCAGCTGCTCATGCTTAATCCAGCAGCTTTGGAA 4194
DB 64605 AGAGGTGCTGATATGCTAGGCGCAGCTGCTCATGCTTAATCCAGCAGCTTTGGAA 64546
QY 4195 GCGGAGGCGGGGCTCACTAAGGTGAGAGTGTGAGACAGCCTGGCAACATGGAGA 4254
DB 64545 GCGGAGGCGGGGCTCACTAAGGTGAGAGTGTGAGACAGCCTGGCAACATGGAGA 64486
QY 4255 AAGCCCATCTCTTCTAATAAATTAACAAATTTAGCGGCTGTGGGGGCACTGGGAGCTGC 4314
DB 64485 AAGCCCATCTCTTCTAATAAATTAACAAATTTAGCGGCTGTGGGGGCACTGGGAGCTGC 64426
QY 4315 CTGTAAATCCAGCTACTCAGAGGCTGAGGCAAGAGATCACTTGAACCCAGAGGCGGC 4374
DB 64425 CTGTAAATCCAGCTACTCAGAGGCTGAGGCAAGAGATCACTTGAACCCAGAGGCGGC 64366
QY 4375 GGTTCGAGTACGCGAGATGTGCTCATTTGCACTCCACCTCCAGCCTGGCAACAGA 4434
DB 64365 GGTTCGAGTACGCGAGATGTGCTCATTTGCACTCCACCTCCAGCCTGGCAACANN 64306

QY 4435 GCCAACTCTGTCTTAATAAATAAATAAAGTGCCTGCATATAAGAGCTGTGCATG 4494
DB 64305 NNN 64246
QY 4495 CAATAGTGGCCAGCAACATGTTAAGAAATGTGAGACTCTGCTT-CCATGCTCTGT 4553
DB 64245 NNN 64186
QY 4554 AAAAAACCACCTCAAGGCCAGGTGCAGTGCCTCATGCTTAATCCACACTTTGGGA 4613
DB 64185 TCATTCATTCATCAATTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 64126
QY 4614 GCGCGAGGCG--GGTGATCAGCTGAGCTGAGAGTTGAGACAGCTGACCAACACACA 4671
DB 64125 GCGTGAGTCAAGTGGAGCTATCTTGGCTCACTGCACACCTGCTCTCTGGTTCAAGCG 64066
QY 4672 TGGTGAATCCACACTCTACTTAATAAATAAATTAAGATAGCATGGTGTGATGCTG 4731
DB 64065 ATTCTCTTGGCTCAGCTCTCTGAGTACTGGGATTAACAGCGGCTGCACCTATGCCAGC 64006
QY 4732 TAATCCACCTACTTGGGAGCTGAGGCAAGAAATCACTAGAACAAGGAG--GCG 4786
DB 64005 TAATGTTTGTATTTTATTAAGAGACAGGATTCACCATGTCAAGCGCTGTCTCGAA 63946
QY 4787 GAGGTGTAGTGAAGCCGAGATCGGCTATGCACTCCAGCTGAGCAATGAGGAAATC 4846
DB 63945 CTGCTGCTCAAAATTAATCTGCCCCCTTGGCTCCCAAGTGTGAGAGTGGGATTA 63886
QY 4847 CATCTCAAAAAACACACACAAAAACCCTCTCTACTCTCCAGGAGCTGGGTACAGAGC 4906
DB 63885 CAGGATGAGACACACACACCCGCGCATTCATTCATTAATTTGTAAGTAAAGAGGCCCTGT 63826
QY 4907 TGGG-----CCATCATGTCAGAGTGTGAGCCACAGAGCTAAAGCGGAGCTG 4955
DB 63825 TAGGTTCTGGGAGACCAAAATATTATTAACTGTGTCCCACTTGAATAATCTCTAGT 63766
QY 4956 CAGGACGCGGAGACAGATTAACAGTGTGATGATGATGATGATGATGATGATGATGATGATG 5015
DB 63765 CTATATGAGATTAATTAACCTAATTTGTGATTAACCAAAACATGCTTAATTAACCAAG 63706
QY 5016 ATTGCTGACCAACGAGGCGGCCCCAACACAGATGCCCCATCCAGTCCACACATCC 5075
DB 63705 AACTACTTATGCTGTGATTAAGAAAGCTTTTTCATTCCTCTTACGTGACCTGA 63646
QY 5076 ACTTCTATCAGAGATGTCTGTTCTTGGCAGCGCTGGGTAATTAAGCAGAGGTGA 5135
DB 63645 GTTTGTATTTGTGACACTGCAAAATGTTTATTAACCAATTTGATTTGATGATGATGATG 63586
QY 5136 CAGTCTTGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5195
DB 63585 AATTTTACTAAGATTTGATTTTAACATGCTTTTAACCTTTTCTTCTTTTAAAAA 63526
QY 5196 TCAAGCCTAGCGGCGGACGCTGACAGCTCCAGGCAAGGCTTGGGCTGTAGAAAACT 5255
DB 63525 AGATAGAGTGGCTGGGCGGCTGACAGCTCCGTAATCTTACACTTTGGAGGCGCAAG 63466
QY 5256 GCGGCTGATCA--CGAGGTCAAGAGTGTGATGATGATGATGATGATGATGATGATGATG 5313
DB 63465 GTGGGCGATCACTGTGAGTGCAGAGTTCCAGACCACTGACCAACATGGAAGAAACCT 63406
QY 5314 GTCTCTACTAATAAATAAATAAATTTAGCGGAGTGTGGGCACTGTAGTCCAGC 5373
DB 63405 GCTCTACTAATAAATG--AAAAATTAACAGGCAAGTGTGATGATGATGATGATGATGATG 63348
QY 5374 TACTCGGAGGCTGAGGCAAGATGCTGAACCCGAGAGGCTAGATTTGAGAGTGC 5433
DB 63347 TACTCGGAGGCTGAGGCAAGATGCTGAACCCGAGAGGCTAGATTTGAGAGTGC 63288
QY 5434 CGAGATCGCGCACTGCACTCCAGCTGGGCGAG--AGAGCAAGCTCATCTGGAAGAA 5492
DB 63287 CGAGATCGCGCACTGCACTCCAGCTGGGCGAGAGGAGGAGAACTCTGCTCAAAAAA 63228
QY 5493 AAAAAAAGCTTACG 5508

Db 63227 AAAAAAAAAAGATGAG 63212

RESULT 9
LOCUS AR156465 2834 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242218.
ACCESSION AR156465
VERSION AR156465.1 GI:15125169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2834)
AUTHORS Treco,D.A., Heartlein,M.W. and Selden,R.F.
TITLE Genomic sequences for protein production and delivery
JOURNAL Patent: US 6242218-A 6 05-JUN-2001;
FEATURES
source location/Qualifiers
1..2834
BASE COUNT 670 a /organism="unknown"
ORIGIN 759 c 817 g 588 t

Query Match 45.5%; Score 2834; DB 6; Length 2834;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2834; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CCGGAGTCCTCAGACCCCTCGTTCGCTCGGCGCTCCTCGCTGGGCTCCACTTC 1949
Db 1 CCGGAGTCCTCAGACCCCTCGTTCGCTCGGCGCTCCTCGCTGGGCTCCACTTC 60

QY 1950 GGTGGCACTTGAAGAGCCCTTCAGCCACCAGCTGCACTGTGGAGCCCTTCTGGGCTG 2009
Db 61 GGTGGCACTTGAAGAGCCCTTCAGCCACCAGCTGCACTGTGGAGCCCTTCTGGGCTG 120

QY 2010 GCCAAGCCAGAGCCGGCTCCCTCAGCTTGCAGAGGAGTGTGAGGAGAGAGGCTCAAGCA 2069
Db 121 GCCAAGCCAGAGCCGGCTCCCTCAGCTTGCAGAGGAGTGTGAGGAGAGAGGCTCAAGCA 180

QY 2070 GGAACCGGGGCTGCGCAGCGGCTTGCGGCCAGCTGAGATTCCGGGTGGGCTTG 2129
Db 181 GGAACCGGGGCTGCGCAGCGGCTTGCGGCCAGCTGAGATTCCGGGTGGGCTTG 240

QY 2130 GGGGGGCCCCGCACTGGAGCAGCGGGCCAGCCCTGCCAGGCCCGGGCAATGAGAGCT 2189
Db 241 GGGGGGCCCCGCACTGGAGCAGCGGGCCAGCCCTGCCAGGCCCGGGCAATGAGAGCT 300

QY 2190 TAGCACCGGGGCGAGGGGCTGGGAGGGTGTACTGGTCCCGACAGATGCCAGCCGCC 2249
Db 301 TAGCACCGGGGCGAGGGGCTGGGAGGGTGTACTGGTCCCGACAGATGCCAGCCGCC 360

QY 2250 GGGGCTGTGCTGCTGATTTCTCACTGGGCTTACAGACCTTCCGCGGGGCGAGGCTC 2309
Db 361 GGGGCTGTGCTGCTGATTTCTCACTGGGCTTACAGACCTTCCGCGGGGCGAGGCTC 420

QY 2310 GGGAGCTGCAAGCCCGCATGCTGAGGCTTCCCTCCATGGGCTCTGTGCGGCCAGGCC 2369
Db 421 GGGAGCTGCAAGCCCGCATGCTGAGGCTTCCCTCCATGGGCTCTGTGCGGCCAGGCC 480

QY 2370 TCCCGACAGACACACCCCTGCTCAAGAGGCCAGTCCCATGACACAGAGGCT 2429
Db 481 TCCCGACAGACACACCCCTGCTCAAGAGGCCAGTCCCATGACACAGAGGCT 540

QY 2430 GAGAAGTGGGGGCGAGCGGACCGGGAGTGGAGGAGAGTACCCCTGGAGCCCTGGTGG 2489
Db 541 GAGAAGTGGGGGCGAGCGGACCGGGAGTGGAGGAGAGTACCCCTGGAGCCCTGGTGG 600

QY 2490 GAATCACTGGTGAAGCAGCTGGGCTCTGAGTCTGTGAGACTTGGAGAACCCTTGA 2549
Db 601 GAATCACTGGTGAAGCAGCTGGGCTCTGAGTCTGTGAGACTTGGAGAACCCTTGA 660

QY 2550 TGTCTAGCTCAGGATCGTAAATACACAATACAGACCCCTGTGTAGCTCAGGCTCTGT 2609

Db 661 TGTCTAGCTCAGGATCGTAAATACACAATACAGACCCCTGTGTAGCTCAGGCTCTGT 720

QY 2610 GAATGACCAATCCACACTGTGTATCTAGTACTGTGATGGGCTTGGAGAACCTTTAT 2669
Db 721 GAATGACCAATCCACACTGTGTATCTAGTACTGTGATGGGCTTGGAGAACCTTTAT 780

QY 2670 GTCTAGCTCAGGATGTAAATACACAATCCGACCTGTATCTAGCTCAAGTGTGA 2729
Db 781 GTCTAGCTCAGGATGTAAATACACAATCCGACCTGTGTATCTAGCTCAAGTGTGA 840

QY 2730 AACACCAATACGACCCCTGTGTCTAGCTCAGGATGTGATGATGACCAATCGACAGTC 2789
Db 841 AACACCAATACGACCCCTGTGTCTAGCTCAGGATGTGATGATGACCAATCGACAGTC 900

QY 2790 TGTATCTGCTACTTTCATATGAGGATCCGTTGTAAGAGACACCAACAGCTTGTGTGA 2849
Db 901 TGTATCTGCTACTTTCATATGAGGATCCGTTGTAAGAGACACCAACAGCTTGTGTGA 960

QY 2850 GCATTAAGCTTCTATCACCCTGGGTGAGGTGGGCTGAGTCCGAAAAAGAGTCAAGCA 2909
Db 961 GCATTAAGCTTCTATCACCCTGGGTGAGGTGGGCTGAGTCCGAAAAAGAGTCAAGCA 1020

QY 2910 GGGAGATTAAGGGGGGGCGGTTTATAGATTTGGTATGAGTAAGGAAAAATACAGTCAA 2969
Db 1021 GGGAGATTAAGGGGGGGCGGTTTATAGATTTGGTATGAGTAAGGAAAAATACAGTCAA 1080

QY 2970 AGGGGGTTTCTCTCGGGGCGAGAGTGGGGGTCGCAAGGTGCTCAGTGGGGGCTGCT 3029
Db 1081 AGGGGGTTTCTCTCGGGGCGAGAGTGGGGGTCGCAAGGTGCTCAGTGGGGGCTGCT 1140

QY 3030 TTTTGAGCAGAGATGACCAAGAAAGACTTTCACAGGTAATGTCAATTAAGGCA 3089
Db 1141 TTTTGAGCAGAGATGACCAAGAAAGACTTTCACAGGTAATGTCAATTAAGGCA 1200

QY 3090 AGGACCGGCAATTAACCTTTTGTGGTGAATCTCATCTTAAGTTGGGGCGAGGC 3149
Db 1201 AGGACCGGCAATTAACCTTTTGTGGTGAATCTCATCTTAAGTTGGGGCGAGGC 1260

QY 3150 ATATTACATCTTTTGTGATTTCTCAGTACTTCAAGGCATCGGCGATATATGTCAG 3209
Db 1261 ATATTACATCTTTTGTGATTTCTCAGTACTTCAAGGCATCGGCGATATATGTCAG 1320

QY 3210 TTACAGGGATGGATGGCTTGGCTGAGAGGCTTGAAGCTACTGTGGGGC 3269
Db 1321 TTACAGGGATGGATGGCTTGGCTGAGAGGCTTGAAGCTACTGTGGGGC 1380

QY 3270 CTTTGAAGATCTTTGTGTGACACCTGTATCTAGTTATCTAGTGGGACGTGGAGAAC 3329
Db 1381 CTTTGAAGATCTTTGTGTGACACCTGTATCTAGTTATCTAGTGGGACGTGGAGAAC 1440

QY 3330 CTTTGTGTAGCTCAGGATTTGTAAACGACCAATCAGCGCCCTGTCAAAACAGACAC 3389
Db 1441 CTTTGTGTAGCTCAGGATTTGTAAACGACCAATCAGCGCCCTGTCAAAACAGACAC 1500

QY 3390 TCGGCTCTACCAATCAGAGATGTGGGTGGGCCAGATTAAGATAAAGCAGGCTGC 3449
Db 1501 TCGGCTCTACCAATCAGAGATGTGGGTGGGCCAGATTAAGATAAAGCAGGCTGC 1560

QY 3450 CCGAGCAGAGTGGCAGACGGCAGAGTCCCTATCCACAAATATGGCAGCTTGTCTTT 3509
Db 1561 CCGAGCAGAGTGGCAGACGGCAGAGTCCCTATCCACAAATATGGCAGCTTGTCTTT 1620

QY 3510 TGTGTGTGGGATTAATCTTGTACTGCTGCGCTTTTGGGTCCACACAGCTTTTATGAGC 3569
Db 1621 TGTGTGTGGGATTAATCTTGTACTGCTGCGCTTTTGGGTCCACACAGCTTTTATGAGC 1680

QY 3570 TGTAACTACACACAGAGGTCTGAGCTTCACTCCTGAAGGCATTAAGACACAGAGCC 3629
Db 1681 TGTAACTACACACAGAGGTCTGAGCTTCACTCCTGAAGGCATTAAGACACAGAGCC 1740

QY 3630 ACCGGGAGGATGAACAACCTCGGCGGCTGCTTAAAGAGCTATTAACCTCACCGCGAA 3689
Db 1741 ACCGGGAGGATGAACAACCTCGGCGGCTGCTTAAAGAGCTATTAACCTCACCGCGAA 1800

Db 1741 ACCGGGAGGAAATGAACAACCTCCGGCCGCTGCTTAAGAGCTATTAACCTACCGCGAA 1800
QY 3690 GGTCGACAGCTTCACTCTCACCAGCGAGACCAAGAACCCACAGAGAGAAATCTC 3749
Db 1801 GGTCTGACAGCTTCACTCTCACCAGCGAGACCAAGAACCCACAGAGAGAAATCTC 1860
QY 3750 GAACACATCTGAACATCAGAGAGAACAACTCCAGATGACCACTTAAGAGCTGTAA 3809
Db 1861 GAACACATCTGAACATCAGAGAGAACAACTCCAGATGACCACTTAAGAGCTGTAA 1920
QY 3810 CTCACCTGCGAGGTCGCGGCTCTCTTGAAGTCAGTGAAGCAAGCACTCACAGTT 3869
Db 1921 CTCACCTGCGAGGTCGCGGCTCTCTTGAAGTCAGTGAAGCAAGCACTCACAGTT 1980
QY 3870 TGGGACACAGCCGAGAGTTGAGATCAGCTGGGCAACATGATGAATGCCCTCTCG 3929
Db 1981 TGGGACACAGCCGAGAGTTGAGATCAGCTGGGCAACATGATGAATGCCCTCTCG 2040
QY 3930 CAAAAAATTTGACAAAAATTTGGCGAGCATGTTGTCCTGCTGTCCTGTCCTG 3989
Db 2041 CAAAAAATTTGACAAAAATTTGGCGAGCATGTTGTCCTGCTGTCCTGTCCTG 2100
QY 3990 CTACGCGGAGGCTAAAGTGGAGAGATCGCTTGAAGCTGGAGGTGAAGACTGCACTGAG 4049
Db 2101 CTACGCGGAGGCTAAAGTGGAGAGATCGCTTGAAGCTGGAGGTGAAGACTGCACTGAG 2160
QY 4050 CTGTATTTGTACCAACAGCCCTTAGGCTGGGGGACAGACTGAGACCTCTTCCCTCG 4109
Db 2161 CTGTATTTGTACCAACAGCCCTTAGGCTGGGGGACAGACTGAGACCTCTTCCCTCG 2220
QY 4110 CAAAAAATTTGACAAAAATTTGAAGAGAGTCTGATATGCTAGGCGCAGTGCAT 4169
Db 2221 CAAAAAATTTGACAAAAATTTGAAGAGAGTCTGATATGCTAGGCGCAGTGCAT 2280
QY 4170 GCTGTATTCAGCAGACTTTGGGAAGCCGAGCGGGGCTCACTAAGTCAAGAGTCT 4229
Db 2281 GCTGTATTCAGCAGACTTTGGGAAGCCGAGCGGGGCTCACTAAGTCAAGAGTCT 2340
QY 4230 GAGACAGGCTGGCCAACTGGAAGAAAGCCATCTTTAAATAATACAAATTAAGCCG 4289
Db 2341 GAGACAGGCTGGCCAACTGGAAGAAAGCCATCTTTAAATAATACAAATTAAGCCG 2400
QY 4290 CTGTGGGGGAGTGTGAGCATGCTGTATTCAGTACTCAGAGGCTGAGGAGGA 4349
Db 2401 CTGTGGGGGAGTGTGAGCATGCTGTATTCAGTACTCAGAGGCTGAGGAGGA 2460
QY 4350 GAATCACTTGAACCCAGAGGCGCGGTTGCAGTGAGCCGAGATCGTCCATTCACCTCC 4409
Db 2461 GAATCACTTGAACCCAGAGGCGCGGTTGCAGTGAGCCGAGATCGTCCATTCACCTCC 2520
QY 4410 ACCCACTCCAGGCTGGGCAACAAAGAGCCAACTCTCTTAAATAATTAAGAGTCTG 4469
Db 2521 ACCCACTCCAGGCTGGGCAACAAAGAGCCAACTCTCTTAAATAATTAAGAGTCTG 2580
QY 4470 CCTGACATTAAGAGGTGTGCAATGCAATGTTGCCAGGCAACATTTAAAGATGTGA 4529
Db 2581 CCTGACATTAAGAGGTGTGCAATGCAATGTTGCCAGGCAACATTTAAAGATGTGA 2640
QY 4530 GCTCTGCTTCATGCTCTGTAAATAATCCACCTCAAGGCGAGGTCAGTGCAT 4589
Db 2641 GCTCTGCTTCATGCTCTGTAAATAATCCACCTCAAGGCGAGGTCAGTGCAT 2700
QY 4590 GCTCTAATCCAGACATTTGGAGGCGAGGCGGTGATACCTGAGAGTCAAGAGTTC 4649
Db 2701 GCTCTAATCCAGACATTTGGAGGCGAGGCGGTGATACCTGAGAGTCAAGAGTTC 2760
QY 4650 GAGACAGGCTGACCAACCAATGTGTAATCCACCTTACTATAAATAACAAATTTAGA 4709
Db 2761 GAGACAGGCTGACCAACCAATGTGTAATCCACCTTACTATAAATAACAAATTTAGA 2820
QY 4710 TGAGCATGTGTGTG 4723
Db 2821 TGAGCATGTGTGTG 2834

RESULT 10
AF388025 5527 bp DNA linear PRI 14-JUN-2001
LOCUS Homo sapiens colony stimulating factor 3 (granulocyte) (CSF3) gene,
DEFINITION complete cds.
ACCESSION AF388025
VERSION AF388025.1 GI:14423572
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 5527)
AUTHORS Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
Yi,Q. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2001) Molecular Biotechnology, University of
Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: SeattleSNPs, NHLBI Program for
Genomic Applications, UW-FHCRC, Seattle, WA (URL:
http://pga.mbl.washington.edu).
FEATURES
source location/Qualifiers
1..5527
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
14..315
/rpt_family="AluX"
/rpt_type=dispersed
28
/frequency="0.43"
/replace="A"
321
/frequency="0.26"
/replace="T"
379
/frequency="0.04"
/replace="T"
649..944
/rpt_family="AluY"
/rpt_type=dispersed
789
/frequency="0.06"
/replace="T"
956..1089
/rpt_family="MIR3"
/rpt_type=dispersed
1158
/frequency="0.18"
/replace="A"
1577
/frequency="0.01"
/replace="T"
1607
/frequency="0.17"
/replace="C"
1619
/frequency="0.01"
/replace="A"
1980
/frequency="0.49"
/replace="G"
2005..4378
/gene="CSF3"
join(2005..2079,2256..2419,2798..2905,3050..3196,
3361..4378)
/gene="CSF3"
/product="colony stimulating factor 3 (granulocyte)"
2024
/gene="CSF3"
/frequency="0.02"

CDS
/replace="G"
join(2040..2079,2256..2419,2798..2905,3050..3196,
3361..3525)
/gene="CSF3"
/codon_start=1
/product="colony stimulating factor 3 (granulocyte)"
/db_xref="GI:14423573"
/translation="MAGPATQSPKIMALQLLHMSALMTVOEATPLGPASSLSQSF
LKCLEQYRKIOGDGALQEKLVSECAVYKCHPELVILGHSIGIIPAPLSSCPGAL
QLAGLSLSLGLFTYGLALEGISELGPPLTDQLDVADEATTIMQMEELGMA
PALOPTGAMPAPASANQRRAGVIVASHQSFLEVSRYLRHHAQ"
2504
variation
/gene="CSF3"
/frequency="0.07"
/replace="G"
2584
variation
/gene="CSF3"
/frequency="0.08"
/replace="T"
2589
variation
/gene="CSF3"
/frequency="0.01"
/replace="C"
2617
variation
/gene="CSF3"
/frequency="0.05"
/replace="T"
2725
variation
/gene="CSF3"
/frequency="0.01"
/replace="C"
2734
variation
/gene="CSF3"
/frequency="0.01"
/replace="A"
2764
variation
/gene="CSF3"
/frequency="0.03"
/replace="T"
3254
variation
/gene="CSF3"
/frequency="0.03"
/replace="A"
3370
variation
/gene="CSF3"
/frequency="0.03"
/replace="A"
3421
variation
/gene="CSF3"
/frequency="0.02"
/replace="A"
3456
variation
/gene="CSF3"
/frequency="0.16"
/replace="A"
3666
variation
/gene="CSF3"
/frequency="0.03"
/replace="T"
4050
variation
/gene="CSF3"
/frequency="0.23"
/replace="T"
4105
variation
/gene="CSF3"
/frequency="0.03"
/replace="C"
4145
variation
/gene="CSF3"
/frequency="0.01"
/replace="A"
4215

/gene="CSF3"
/frequency="0.47"
/replace="T"
4480
variation
/frequency="0.16"
/replace="G"
4522
variation
/frequency="0.02"
/replace="T"
4530..4762
repeat_region
/rpt_family="L2"
/rpt_type=dispersed
4993
variation
/frequency="0.02"
/replace="T"
5168
variation
/frequency="0.47"
/replace="G"
BASE COUNT 1195 a 1571 c 1673 g 1088 t
ORIGIN

Query Match 25.9% Score 1612.4; DB 9; Length 5527;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1663; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

QY 4557 AACCCACCTCAGGCGCAGGTGCAAGTGGCTCATCTATTAATCCACACTTTGGAGGC 4616
DB 1 AACCCACCTCAGGCGCAGGTGCAAGTGGCTCATCTATTAATCCACACTTTGGAGGC 60
QY 4617 CGAGCGGGGAGTACCTGAGTGCAGAGTTCGAGACGAGCCGACACCAATCATGTG 4676
DB 61 CGAGCGGGGAGTACCTGAGTGCAGAGTTCGAGACGAGCCGACACCAATCATGTG 120
QY 4677 AATCCACCTCTACTATAAATACAAATTAGATGACCATGTGTGTCATGCTGTATC 4736
DB 121 AATCCACCTCTACTATAAATACAAATTAGATGACCATGTGTGTCATGCTGTATC 180
QY 4737 CCACCTACTTGGAGGCTGAGGCGAGAAATCACTAAGACGAGGAGCGGAGGTTAG 4796
DB 181 CCACCTACTTGGAGGCTGAGGCGAGAAATCACTAAGACGAGGAGCGGAGGTTAG 240
QY 4797 TGAGCGAGATCGTGCATTCGACCTGAGCAATGAGCGAACTCCATCTCAAA 4856
DB 241 TGAGCGAGATCGTGCATTCGACCTGAGCAATGAGCGAACTCCATCTCAAA 300
QY 4857 AACACACACAAAAACCACTCTCTACTCCAGGAGCTGGGTACAGAGCTGGGCACAT 4916
DB 301 AACACACACAAAAACCACTCTCTACTCCAGGAGCTGGGTACAGAGCTGGGCACAT 360
QY 4917 CAGTGCAGAGTGTGAGCCACAGACTTAAGCGGAGCTGCAGACCGCGGACGATPAC 4976
DB 361 CAGTGCAGAGTGTGAGCCACAGACTTAAGCGGAGCTGCAGACCGCGGACGATPAC 420
QY 4977 AGTGTGAGATCGATGTGTGAGATCAGAGCTCCCTGCATTTGGTGAACCAACAGGGGCC 5036
DB 421 AGTGTGAGATCGATGTGTGAGATCAGAGCTCCCTGCATTTGGTGAACCAACAGGGGCC 480
QY 5037 CCCAAGCAGCAGAGATGGCCCATCAGTACACCATCCATTCTCATCCAGAGATGCT 5096
DB 481 CCCAAGCAGCAGAGATGGCCCATCAGTACACCATCCATTCTCATCCAGAGATGCT 540
QY 5097 GTTCTTGGCAGCGTGGGGTAAATTAGACAGAAAGTACAGTCTGGGTGTGTCAGTC 5156
DB 541 GTTCTTGGCAGCGTGGGGTAAATTAGACAGAAAGTACAGTCTGGGTGTGTCAGTC 600
QY 5157 AGACTGCCCGCAGGAGCTTGTGTGCTGTAGAAAAGTTCAGGCTCAGGCGGCGACGG 5216
DB 601 AGACTGCCCTTATTCTGCTTGTGCTGTAGAAAAGTTCAGGCTCAGGCGGCGACGG 660
QY 5217 TGCTCAGCGCTGTAAATCCAGCACTTTGGAGGCGGAGCGGCTGATACGAGGTACG 5276
DB 661 T-GCTCAGCGCTGTAAATCCAGCACTTTGGAGGCGGAGCGGCTGATACGAGGTACG 719


```
* 30257 30356: gap of unknown length
* 30357 30356: contig of 2627 bp in length
* 32984 32983: gap of unknown length
* 33083 33083: contig of 2376 bp in length
* 33084 33083: gap of unknown length
* 35460 35459: gap of unknown length
* 35559 35559: gap of unknown length
* 39128 39128: contig of 3569 bp in length
* 39129 39128: gap of unknown length
* 39229 39228: contig of 3380 bp in length
* 42609 42708: gap of unknown length
* 42709 42708: contig of 4359 bp in length
* 47068 47167: gap of unknown length
* 47168 50792: contig of 3625 bp in length
* 50793 50893: gap of unknown length
* 50893 55282: contig of 4390 bp in length
* 55283 55382: gap of unknown length
* 55383 59386: contig of 4004 bp in length
* 59387 59486: gap of unknown length
* 59487 64208: contig of 4722 bp in length
* 64209 64308: gap of unknown length
* 64309 68973: contig of 4665 bp in length
* 68974 69073: gap of unknown length
* 69074 73514: contig of 4441 bp in length
* 73515 73614: gap of unknown length
* 73615 79235: contig of 5621 bp in length
* 79236 79335: gap of unknown length
* 79336 84273: contig of 4938 bp in length
* 84274 84373: gap of unknown length
* 84374 89567: contig of 5194 bp in length
* 89568 89667: gap of unknown length
* 89668 95452: contig of 5785 bp in length
* 95453 95552: gap of unknown length
* 95553 101367: contig of 5815 bp in length
* 101368 101467: gap of unknown length
* 101468 108294: contig of 6827 bp in length
* 108295 108394: gap of unknown length
* 108395 115531: contig of 7137 bp in length
* 115532 115631: gap of unknown length
* 115632 125051: contig of 9420 bp in length
* 125052 125151: gap of unknown length
* 125152 134705: contig of 9554 bp in length
* 134706 134805: gap of unknown length
* 134806 145490: contig of 10685 bp in length
* 145491 145590: gap of unknown length
* 145591 155823: contig of 10233 bp in length
* 155824 155923: gap of unknown length
* 155924 170624: contig of 14701 bp in length
* 170625 170724: gap of unknown length
* 170725 184829: contig of 14105 bp in length
* 184830 203099: gap of unknown length
* 203099 203199: contig of 18170 bp in length
* 203100 221484: gap of unknown length
* 221484 221484: contig of 18285 bp in length.

FEATURES
    source
        1. .221484
            Location/Qualifiers
                1. .221484
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /chromosome="17"
                    /clone="RP11-387H17"
                    1. .1523
                        misc_feature
                            /note="assembly_name:Contig17"
                            1624. .2830
                                misc_feature
                                    /note="assembly_name:Contig18"
                                    2931. .4445
                                        misc_feature
                                            /note="assembly_name:Contig19"
                                            4546. .5643
                                                misc_feature
                                                    /note="assembly_name:Contig20"
                                                    5744. .7022
                                                        misc_feature
                                                            /note="assembly_name:Contig21"
                                                            7123. .8983
                                                                misc_feature
                                                                    /note="assembly_name:Contig22"
                                                                    9084. .11092
                                                                        misc_feature
                                                                            /note="assembly_name:Contig23"

misc_feature 11193. .12752
                /note="assembly_name:Contig24"
                12853. .14247
                    misc_feature
                        /note="assembly_name:Contig25"
                        14348. .16451
                            misc_feature
                                /note="assembly_name:Contig26"
                                16552. .18402
                                    misc_feature
                                        /note="assembly_name:Contig27"
                                        18503. .21089
                                            misc_feature
                                                /note="assembly_name:Contig28"
                                                21190. .24337
                                                    misc_feature
                                                        /note="assembly_name:Contig29"
                                                        24438. .27881
                                                            misc_feature
                                                                /note="assembly_name:Contig30"
                                                                27982. .30256
                                                                    misc_feature
                                                                        /note="assembly_name:Contig31"
                                                                        clone_end:SP6
                                                                        vector_side:left"
                                                                        30357. .32983
                                                                            misc_feature
                                                                                /note="assembly_name:Contig32"
                                                                                33084. .35459
                                                                                    misc_feature
                                                                                        /note="assembly_name:Contig33"
                                                                                        35560. .39128
                                                                                            misc_feature
                                                                                                /note="assembly_name:Contig34"
                                                                                                39229. .42608
                                                                                                    misc_feature
                                                                                                        /note="assembly_name:Contig35"
                                                                                                        42709. .47067
                                                                                                            misc_feature
                                                                                                                /note="assembly_name:Contig36"
                                                                                                                47168. .50792
                                                                                                                    misc_feature
                                                                                                                        /note="assembly_name:Contig37"
                                                                                                                        50893. .55282
                                                                                                                            misc_feature
                                                                                                                                /note="assembly_name:Contig38"
                                                                                                                                55383. .59386
                                                                                                                                    misc_feature
                                                                                                                                        /note="assembly_name:Contig39"
                                                                                                                                        59487. .64208
                                                                                                                                            misc_feature
                                                                                                                                                /note="assembly_name:Contig40"
                                                                                                                                                64309. .68973
                                                                                                                                                    misc_feature
                                                                                                                                                        /note="assembly_name:Contig41"
                                                                                                                                                        69074. .73514
                                                                                                                                                            misc_feature
                                                                                                                                                                /note="assembly_name:Contig42"
                                                                                                                                                                73615. .79235
                                                                                                                                                                    misc_feature
                                                                                                                                                                        /note="assembly_name:Contig43"
                                                                                                                                                                        79336. .84273
                                                                                                                                                                            misc_feature
                                                                                                                                                                                /note="assembly_name:Contig44"
                                                                                                                                                                                84374. .89567
                                                                                                                                                                                    misc_feature
                                                                                                                                                                                        /note="assembly_name:Contig45"
                                                                                                                                                                                        89668. .95452
                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                /note="assembly_name:Contig46"

Query Match      22.9%; Score 1424.8; DB 2; Length 221484;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1480; Conservative 0; Mismatches 17; Indels 5; Gaps 4;
```


QY	5032	GGGGCCCCAAGCACACAGAGATGGGCCCATCCAGTCCACACACATCCACTTCATCCACAGGA	5091
Db	299	GGGGCCCCAAGCACACAGAGATGGGCCCATCCAGTCCACACACATCCACTTCATCCACAGGA	358
QY	5092	TGTCCTGTTTCTTGGACAGCTGGGGGTAAATTAGACAGAAAGGTGACAGTCTTGSGTGTGT	5151
Db	359	TGTCCTGTTTCTTGGACAGCTGGGGGTAAATTAGACAGAAAGGTGACAGTCTTGSGTGTGT	418
QY	5152	CAGTCAGACTGCCCCAGGCAAGGCCCTTGTGGCCTGTAGAAAAAGTTCAAGGCCCTAGCCGGG	5211
Db	419	CAGTCAGACTGCCCCAGGCAAGGCCCTTGTGGCCTGTAGAAAAAGTTCAAGGCCCTAGCCGGG	478
QY	5212	CACGGGTGCTACGCCCTGTATATCCACAGACTTTTGGAGGCGGAGGGGGGTGATACAGAG	5271
Db	479	CACGGGTGCTACGCCCTGTATATCCACAGACTTTTGGAGGCGGAGGGGGGTGATACAGAG	538
QY	5272	GTCAGAGATGCTGATCATCCTGGCTTAACAGGGGAACCCCGTCTACTAAAAATACA	5331
Db	539	GTCAGAGATGCTGATCATCCTGGCTTAACAGGGGAACCCCGTCTACTAAAAATACA	598
QY	5332	AAAAATTTGGCCGGGCATGATGGCGGCGACCTGTATGTTCCAGCTACTGTGGAGGCTGAGGC	5391
Db	599	AAAAATTTGGCCGGGCATGATGGCGGCGACCTGTATGTTCCAGCTACTGTGGAGGCTGAGGC	658
QY	5392	AGGAGATTTGGCGTGTAAACCCAGAGGCGAGAGTTTCCAGTGAAGCCGAGATCCGCCACATGCA	5451
Db	659	AGGAGATTTGGCGTGTAAACCCAGAGGCGAGAGTTTCCAGTGAAGCCGAGATCCGCCACATGCA	718
QY	5452	CTCCAGGCTGGGGCGACAGAGCAACATCTGTGAAAAAGAAAAAGAAACGTTCAAGTGC	5511
Db	719	CTCCAGGCTGGGGCGACAGAGCAACATCTGTGAAAAAGAAAAAGAAACGTTCAAGTGC	778
QY	5512	TGAGCCAGAGAGCCGAGGCTGTATATCTGTCACTTACCATGACCTTTGGGCAAGGACTTTC	5571
Db	779	TGAGCCAGAGAG - CCAGGCTGTATATCTGTCACTTACCATGACCTTTGGGCAAGGACTTTC	837
QY	5572	TTCCCTGGCCAGTTTCACAGGGGGTTGGATGCACTCCAAAGCTCCCTTCCAGCATTAACGCT	5631
Db	838	TTCCCTGGCCAGTTTCACAGGGGGTTGGATGCACTCCAAAGCTCCCTTCCAGCATTAACGCT	897
QY	5632	GCATGGTTCTTAAGATGAGAAAGATGGGGCAGTTTCCCTCTCTACCCACGCCGCGTGTCCA	5691
Db	898	GCATGGTTCTTAAGATGAGAAAGATGGGGCAGTTTCCCTCTCTCTACCCACGCCGCGTGTCCA	957
QY	5692	CTTTCAGGTGATATACACAGGGAATGTACAGTGTCCCAATCCCGCAGTTTCCAAAGGCTTTGG	5751
Db	958	CTTTCAGGTGATATACACAGGGAATGTACAGTGTCCCAATCCCGCAGTTTCCAAAGGCTTTGG	1017
QY	5752	GGACCCCTACTGTCAAGGCTGTGCACAGAGAGGTGAAGTCAAGTGAAGCCCAATGCGCTCGA	5811
Db	1018	GGACCCCTACTGTCAAGGCTGTGCACAGAGAGGTGAAGTCAAGTGAAGCCCAATGCGCTCGA	1077
QY	5812	AGGGTCTTGGCTCATTTGGGGGACACAAATCCGCGTTCTCTGTGGGCTTACCGGGATTTCTAGG	5871
Db	1078	AGGGTCTTGGCTCATTTGGGGGACACAAATCCGCGTTCTCTGTGGGCTTACCGGGATTTCTAGG	1137
QY	5872	GGCTTTTACCGGAATGAGTCAATGGGGGCGGGGGGGTTCCTGGGGGAGTTCACCACTAATC	5931
Db	1138	GGCTTTTACCGGAATGAGTCAATGGGGGCGGGGGGGTTCCTGGGGGAGTTCACCACTAATC	1197
QY	5932	AACCTTGGGACAGGACACCTGTGAATCTTCGATGTGTGCTTATCCAAAGTGTGGGGTGGCAC	1257
Db	1258	AACCTTGGGACAGGACACCTGTGAATCTTCGATGTGTGCTTATCCAAAGTGTGGGGTGGCAC	1317
QY	5992	AGCAGCCAAAGCCCAATGTCTTATCTTCAGTTAGGGGCTCAGAGAGTCTCCCAACAGGC	6051
Db	1318	AGCAGCCAAAGCCCAATGTCTTATCTTCAGTTAGGGGCTCAGAGAGTCTCCCAACAGGC	6052
QY	6052	AGCCTCCGAGAGTTTGGGGGTAGAGATGGGAGCAACAGGCTCTTTTCTTCTCTCTTA	6111
Db	1318	AGCCTCCGAGAGTTTGGGGGTAGAGATGGGAGCAACCA - GCTTCTTTTCTTCTCTCTTA	1376
QY	6112	GAATTTGGGGGCTTTGGGGGACAGGCTTGAGATCCCAAAGAGAGAGGGGCAAAAGACACTC	6171

Db	1377	GAATTTTGGGGGCTTTGGGGGGACAGGCTTGAGATATCCAAAGAGAGAGGGGCAAAAGGACACTGC	1436
QY	6172	CCCCACAAGTCTGCCAGAGCGAGAGAGAGACCCGCACTCAGCTGCACCTTCCCAACAG	6231
Db	1437	CCCCGCAAGTGTGCACAGGC-AGAGAGAGAGAGACCCGCACTCAGCTGCACCTTCCCAACAG	1495
QY	6232	GC 6233	
Db	1496	GC 1497	
RESULT 12			
LOCUS	ARI56466	1252 bp	DNA
DEFINITION	Sequence 7 from patent US 6242218.	linear	PAT 08-Aug-2001
ACCESSION	ARI56466		
VERSION	ARI56466.1	GI:15125170	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1252)		
TITLE	Treco,D.A., Heartlein,M.W. and Selden,R.F.		
JOURNAL	Genomic sequences for protein production and delivery		
FEATURES	Patent: US 6242218-A 7 05-JUN-2001;		
source	location/Qualifiers		
	1..1252		
	/organism="unknown"		
BASE COUNT	300 a 337 c 372 g 243 t		
ORIGIN			
Query Match	20.1%; Score 1252; DB 6; Length 1252;		
Best Local Similarity	100.0%; Pred. No. 4,2e-292;		
Matches 1252; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	4728	CCGTGTAATCCACCTACTTGGGAGGCTGAGGAGGAAATCATAAGAACGAGAGGCGG	4787
Db	1	CCTGTAATCCACCTACTTGGGAGGCTGAGGAGGAAATCATAAGAACGAGAGGCGG	60
QY	4788	AGGTTGTATGAGGCGGAGATGTCCTCATGTGACTCCAGCCTGAGACATGAGCCAAATCC	4847
Db	61	AGGTTGTATGAGGCGGAGATGTCCTCATGTGACTCCAGCCTGAGACATGAGCCAAATCC	120
QY	4848	ATCTCAAAAAAACAACAACAAACCACTCTATCCAGGAGGCTGGGTACAGAGCT	4907
Db	121	ATCTCAAAAAAACAACAACAAACCACTCTATCCAGGAGGCTGGGTACAGAGCT	180
QY	4908	GGGCGCATCATGTCGAAGTGCTTGAAGCCACAGAGCTAAGGCGGAGCTGCAGAGCCGCGGA	4957
Db	181	GGGCGCATCATGTCGAAGTGCTTGAAGCCACAGAGCTAAGGCGGAGCTGCAGAGCCGCGGA	240
QY	4968	CCAATATAACAGTGTGTGAGATCATGTGTGATACAAACCTCCCTGCCATGTGTGACAC	5027
Db	241	CCAATATAACAGTGTGTGAGATCATGTGTGATACAAACCTCCCTGCCATGTGTGACAC	300
QY	5028	CAGGGGGGCCCAAGACACAGAGATGGGCCCATCGACTCAGACACATCCACTTTCATCA	5087
Db	301	CAGGGGGGCCCAAGACACAGAGATGGGCCCATCGACTCAGACACATCCACTTTCATCA	360
QY	5088	GAGATGTCTGTTTCTTGGACGCTGGGGGTAAATTAGACAGAGAGGTGACACTTGGGTG	5147
Db	361	GAGATGTCTGTTTCTTGGACGCTGGGGGTAAATTAGACAGAGAGGTGACACTTGGGTG	420
QY	5148	TGTCATCATCAGCTGCCCGCCAGGAGGCTTGTGGCTGTGAAAACGTTACGGGCTAGCC	5207
Db	421	TGTCATCATCAGCTGCCCGCCAGGAGGCTTGTGGCTGTGAAAACGTTACGGGCTAGGC	480
QY	5208	CGGGCAGGAGTGCTCAGCGCTGTATATCCACAGCATTTTGGAGGCGGAGGCGGAGTCA	5267
Db	481	CGGGCAGGAGTGCTCAGCGCTGTATATCCACAGCATTTTGGAGGCGGAGGCGGAGTCA	540
QY	5368	CGAGGTGAGGAGATCGTACCATCTGGGCTTAACACGGGTGAACCCCGTCTTACTATAAAA	5327

```

Db      541 CGAGGTGAGGATGTCATCCTGCTAACGAGGTAACCCCGTCTCTACTAATAA 600
Qy      5338 TACAAAAAATGGCGGCGATGTCGGGGCAGCTGTAGTTCCAGCTACTCGGAGGCTG 5387
Db      601 TACAAAAAATGGCGGCGATGTCGGGGCAGCTGTAGTTCCAGCTACTCGGAGGCTG 660
Qy      5388 AGCGAGGAATGGGCGTGAACCCGAGAGAGAGTTTTCAGAGACCGAGATCGCGCAC 5447
Db      661 AGCGAGGAATGGGCGTGAACCCGAGAGAGAGTTTTCAGAGACCGAGATCGCGCAC 720
Qy      5448 TGCACCTCCAGCTGGGCGACAGAGCAACATCTCATCTGAAAAAGAAAAAGAAAGCTTCA 5507
Db      721 TGCACCTCCAGCTGGGCGACAGAGCAACATCTCATCTGAAAAAGAAAAAGAAAGCTTCA 780
Qy      5508 GGTCTGAGCCAGAGGCGCCAGGCTGTAAATTCGTCTACTTACATGACCTTTGGGCAAGGAC 5567
Db      781 GGTCTGAGCCAGAGGCGCCAGGCTGTAAATTCGTCTACTTACATGACCTTTGGGCAAGGAC 840
Qy      5568 TTCTCTCCCTGGCCAGTTCAAGGGGTTGGAATGACATCCCAAGGCTCTTCCAGATTA 5627
Db      841 TTCTCTCCCTGGCCAGTTCAAGGGGTTGGAATGACATCCCAAGGCTCTTCCAGATTA 900
Qy      5628 CGCTGCATGTTCTTAAGATGAGAAAGATGGGCGAGTTCCCTCTCTACCCAGCCGCTG 5687
Db      901 CGCTGCATGTTCTTAAGATGAGAAAGATGGGCGAGTTCCCTCTCTACCCAGCCGCTG 960
Qy      5688 TCCACTTCAGGTGAATGAGCAAGGAAAGTCACTGTTCCCAATCCCGAGTTCCAAAGCC 5747
Db      961 TCCACTTCAGGTGAATGAGCAAGGAAAGTCACTGTTCCCAATCCCGAGTTCCAAAGCC 1020
Qy      5748 TTGGGAGACCTTACTGTGAGGTCGTGCACGAGAGAGTGAAGTCAAGTGAAGCAATGCC 5807
Db      1021 TTGGGAGACCTTACTGTGAGGTCGTGCACGAGAGAGTGAAGTCAAGTGAAGCAATGCC 1080
Qy      5808 TCGAAGGCTTTCCTCATTCCTGCGACACATCCGCTTCTCTGCTCTACCGGATTC 5867
Db      1081 TCGAAGGCTTTCCTCATTCCTGCGACACATCCGCTTCTCTGCTCTACCGGATTC 1140
Qy      5868 TAGGGGCTTTCAGCGAATGAGTCAATGGGGGCGGGGGGTTTCGGGGAGTTCCAGCT 5927
Db      1141 TAGGGGCTTTCAGCGAATGAGTCAATGGGGGCGGGGGGTTTCGGGGAGTTCCAGCT 1200
Qy      5928 AATCACTTGGGACAGGACACCTGGAATCTTCATGATGCTTCCAAAGTG 5979
Db      1201 AATCACTTGGGACAGGACACCTGGAATCTTCATGATGCTTCCAAAGTG 1252

RESULT 13
BX470173
LOCUS      110779 bp      DNA      linear      PRI 21-MAY-2003
DEFINITION Human DNA sequence from clone Rp11-739c15 on chromosome 1, complete
sequence.
ACCESSION BX470173
VERSION    BX470173.5      GI:31043711
KEYWORDS   HTG.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 110779)
AUTHORS    Githero, R.
TITLE      Direct Submission
JOURNAL    Submitted (21-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
            On May 22, 2003 this sequence version replaced gi:30962389.
            ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquerry@sanger.ac.uk
            -----
COMMENT

```

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the rare assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., MORBERP; Information on the MORBERP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormrep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl> Rp11-739c15 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6.

FEATURES

```

source      1..110779
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /chromosome="1"
             /clone="Rp11-739c15"
             /clone_11b="RPCI-11.3"
BASE COUNT  32271 a 25614 c 24906 g 27988 t
ORIGIN

```

```

Query Match      19.1%; Score 1189.4; DB 9; Length 110779;
Best Local Similarity 66.9%; Pred. No. 1.6e-276;
Matches 2028; Conservative 0; Mismatches 816; Indels 189; Gaps 16;

Qy      1862 TGGCTGAGCGCTGAGAGTGACAGATGCGGCGAGCTCTACAGCCCTCGTGCCTCG 1921
Db      89252 TGGATTCTTCTTGAGAGGTGACAGCTGCTGCGACGCTCAGACCTCGTGCCTCG 89311
Qy      1922 GCGCCTCCTTGCCTGCGCTCCACTTGCCTGAGCTGAGAGAGCCCTCAGCCACCG 1981
Db      89312 GCACCTCCTTGCCTGCGCTCCACTTGCCTGAGAGAGCTTGAAGAGCCCTTCAAGCCACCG 89371
Qy      1982 TGCACGTGTGGAGCCCTTCTGCGCTGCGCCAGAGAGCCGCTCCTCAGCTTGCA 2041
Db      89372 TGCCTGTGGAGCCCTTCTGCGCTGCGCCAGAGAGCCGCTCCTCAGCTTGCA 89431
Qy      2042 GGGAGGTGTGGAGGAGAGGCTCAAGCAGAACCCGGGGCTGCGACGCGCTTGGGGCC 2101
Db      89432 GGGAGGTGTGGAGGAGAGGCTCAAGCAGAACCCGGGGCTGCGACGCGCTTGGGGCC 89489
Qy      2102 AGCTGAGATTCCGGGTGGGCTTGGCGGGGCCCGGCACTGAGAGAGCGGGCCAGC 2161
Db      89490 AGCTGAGATTCCAGAGTGGGCTTGGCGGGGCCCGGCACTGAGAGAGCGGGCCAGC 89549
Qy      2162 CTGTC-----CAGGCCCGGGCAATGAGAGGCTTGAACCCCGGGCCAGCGCTTGGCG 2213
Db      89550 CTGTCAGAGGCTTCCCGGCCCGGGCAATGAGAGGCTTGAACCCCGGGCCAGCGCTTGGCG 89609
Qy      2214 AGGCTGACGTGGGTGCGCCAGAGAGTGCACAGCCCGCGGCGCTGCTGCTCATTTCTC 2273
Db      89610 AGGATGACGTGGGTGCGCCAGAGAGTGCACAGCCCGCGGCGCTT-----CGTCTCATTTCTC 89665
Qy      2274 ACTGGGCTTACAGAGCTTCCCGCGGGCGAGGCTGCGGAGCTGAGAGCCCGCATGCTG 2333
Db      89666 ACCGGGCTTACAGCTTCCCGCGGGCGAGGCTGCGGAGCTGAGAGCCCGCATGCTG 89725

```


Db	91722	CAACTGTGCTGGCCAAACAAGACACTCTTAATATGATGATCTTCATTAATAACTTAAAACT		91761
QY	4547	TCCTGTTAAAAACCCACCCCTCAAGGCCAGGTGCAGTGGCTCATGTGCTATTAATCCACGAC		4606
Db	91782	TTCAATTTTAAAGAACACCTCTGGGGGTGTGGTGGCTCAAGTCTGTAAACCTTGACAC		91841
QY	4607	TTTGGAGGCGGAGGCGGGTGGATCACTGAGTCAAGAGATTGAGACCCAGCCTGACAC		4666
Db	91842	TTTGGAGGCGAGAGGTGGTGGATCATCTTGAGTCAAGAGTTGAAACCAACCTG---GC		91898
QY	4667	CAACATGTTAAATCCACCTCTACTATAAAATAC-AAAATTAGATGAGCATGGTGTGCA		4725
Db	91899	CAACATGTTAAACCCCGTCTCTACTATAAAATACAAAATAGAACCGAGTGTGGCGCA		91958
QY	4726	TGCTGTAAATCCACCTACTTTGGAGGCTGAGGCAAGAAATACTAGAACACGAGGAC		4785
Db	91959	CGCTGTAAATCCACGCTACTGAGAGGCTGAGGCAAGAAATAGTTGAACCCGGGAGGC		92018
QY	4786	GGAAGTGTAGTGAAGCCGAGATGTTGCATTGGCACTCAAGCCTGAGCAATGAGCGAAACT		4845
Db	92019	GGAGTGTGCAGTGAGTGGGATGCAACATGCACTCCAGCCTGGTGTGACAGAACAGAT		92078
QY	4846	CCATCTAAAAAACAACAACAAACCACTC	4878	
Db	92079	CCATCTCAAAAAAAAAAAAAAAAAAAGCAC	92111	

RESULT	14
AL732292	
LOCUS	AL732292
DEFINITION	AL732292 51015 bp DNA linear PRI 19-JUN-2002 Human DNA sequence from clone RP4-597N16 on chromosome 1, complete sequence.
ACCESSION	AL732292
VERSION	AL732292.12 GI:21531517
KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 51015) Lad,H.
REFERENCE	Direct Submission
AUTHORS	Submitted (19-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humangene@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 21, 2002 this sequence version replaced gi:21065403.
TITLE	
JOURNAL	
COMMENT	

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping

group. Further information can be found at <http://www.sanger.ac.uk/NGP/Ch1R4-597IN16> is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCIPAC2.

FEATURES	SOURCE
Location/Qualifiers	1. .51015
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
/chromosome="1"	
/clone="RP4-597N16"	
/clone_1lb="RPC1-4"	
BASE COUNT	14768 a 11872 c 10934 g 13381 t
ORIGIN	

Query Match	19.1%;	Score 1187.8;	DB 9;	Length 51015;
Best Local Similarity	66.8%;	Pred. No. 3.3e-276;		
Matches 2027; Conservative	0;	Mismatches 817;	Indels 189;	Gaps 1

QY	1862	TGGCTTAAAGCCTGAGAGCTACACAGCAAGCCGGGCAAGTCTCACAGACCCCTGTTGGCTCTG	1921
Db	46767	TGATTTCTTCTGAGAGGTGACAGCGTGGTGGGACGTCTTCAGAGCCCTGCTGCTCTCC	46822
QY	1922	GCGCCTCTCTGCTGGGCTCCCACTTCGGTGGCACTTGAGAGACCCCTTACGCCACCGC	1981
Db	46827	GCACCTCTCTGCTGGGCTCCCACTTTCAGGACACTTGGAGAGCCCTTCAGGCCACCGC	46886
QY	1982	TGCATCTGGAGAGCCCTTCTGGGCTGGCCAAAGGCGAGAGCGGCGCCCTCAGCTTGGCA	2041
Db	46887	TGCCTTCTGGAGAGCCCTTCTGGGCTGGCCAAAGGCGAGAGCGGCGCCCTCAGCTTGGCA	46948
QY	2042	GGAGAGTGTGAGAGGAGAGGCTCAAGCAGGAACCGGGGCTGCGACAGCGCTTGCGGGCG	2101
Db	46947	GGAGAGTGTGAGAGGAGAGGCGGAGAGTGGGAACACGAGGCTGCG - CGGGCTTGGGGGCG	47004
QY	2102	AGCTGAGATTCGGGGTGGCGTGGGCTTGGCCGGGCCCCGCACCTCGAGACAGCGGCGACG	2161
Db	47005	AGCTGAGATTCAGAGTGGGGTGGCGTGGGCGGCCCCGCACCTCGAGACAGCGGCGGCG	47064
QY	2162	CCCTCC-----CAGGCCCCGGGGCAATGAGAGGCTTAGACCCGGGGCCAGCGGGCGGG	2213
Db	47065	CCCTCAGAGCCCTCGCGGGCCCCGGGGCAATGAGGGGCTTAGACCCGGGGCCAGTGGCTGGCG	47122
QY	2214	AGGGTACTGAGGGTGGCCCCAGACAGTGGCACCCGCGGGCGCTGTGCTGCATTTCTC	2273
Db	47125	AGAGTACTAGGGTGGCCCCAGAGTGGCAACCCACTGCGGCTA-----CGTGCATTTCTC	47186
QY	2274	ACTGGGCTTAGACAGCCTTCCCGGGGGGAGGGCTGGGACCTGACAGCCCGCATCTCG	2333
Db	47181	ACCGGGCTTAGAGCTTCTCCCGAGGGTGGGACCTGACAGCCCGCATCTCTG	47240
QY	2334	AGCCT-----CCCTTCATGGGCTCCGTGTCGGGCGGAGCTCTCCCGAGAGCACACCC	2388
Db	47241	AGCCTCCACCCCTTCATGGGCTCTGTGCGGCGGAGCTCTCCCGAGAGCACACCC	47300
QY	2389	CCTGCTCAGAGCGCCAGTCCCATCGACACCAAGAGGCTGAGATGGCGGCGACAGG	2448
Db	47301	CTGTCTCAGAGCGCCAGTCCCATCGACACCAAGAGGCTGGGAGTGCAGGCGGACGG	47366
QY	2449	CACCGGAGCTGGCAGCGAGCTACCCCTGACGCGCTGTGCGGAATCCACTGGGTGAAGCC	2508
Db	47361	CA-TGGAGTTGGCAGGAGCTCACCTGACAGCCCGGTGAGGATCCACTGGGTGAAGCC	47419
QY	2509	AGCTGGGCTCTGAGTGTGGTGGAGACTTGGAGAACCTTTATGTCTAAGCTCAGGATCGT	2568
Db	47420	AGCTGGGCTCTCGAGTGTGGTGGGAGTGTGAGAACCTTTATGTCTAAGCTCAGGAGTGTG	47479
QY	2569	AAATACACCAATAGACACCTGTGTCTAAGCTCAGGCTGTGAATGCACCAATCCACACT	2628
Db	47480	AAATACACCAATAGACACCTGTGTCTAAGCTCAGGCTGTGTGAATGCACCAATCCACACT	47539

OY 2629 CTGATCTAGCTACTGTGATGGGCTTGAGAACCTTTATGCTAGCTCAGGATTTGA 2688
 Db 47540 CTATATCTAGCTACTGTGATGGGCTTGAGAACCTTTATGCTAGCTCAGGATTTGA 47599
 OY 2689 AATACCAATCGGACCTCTGTATCTAGCTCAAGTTTGTAAACACCAATCAGACCC 2748
 Db 47600 AATACCAATCGGACCTCTGTATCTAGCTCAAGTTTGTAAACACCAATCAGACCC 47659
 OY 2749 TGTGTAGCTCAGGATTTGATGATGCAACATGCAAGTCTGTATCTGCTACTTCAAT 2808
 Db 47660 TGTGTAGCTCAGGATTTGATGATGCAACATGCAAGTCTGTATCTGCTACTTCAAT 47719
 OY 2809 GGGCATCCGTGTGAAGAGCCCAACAGAGCTTTGTGTGACCAATTAAGCTTCTATAC 2868
 Db 47720 GGG-----GCTTGACAACTTTATGCTGACGAGGATTTGAATTA 47763
 OY 2869 CTGGGTGCAAGTGGGCTGAGTCCGAAAGAGAGTCAAGGAGGAGATTAAGGCTGGGCC 2928
 Db 47764 C-----AAC 47767
 OY 2929 GTTTATAGATTTGGTAGTGAAGAAATTAACATCAAGGGGGTTTGTCTCTGAGC 2988
 Db 47768 AATCGGACCTCTGTATCTAGCTCAAGTTTGTAAACACCAATCGGACCTGTCTTTA 47827
 OY 2989 GGGCAGAGTGGGGGCTGCAAGTGTCTAGTGGGGGCTTTTGTAGCCAGATGAGCC 3048
 Db 47828 GCTCAAGGTTTGTAGTCAACCAATGCACTCTGTAT-CTAGTCTCTGTGGGGCT 47886
 OY 3049 AGGAAGAGACTTTCACAGGTAATGTCAATTAAGGCAAGGACCCGCTTTTACCC 3108
 Db 47887 TGGACAACTTATCTAGCTCAGGGGTTGTAAATACCAATCGGACCTGTATCTA 47946
 OY 3109 TCTTTGTGATGATGATCAATGATTAAGTTGGGAGGAGCAATTAATCTTTTGTGA 3168
 Db 47947 GCTCAAGTTTAAACACCA----- 47969
 OY 3169 TTTCTCAGTACTTACAGGACATCTGGGCTATATGTGCAATTAAGGAGGATCGATGCG 3228
 Db 47970 ---ATCAGACCTCTGTATCTAGCTCAGGGTTTGTAGTGCACCAATCGATCTGTATC 48026
 OY 3229 TTGGCTTGGGCTCAAGGCTTACAGCTACTGTGTGGGGCTTGTGAGCAATTTTGTGTC 3288
 Db 48027 T-----AGTCTCTGTGGGGCTTGTGAGCAATCTTGTGTGTC 48063
 OY 3289 GACACTCTGTATCTAGTAACTAGTGGGAGCTGAGAGAACTTTGTCTGCTCAGG 3348
 Db 48064 GATCTCTGTATCTAGTAACTAGTGGGAGCTGAGAGAACTTTGTCTGCTCAGG 48123
 OY 3349 ATTGTAAAGCACAATCAGCGCTGTCAAAACAGACACTCGGCTTACCAATCAGCA 3408
 Db 48124 ATTGTAAAGCACAATCAGCGCTGTCAAAACAGACACTCGGCTTACCAATCAGCA 48183
 OY 3409 GGATGTGGGTGGGCGCAGATTAAGATTAAGAGAGAGCTGCCGAGCAGAGTGGCAAC 3468
 Db 48184 GGATGTGGGTGGGCGCAGATTAAGATTAAGAGAGAGCTGCCGAGCAGAGTGGCAAC 48243
 OY 3469 GGGCAGAGTCCCTTCAACATATGAGCAGCTTTGTCTTTGTGCTTTTGTGCAATATCT 3528
 Db 48244 CCACGTGGGTCCCTTCAACATATGAGCAGCTTTGTCTTTGTGCAATATATCT 48303
 OY 3529 TGTCTAGCTCTGCTTTTGGGTCACACACTGCTTTATGAGCTGTAACTCAGCAGAG 3588
 Db 48304 TGTCTAGCTCTGCTTTTGGGTCACACACTGCTTTATGAGCTGTAACTCAGCAGAG 48363
 OY 3589 GTCTCAGCTTCTCTGTAAGCCATTAAGACACAGAGCCACCGGAGGAATGAACAC 3648
 Db 48364 ATCTCAGCTTCTCTGTAAGCCATTAAGACACAGAGCCACCGGAGGAATGAACAC 48423
 OY 3649 TCCGGCCGCTGCTTAAAGCTTAACTTAACTCAGCCGAGAGGCTTGCAGCTTCACTCT 3708
 Db 48424 TCCAGACCGCTGCTTAAAGCTTAACTTAACTCAGCCGAGAGGCTTGCAGCTTCACTCT 48483
 OY 3709 CAGCCAGGAGACCAACCAACCAAGAAAGAACTGCGAACAATCTCAATCTGAG 3768

Db 48484 GAGCAGTGTAGACACCAAGCCACCAAGAAAGAAATCCGAAACAAATCCGAACATCAG 48543
 OY 3769 AAGGAACAACTCCAGATGCAACCACTTAAGAGCTGTAACTCAGCTCGAGGGCTCCCG 3828
 Db 48544 AAGGAACAACTCCAGAGCACCACTTAAGAGCTGTAACTCAGCTCGAGGGCTCCCG 48603
 OY 3829 GCTCTCTCTTGAATCAGTGTAGACCAAGCACTCAGAGTTTGTGACCAAGCCAGAG 3888
 Db 48604 GCTTATCTTAAAGTCACTGTAGACCAAGCACTCAGAGTTTGTGACCAAGCCAGAG 48652
 OY 3889 TTTGATCAGCTGGGCAACATGTAATGCTCTCTGTGCAAAAAAATTAATAC 3948
 Db 48653 -----ATCTCTGTGTGAGAGAAAGGCTAAGCTGTAGGGAGGATGAGCAACCTG 48706
 OY 3949 AAAAATGGCGAGCATGGTGGTCCGTGCTGTGCTCCAGCTAGCCGAGAGCTTAAGT 4008
 Db 48707 TCACTCCAGGACAGAGAAAGACCTTACAGCCGAGAGAAAGGAGAGTCCAGTACGG 48766
 OY 4009 GGGAGATGCTTGAAGCTGGGAGGTGAAGACTGCAAGTGTGATTTGACACAGCC 4068
 Db 48767 GGGG-GAGGTGGGAAACATCTCTGTATATCCCAATTAAGTACAAAGGCTTTGGCAC 48825
 OY 4069 CTCTAGGCTGGGGACAGACTGACCTGTTCCCTCCGCAAAAAAATTAATGACAAAGT 4128
 Db 48826 AGCTTGGCTGCCCCGGAAGAAAGCCCTGATCAGTGTGCACTCTGAGACAGCAAACT 48885
 OY 4129 GTAAATAGAGTGTCTGATATGCTAGAGGCTAGGCTGATATGCTGTATATCCACACT 4188
 Db 48886 AAGACAAAGACAGAGAGACCTGCTGCGCCACTCCACCAACATCAAGCAAGCACTGAC 48945
 OY 4189 TGGGAAGCCGAGGGGGGCTCACCCTAAGTCAAGAGTGTAGACCAAGCCGCAACA 4248
 Db 48946 AAGCAATAGAC-----TTTTTTATTTTGAAGAGAGTTTCTCTTCTGAGTCA 48996
 OY 4249 TGGGAAGCCCACTCTTTTAAATTAACAAATTAAGCCGCTGTGGGGAGTGTGA 4308
 Db 48997 GCGTGAAGTCAATGAGATGATCTGCGCTCACTGCACTCACTCACTCACTCACTCACT 49056
 OY 4309 GCATGCTGTATCCAGCTACTCAGAGAGCTGAGAGCAGAGCAATCATTGAACCCAGCA 4368
 Db 49057 ATTCTCTGCTTCAAGCTTCCAAATAGCTGGGATTAACAGCCACCACTCTGTGTC 49116
 OY 4369 GCGGGGCTTGAAGAGAGCCGAGATGCGCATGTCAGTCACTCCACCACTCAGCTGGCA 4428
 Db 49117 TTAATTTTGTATTTTGAAGAGAGCGGCTTCCACAGCTTGGCCAGCTGTCTTAA 49176
 OY 4429 ACNAGAGCCAACTCTGCTTAAAAAATTAAGAGAGTGGCTGACATTAAGAGTGT 4488
 Db 49177 TCTGACCTCAAGTATATCGCCCACTTGAAGTCAATTAAGTAACT 49236
 OY 4489 GCA--ATGCAATAGTCCAGGCAACATGTTTAAAGATGAGAGCTCTGCTTCATG 4546
 Db 49237 CCAGTGTGCTGGCAACCAAGCACTCTTAATGAGATCTCAATAAATTTAAACT 49296
 OY 4547 TCTGTAAAAAACCACCTCAAGCCAGTGCATGCTGTATGCTTAATCCAGAC 4606
 Db 49297 TTTCAATCTTAAAGACACCTCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 49356
 OY 4607 TTTGGAGGCCGAGGCTGTGATCAGCTGAGAGTGTGAGAGTGTGAGAGCTGAGAG 4666
 Db 49357 TTTGGAGGCCGAGGCTGTGATCAGCTGAGAGTGTGAGAGTGTGAGAGCTGAGAG 49413
 OY 4667 CAACATGTGTAATCCACCTTCTAATAAATATC--AAATTAAGATGAGATGAGTGTGA 4725
 Db 49414 CAACATGTGTAATCCACCTTCTAATAAATATC--AAATTAAGATGAGATGAGTGTGA 49473
 OY 4726 TCCCTGTATCCCACTTCTTGGAGGCTGAGAGCAGAGAAATCATTGAACAGGAGG 4785
 Db 49474 CCGTGTATATCCCACTTCTTGGAGGCTGAGAGCAGAGAAATCATTGAACAGGAGG 49533
 OY 4786 GGAGGTTGTAGTGAAGCCGAGATGCTGATGCACTTCAAGCTTGAAGTGAAGCAACT 4845

Db	49534	GGAGCTTGCAGTGAGTGGGATGCGACCACTGCACTCGACCGTGGACAGAGCAAGGANT	49534
Qy	4846	CCATCTCAAAAAACAACAACAAACCACCTC	4878
Db	49594	CCAACTCAAAAAAAAAAAAAAAAAAGACAC	49526
RESULT 15			
AC104212			
LOCUS	AC104212	196806 bp	DNA linear PRI 27-APR-2002
DEFINITION	Homo sapiens chromosome 8, clone RP11-94IH19, complete sequence.		
ACCESSION	AC104212		
VERSION	AC104212.3	GI:20149422	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Bliren,B., Linton,L., Nusbaum,C. and Lander,E.		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 196806)		
REFERENCE	Bliren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collumore,A., Cook,A., Cooke,P., Deatrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Gage,D., Graham,L., Grand-Pierre,N., Hago,B., Heaford,A., Horton,L., Hultine,W., Illey,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Laroque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Marguis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPeters,R., Meldrim,J., Menus,L., Mihova,T., Mlenge,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Piere,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnpack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stolanovic,N., Straus,N., Subramanian,A., Talams,J., Testfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trifillo,J., Vassiliev,H., Vye,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 330 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 196806)		
AUTHORS	Bliren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collumore,A., Cook,A., Cooke,P., Deatrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hago,B., Horton,L., Hultine,W., Illey,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Laroque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marguis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Menus,L., Mihova,T., Mlenge,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Piere,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnpack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stolanovic,N., Straus,N., Subramanian,A., Talams,J., Testfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trifillo,J., Vassiliev,H., Vye,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Submitted (15-APR-2002) Whitehead Institute/MIT Center for Genome		
JOURNAL	Submitted (15-APR-2002) Whitehead Institute/MIT Center for Genome		

REFERENCE	Research, 320 Charles Street, Cambridge MA 02141, USA
REFERENCE	4 (bases 1 to 196806)
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, K., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Fardo, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Herold, S., Hulme, W., Iliev, T., Johnson, R., Jones, C., Kamat, A., Karates, A., Kellis, C., Labrecque, K., Lamazares, R., Landers, T., Lenczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McKwan, P., McKernan, K., Meltrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, D., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K. C., Phunkhang, P., Piere, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schuppach, R., Seaman, S., Severy, P., Spencer, B., Stange-Themann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trifillio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted (27-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Apr 15, 2002 this sequence version replaced g1:2018254. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
FEATURES	Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence.submissions@genome.wi.mit.edu ----- Project Information Center project name: L19698 Center Clone name: 941_H_19 ----- location/Qualifiers 1. 196806 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="8" /map="8" /clone="RP11-941H19" /clone_lib="RPC1-11 Human Male BAC" 641. 823 /rpt_family="L1ME4A" 896. 1076 /rpt_family="MER5A" 1804. 1848 /rpt_family="(CA)n" complement(2152..2310) /rpt_family="AluYo" 2311. 2338 /rpt_family="(TG)n" complement(2339..2455) /rpt_family="AluYo" 3038. 3469 /rpt_family="THE1B" 3470. 4964 /rpt_family="THE1B-int" 4966. 5330 /rpt_family="THE1B" 5420. 5858 /rpt_family="L1R54B" 6492. 6791 /rpt_family="AluXx" 8656. 8746 /rpt_family="(CA)n"

Query Match	18.1%	Score 1129.8	DB 9:	Length 196806
Best Local Similarity	69.6%	Pred. No. 4.9e-262		
Matches 1825: Conservative	0	Mismatches 652	Indels 144	Gaps 16
DB	85566	GGCACAATGGCTATGCACTATCTCCAGACACTTTGGAGAGCCGAGAGTGGAG-----	85618	
QY	1867	TGAGCCTGAGAGGTGACAGCATCGGACAGTCTCTCAACAGCCTCGTTGCTCTCGGCGCC	1926	

[illegible]

Db 86651 ATGTCTAGCTCAGGGATTGTAAACACACTAATCAGACCCCTGTGTTAGCTCAGGGTTTG 86710
QY 3001 GGGGTGCAGAGTCTCTAGTGGGGTGTCTTTTATGACCGAGATATAGCCAGGAAAAAGCACT 3060
Db 86711 TGAATGCACCAANTGACACTCTGTAT-CTAGCTCTCTGTGGGGCTTGGAGAACCTTTT 86769
QY 3061 TTCACAGATTAATGTCAATCAATTAAGCAAGGACCCGCAATTTACACTCTTTTGTGGTG 3120
Db 86770 ATGTCTAGCTCAGGGATTGTAAATACACAAATCAGCACTGTGTATCAGCCCAAGTTTG 86829
QY 3121 GAATGTCAATCAATTAATGTGGGGCAGGCAATATTCCTTTTGTGATTCCTTACAGTTAC 3180
Db 86830 TAAACACACCAATCA-----GCAACCTGTGTTTAG 86859
QY 3181 TTACAGCCATCTGGGCGCTATATGTGCAAGTTACAGGGATCCATGGCTTGGGCT 3240
Db 86860 CTCAAGGTTTGTGTGTCACCAATTA----- 86886
QY 3241 CAGAGGCTTACACACTCTCTGTGGGGCTTGGAGAAATGTTGTGCACTCTGTAT 3300
Db 86887 CACTGTATCTAGCTCTCTGTGGGGCTTGGAGAACTTTGTGTGATCTCTGTAT 86946
QY 3301 CTAGTTAATCTAGTGGGAGCTGAGAACCTTTGTCTAGCTCAGGGATTGTAAACGCA 3360
Db 86947 CTAACTAATCTGATGGGAGCTGAGAACAGTTATCTAGCTCAGGGATTGTAAAGCA 87006
QY 3361 CCATACAGCCGCTGTAAAAACAGACACCTGGCTCTACCAATACAGAGATGTGGGTGG 3420
Db 87007 CCATACAGACCTGTAAAAATAGCACTGGCTCTACCAATACAGGGATGTGGGTGG 87066
QY 3421 GGGCAGATTAAGAGAAATAAAGCAGGCTGCCGAGCAGAGTGGCAACGGCAGACAGTTC 3480
Db 87067 GGGCAGATTAAGAGAAATAAAGCAGGCTGCCGAGCAGAGTGGCAACGGCTGGGTTC 87126
QY 3481 CTATCCAAATATGCGACGCTTTGTTCTTTGCTGTTGCGATTAATCTTCTACTGCTCG 3540
Db 87127 CTTTCCAGCTGTGGAGCTGTGTTCTTTGTTCTTGAATTAATCTTGTGCTGCTCA 87186
QY 3541 CTTTGGGGTCCACAGCTTTTATGAGC-----TGTAACACTCAGCAGAAAGCTGTGAG 3596
Db 87187 GTCTTTGGTCCACAGCTTTTATGAGCTGTATGATTAACACTCAGCAGAAAGCTGTGAG 87246
QY 3597 CTTTACTCTGTAAGCCACTTAAGACACAGACCCACCGGAGGAATGAACAACCTCCGGCG 3656
Db 87247 CTTTACTCTGTAAGCCACTTAAGACACAGACCCACCGGAGGAATGAACAACCTCCAGACA 87306
QY 3657 CGCTGCTTAAGAGCTTAACACTCAGCGGGAAGTCTGCAAGCTTCACTCCTCAGCCAGC 3716
Db 87307 CGCTGCTTAAGAGCTTAACACTCAGCGGGAAGTCTGCAAGCTTCACTCCTGAGCCAGT 87366
QY 3717 GAGACCAAGAACCCACCAAGAGAAAGAACTGGGAACACATCTGAACATCAGAAAGACA 3776
Db 87367 GAGACTTACGAACCCACCAAGAGAAAGAACTGGGAACACATCTGAACATCAGAAAGACA 87426
QY 3777 AACTCAGATGACACACTTAAGAGCTTAACACTCAGAGGCTCGCGGGCTTCTT 3836
Db 87427 GACTCCAGATGACACCGCTTAAGAGCTTAACAGGCGCGCGCGGT---GGCTCAGGCC 87483
QY 3837 CTTGAAGTCAGTAGAACCAAGCACTCAGAGTTTGGACACAAAGCCAGAGATTGAGAT 3896
Db 87484 TGTAAACCCGCACTTTGGAGGCCGAGGCGGCGGATCAGAGGTGAGAGATCAGAC 87543
QY 3897 CAGCCTGGGCAATATGAAATGCGCTCTCTGCAAAAAAATTAACAAAAATG 3956
Db 87544 CATCCCGGCTAAAGCGTGAACCCGCTCTCTACTAAATAATACA-----AAAAATTA 87595
QY 3957 GCGGAGCATGTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4016
Db 87596 GCGGAGCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 87655
QY 4017 CGCTTACGCTGGGAGGTGAAGACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4076
Db 87656 GCGGTGAACCCGAGGAGGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 87715

QY 4077 TGGGGACAGACTAGACACTGTGTTCCCTCCGCAAAAAATTAACAAA---GTGTAA 4132
Db 87716 TGGAGACAAAGCAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAGCTGTAA 87775
QY 4133 TAAAGGAGCTGATTAAGGCTAAGGCGAGTGGCTCATGCCCTTAATCCAGCACTTTGGG 4192
Db 87776 CACTCATGTGCAAGGCTCGCGGCTTTCTTTTGAAGTCAAGTGAAGCAAGAACCCAGAA 87835
QY 4193 AAGCCAGAGCGCGGCTGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 4252
Db 87836 TCCGGAACCCAGAGGATGTTGTTGAAGTCAAGTGAAGCAAGCTTGGGCAACAAAGT 87895
QY 4253 GAAAGCCATCTCTTAAATAATTAAGCCGCTGTGGGGCAGTGTGAGCAT 4312
Db 87896 ATAGTAAGACCTCTTCTGCAAAAAATGAATTAAGTGTGGTGTGTGTGC 87955
QY 4313 GCCCTAATCCACTACTCTCAGAGGCTGAGGCGAGAGGAATCACTTAACCCAGAGCGC 4372
Db 87956 ACATGTAGTCCCACTACTGTGGGGAAGCTGAGGTGAGGGAATTAATTAACCCAGAGGTC 88015
QY 4373 GCGGTCAGTGAAGCCAGATCTGCAATTCACCTCACC 4413
Db 88016 AAGGCTGAGTGAAGCCCTGGCAGCACCGCTGTAGTCCAGCC 88056

Search completed: August 16, 2003, 20:10:10
Job time : 14696 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 22:51:15 ; Search time 998 Seconds

(without alignments)
10864.726 Million cell updates/sec

Title: US-09-845-020A-5

Perfect score: 6235
Sequence: 1 gatcacttgagacagtagt.....tgcactcccccacagcct 6235

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_19Jun03:.*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6235	100.0	6235	21	AAZ29169 Human G-CSF genomic partial sequence o
2	6235	100.0	6679	21	AAZ29170 Human granulocyte
3	6235	100.0	6679	22	AAZ29173 Human interleukin a
4	3725	59.7	6753	22	AAZ29173 Human interleukin a
5	2834	45.5	2834	21	AAZ29174 Human granulocyte
6	2220.4	35.6	2515	22	AAZ29174 Targeting sequence
7	1252	20.1	1252	21	AAZ29174 Targeting sequence
8	773.4	12.4	50000	21	AAA96363 Polymorphic repeat

C	9	757.4	12.1	163350	24	AAZ29169	AAZ29169
C	10	744.8	11.9	260209	24	AAZ29169	AAZ29169
C	11	733.2	11.8	121724	24	AAZ29169	AAZ29169
C	12	710.8	11.4	49999	20	AAZ29169	AAZ29169
C	13	708.4	11.4	55235	22	AAZ29169	AAZ29169
C	14	693.8	11.1	22081	22	AAZ29169	AAZ29169
C	15	669.2	10.7	1831	21	AAZ29169	AAZ29169
C	16	668	10.7	185371	24	AAZ29169	AAZ29169
C	17	652.8	10.5	10351	24	AAZ29169	AAZ29169
C	18	614.2	9.9	5236	22	AAZ29169	AAZ29169
C	19	608.6	9.8	2610	22	AAZ29169	AAZ29169
C	20	606.2	9.7	19974	24	AAZ29169	AAZ29169
C	21	593.6	9.5	1914	24	AAZ29169	AAZ29169
C	22	593	9.5	249999	25	AAZ29169	AAZ29169
C	23	592.6	9.5	122888	24	AAZ29169	AAZ29169
C	24	584.8	9.4	1872	23	AAZ29169	AAZ29169
C	25	583.8	9.4	6766	22	AAZ29169	AAZ29169
C	26	583.8	9.4	6766	23	AAZ29169	AAZ29169
C	27	583.2	9.4	2597	22	AAZ29169	AAZ29169
C	28	576.6	9.2	1405	23	AAZ29169	AAZ29169
C	29	573	9.2	1474	23	AAZ29169	AAZ29169
C	30	564.4	9.1	28818	22	AAZ29169	AAZ29169
C	31	564.4	9.1	28818	25	AAZ29169	AAZ29169
C	32	563.8	9.0	9704	24	AAZ29169	AAZ29169
C	33	563.8	9.0	9704	25	AAZ29169	AAZ29169
C	34	560.4	9.0	32127	22	AAZ29169	AAZ29169
C	35	560.4	9.0	32127	22	AAZ29169	AAZ29169
C	36	560.4	9.0	72215	22	AAZ29169	AAZ29169
C	37	560	9.0	1503841	24	AAZ29169	AAZ29169
C	38	560	9.0	1503841	24	AAZ29169	AAZ29169
C	39	560	9.0	1503900	22	AAZ29169	AAZ29169
C	40	560	9.0	1503900	22	AAZ29169	AAZ29169
C	41	551.8	8.9	2943	23	AAZ29169	AAZ29169
C	42	549.2	8.8	3167	22	AAZ29169	AAZ29169
C	43	546	8.8	1349	23	AAZ29169	AAZ29169
C	44	542.8	8.7	14273	22	AAZ29169	AAZ29169
C	45	542.8	8.7	14273	22	AAZ29169	AAZ29169

ALIGNMENTS

RESULT 1	AAZ29169	standard: DNA; 6235 BP.
AC	AAZ29169;	
DT	21-FEB-2000	(first entry)
DE	Human G-CSF genomic sequence upstream of transcription start site.	
XX	Granulocyte colony stimulating factor; G-CSF; genomic sequence;	
KW	transcription start site; 5' non-coding sequence; DNA construct;	
KW	targeting sequence; regulatory region; marker gene; selection;	
KW	homologous recombination; gene therapy; delivery system; upstream;	
KW	hematopoietic progenitor cell; chemotherapy-induced neutropenia;	
KW	bone marrow transplantation; congenital neutropenic disorder;	
KW	chronic idiopathic disorder; ds.	
OS	Homo sapiens.	
XX		
PN	W09957291-A1.	
XX		
PD	11-NOV-1999.	
XX		
PF	05-MAY-1999; 99WO-US09924.	
XX		
PR	07-MAY-1998; 98US-0084649.	
XX		
PA	(TRAN-) TRANSKARYOTIC THERAPIES INC.	
XX		
PI	Treco DA, Heartlein MW, Selden RF;	

Human tumour suppressor
Human SUF2 genomic
Human osteoblast d
Human LOBO homolog
Human immune/haema
Human neuroblastom
5'HS5 endogenous r
Human breast cancer
Human CDLE CDNA.
Human immune/haema
Human full-length
Invertebrate forag
Human cancer promo
Human transdormin ge
Human cDNA differ
DNA encoding novel
Human immune/haema
Genomic sequence #
Human cDNA sequenc
DNA encoding novel
DNA encoding novel
Human musculoskele
cDNA encoding nove
Genomic DNA of an
Human aminocyclase
Human excretory re
Human kidney relat
Human immune/haema
Human neuroregulin 1
Human neuroregulin 1
Human neuroregulin-1
Human encoding novel
DNA encoding novel
DNA encoding novel
Human pancreatic c
Human digestive sy

XX WPI: 2000-072235/06.
XX Novel genomic sequences used for treating human diseases and disorders

PS Claim 1: Fig 5: 58pp; English.

CC The present DNA sequence is the human genomic sequence from a region
CC upstream of the transcription start site of granulocyte colony-
CC stimulating factor (G-CSF). This sequence represents nucleotides -6578
CC to -364 relative to the translation start site. G-CSF gene contains five
CC exons and four introns. A DNA construct comprising a targeting sequence
CC homologous to the 5' non-coding sequence of G-CSF, a transcriptional
CC regulatory sequence that differs from the endogenous G-CSF gene, and a
CC selectable marker gene for selection of recombinant cells is generated.
CC It can be used by homologous recombination to modify the expression of
CC endogenous G-CSF. These recombinant cells which express G-CSF are useful
CC for in vitro production of the protein and gene therapy. Such cells may
CC also be used in a delivery system for stimulating the proliferation and
CC differentiation of hematopoietic progenitor cells, or for other
CC conditions that can be treated with G-CSF, like chemotherapy-induced
CC neutropenia, to treat patients undergoing bone marrow transplantation,
CC chronic idiopathic and congenital neutropenic disorders.

XX Sequence 6235 BP; 1586 A; 1610 C; 1708 G; 1331 T; 0 other;

Query Match 100.0%; Score 6235; DB 21; Length 6235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCAGCTGAGGACAGTCTCAAGACACCTGGGAGCATGAGAGACTGTCTACG 60
DB 1 GATCAGCTGAGGACAGTCTCAAGACACCTGGGAGCATGAGAGACTGTCTACG 60
QY 61 AAAATCAAAAAATTTATGGCGGAGCATGTGGCTACCTGTAATCCGTAACCTTGGG 120
DB 61 AAAATCAAAAAATTTATGGCGGAGCATGTGGCTACCTGTAATCCGTAACCTTGGG 120
QY 121 ACATCAAGGCAAGTGTGATCACTTGAAGTTCAGAGTTCAGAGTACCTGTCGCAACATGCT 180
DB 121 ACATCAAGGCAAGTGTGATCACTTGAAGTTCAGAGTTCAGAGTACCTGTCGCAACATGCT 180
QY 181 GAAACCCCTATCTCCACTCAAAAAATTAACGAGCATGTGGTGGCAGCACTGTA 240
DB 181 GAAACCCCTATCTCCACTCAAAAAATTAACGAGCATGTGGTGGCAGCACTGTA 240
QY 241 ATCCGCGCTACTCAGAGGCTGAGGAGCATGAGTACCTTGAACCCAGGAGGAGGTTG 300
DB 241 ATCCGCGCTACTCAGAGGCTGAGGAGCATGAGTACCTTGAACCCAGGAGGAGGTTG 300
QY 301 CAGTGAAGCTGAGTACACACCATGCTCAGGCTGGGTGACAGAGCAAGACTCTATCTC 360
DB 301 CAGTGAAGCTGAGTACACACCATGCTCAGGCTGGGTGACAGAGCAAGACTCTATCTC 360
QY 361 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 361 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY 421 CTACTCAGAGGCTGAGGAGTGGAGATCACTTGAACCTGGGAGCATGAGAGACTGTA 480
DB 421 CTACTCAGAGGCTGAGGAGTGGAGATCACTTGAACCTGGGAGCATGAGAGACTGTA 480
QY 481 GCCAAGATCATGCGACTACACTCAGCTGGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 GCCAAGATCATGCGACTACACTCAGCTGGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
DB 541 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
QY 601 ATGTATATAGTTCGAAAGATCCAGATAGTCAATTTTATGGGCTGGGGCGCT 660
DB 601 ATGTATATAGTTCGAAAGATCCAGATAGTCAATTTTATGGGCTGGGGCGCT 660

DB 601 ATGTATATAGTTCGAAAGATCCAGATAGTCAATTTTATGGGCTGGGGCGCT 660
QY 661 ATGTCTCTGTCAACATCACTGTCCCTGTCTTTCAGACAAAGCAGCTATTAACAT 720
DB 661 ATGTCTCTGTCAACATCACTGTCCCTGTCTTTCAGACAAAGCAGCTATTAACAT 720
QY 721 ACATACATGAATTTTATAGACATGAGATTTGAATTTATATGATTTTATACATTTTAT 780
DB 721 ACATACATGAATTTTATAGACATGAGATTTGAATTTATATGATTTTATACATTTTAT 780
QY 781 AAAATATCTTTTAAAAATTTTCCCTAACCATTTTAAAGTAAAAAGCGGCACGCG 840
DB 781 AAAATATCTTTTAAAAATTTTCCCTAACCATTTTAAAGTAAAAAGCGGCACGCG 840
QY 841 GCCATCTCAGCGCTGTAAATTCAGACACTTTGGAGGCTGAGGAGGAGATCACTTGAG 900
DB 841 GCCATCTCAGCGCTGTAAATTCAGACACTTTGGAGGCTGAGGAGGAGATCACTTGAG 900
QY 901 ATCAAGCTTCGAGACACGCTGGCCAACTAGCAAAACCCATTTCTACTAAAAATAAA 960
DB 901 ATCAAGCTTCGAGACACGCTGGCCAACTAGCAAAACCCATTTCTACTAAAAATAAA 960
QY 961 AAAATTAAGTGGGATAGTGTGTCACACCTGTATCCACCTTGGAGGCTGAGGCA 1020
DB 961 AAAATTAAGTGGGATAGTGTGTCACACCTGTATCCACCTTGGAGGCTGAGGCA 1020
QY 1021 GGAGAAATCGCTTGAACCTGGGAAAGGAGGTTGAGTGCAGTGCACATCATGTCAC 1080
DB 1021 GGAGAAATCGCTTGAACCTGGGAAAGGAGGTTGAGTGCAGTGCACATCATGTCAC 1080
QY 1081 TCCAGCTGGGTGACAGAGTGAAGTCTGTCTCAACGAAAAAAAGTAAAGGCAT 1140
DB 1081 TCCAGCTGGGTGACAGAGTGAAGTCTGTCTCAACGAAAAAAAGTAAAGGCAT 1140
QY 1141 TCCATTAATGATGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TCCATTAATGATGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 ACCGTGAAAGTAGAGTGTGTCAGAGGATACATTTTCAATTTCAATTTCAATTTCAAT 1260
DB 1201 ACCGTGAAAGTAGAGTGTGTCAGAGGATACATTTTCAATTTCAATTTCAATTTCAAT 1260
QY 1261 ACCAAGTTCGATTCGAAAGGAGGTTTTTTTTTACATTTCACTCCCCCAGCAACAAT 1320
DB 1261 ACCAAGTTCGATTCGAAAGGAGGTTTTTTTTTACATTTCACTCCCCCAGCAACAAT 1320
QY 1321 GAGAGTACTCCAGATCTTTTAAAGATGCTCTAAGCCAGTACAGATGAAGAAAGGA 1380
DB 1321 GAGAGTACTCCAGATCTTTTAAAGATGCTCTAAGCCAGTACAGATGAAGAAAGGA 1380
QY 1381 AGTGGAGGGAAGCTGCGACGCTTCTTAACATGAAGAAATACCTGTAGAGCTTCT 1440
DB 1381 AGTGGAGGGAAGCTGCGACGCTTCTTAACATGAAGAAATACCTGTAGAGCTTCT 1440
QY 1441 GATAGCTGGAAGATGAATTAACGGGGTCTCTGAGGCTGCCCCCTGTCAAGTCACTGTG 1500
DB 1441 GATAGCTGGAAGATGAATTAACGGGGTCTCTGAGGCTGCCCCCTGTCAAGTCACTGTG 1500
QY 1501 ACTTCTGAGGCTCAGATCCAGTCTCAGGCCCATGTGTCAATGGGAGGAGGAGGCTT 1560
DB 1501 ACTTCTGAGGCTCAGATCCAGTCTCAGGCCCATGTGTCAATGGGAGGAGGAGGCTT 1560
QY 1561 CACTCTCTGTTTGTCTTATTTCTCCCATGTGGGGCTGAAGTCTGATTTGAGCCGTTAT 1620
DB 1561 CACTCTCTGTTTGTCTTATTTCTCCCATGTGGGGCTGAAGTCTGATTTGAGCCGTTAT 1620
QY 1621 TCAAGATGTACAGCTTTCTTGACAGAAAGTATGTCAAGAAACAGCAGGGCTTGGCA 1680
DB 1621 TCAAGATGTACAGCTTTCTTGACAGAAAGTATGTCAAGAAACAGCAGGGCTTGGCA 1680
QY 1681 AGATGATCTTAACCTGCAAAATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1740
DB 1681 AGATGATCTTAACCTGCAAAATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1740

OY	1741	AAAGTTTTTCACTTCTCTGAGGCCATCCCTTGGCTACAAACACACCACTGTGGTTGACAGGA	1800
Db	1741	AAAGTTTTTCACTTCTCTGAGGCCATCCCTTGGCTACAAACACACCACTGTGGTTGACAGGA	1800
OY	1801	TGAATATGACGAAGTCCCTTACACCTGTATCCAGACACTTGGAGAGCCCAAGGGGGGG	1860
Db	1801	TGAATATGACGAAGTCCCTTACACCTGTATCCAGACACTTGGAGAGCCCAAGGGGGGG	1860
OY	1861	ATGGCTTGAGCCTTGAGAGGTGACAGCATGCCGGCAGTCTTCACAGACCCTCGTTCGCTTC	1920
Db	1861	ATGGCTTGAGCCTTGAGAGGTGACAGCATGCCGGCAGTCTTCACAGACCCTCGTTCGCTTC	1920
OY	1921	GGCGCTCCTCTGGCTGGGGCCCACTTCGGTGGCAGTTGGAGAGCCCTTACAGCCACCG	1980
Db	1921	GGCGCTCCTCTGGCTGGGGCCCACTTCGGTGGCAGTTGGAGAGCCCTTACAGCCACCG	1980
OY	1981	CTGCAGTGTGGAGACCCCTTCTTGGGGCTGGCCAGAGCCAGCGGCTCCCTCACTAGCTTC	2040
Db	1981	CTGCAGTGTGGAGACCCCTTCTTGGGGCTGGCCAGAGCCAGCGGCTCCCTCACTAGCTTC	2040
OY	2041	AGGAGGTGTGAGGAGAGAGGCTCAACGAGAACCCGGGGCTGGCCAGGGGCTTGGGGGC	2100
Db	2041	AGGAGGTGTGAGGAGAGAGGCTCAACGAGAACCCGGGGCTGGCCAGGGGCTTGGGGGC	2100
OY	2101	CAGCTGAGATTCCCGGTGGGGGCTGTGGCGGGCCCGCACATCTGGAGACAGCGGGCCAG	2160
Db	2101	CAGCTGAGATTCCCGGTGGGGGCTGTGGCGGGCCCGCACATCTGGAGACAGCGGGCCAG	2160
OY	2161	CCCTGGCCAGGCCCCGGGGCAATGAAAGGCTTATAGCACCCGGGCCACAGCGGCTCGGAGGCTGT	2220
Db	2161	CCCTGGCCAGGCCCCGGGGCAATGAAAGGCTTATAGCACCCGGGCCACAGCGGCTCGGAGGCTGT	2220
OY	2221	ACTGGGTGCCCAACAGTGCAGCGCCCGCGGGCGGTGTGCTGCCTGCATTTCTCACTGGGC	2280
Db	2221	ACTGGGTGCCCAACAGTGCAGCGCCCGCGGGCGGTGTGCTGCCTGCATTTCTCACTGGGC	2280
OY	2281	CTTATGACAGCCTTCCCGGGGGCGAGGGCTCGGGACCTTGACAGCCGCCATGCTGTAGCCTCC	2340
Db	2281	CTTATGACAGCCTTCCCGGGGGCGAGGGCTCGGGACCTTGACAGCCGCCATGCTGTAGCCTCC	2340
OY	2341	CCTCATAGGGGTCCGTGTCGGGCGGGCGAGGCTCCCGAGAGACACACCCCTGCTGCACAG	2400
Db	2341	CCTCATAGGGGTCCGTGTCGGGCGGGCGAGGCTCCCGAGAGACACACCCCTGCTGCACAG	2400
OY	2401	CGCCCACTCCCATGACACACGAAAGGGCTGAAAGTGGGGCGACAGCGACACCGGAGCTGG	2460
Db	2401	CGCCCACTCCCATGACACACGAAAGGGCTGAAAGTGGGGCGACAGCGGACACCGGAGCTGG	2460
OY	2461	CAGGACAGTACCCTTGCAGACCCCTGTGGGATCACATGGGTGGAAGCCAGCTGGGGCTCT	2520
Db	2461	CAGGACAGTACCCTTGCAGACCCCTGTGGGATCACATGGGTGGAAGCCAGCTGGGGCTCT	2520
OY	2521	GAGCTGTGGTGGAGACTTGGAGAACCTTATATCTAGCTCAGAGATCGTAATTAACCAAT	2580
Db	2521	GAGCTGTGGTGGAGACTTGGAGAACCTTATATCTAGCTCAGAGATCGTAATTAACCAAT	2580
OY	2581	CAGACACCCCTGTCTAGCTCAGGGCTGTGTGATGCACCAATCCACACTCTGTATCTAGCT	2640
Db	2581	CAGACACCCCTGTCTAGCTCAGGGCTGTGTGATGCACCAATCCACACTCTGTATCTAGCT	2640
OY	2641	ACTCTGATAGGGGCTTGGAGAACCTTATATGCTTAGCTCAGGAGATTGTAATTAACCAATC	2700
Db	2641	ACTCTGATAGGGGCTTGGAGAACCTTATATGCTTAGCTCAGGAGATTGTAATTAACCAATC	2700
OY	2701	GGCACTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTCTAGCTC	2760
Db	2701	GGCACTGTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTCTAGCTC	2760
OY	2761	AGGCTATGTGATACGACCAATTCGACAGTCTGTATCTGGCTACTTTCAATGGGCATCGCTGT	2820
Db	2761	AGGCTATGTGATACGACCAATTCGACAGTCTGTATCTGGCTACTTTCAATGGGCATCGCTGT	2820

QY	2821	GAAGAGACCCAAACAGGCTTTGTGTGACATAAAGCTTTATCACTGGGTGCAAGT	2880
Db	2821	GAAGAGACCCAAACAGGCTTTGTGTGACAAATAAAGCTTCTATCACCTGGGTGCAAGT	2880
QY	2881	GGGCGTACTCCGAAAAGAGACTCAGCGAAGGAGATPAAGGTGGGGCGTTTATATGAGAT	2940
Db	2881	GGGCGTACTCCGAAAAGAGACTCAGCGAAGGAGATPAAGGTGGGGCGTTTATATGAGAT	2940
QY	2941	TTGGGTAGGTAAAGAAAATTATCACTCAAGGGGGTTGTCTCTGGCGGGCAGAGATGG	3000
Db	2941	TTGGGTAGGTAAAGAAAATTATCACTCAAGGGGGTTGTCTCTGGCGGGCAGAGATGG	3000
QY	3001	GGGGTGCAGGTGCTCACTAGTGGGGTCTTTTGTAGCCAGAGATGAGCCAGAGAAAGACT	3060
Db	3001	GGGGTGCAGAGTGTCTCACTAGTGGGGTCTTTTGTAGCCAGAGATGAGCCAGAGAAAGACT	3060
QY	3061	TTCCAAAGATATGTCAATATPAAGGCAAGGACCGGCCATTTACACTCTTTTGTGAGTG	3120
Db	3061	TTCCAAAGATATGTCAATATPAAGGCAAGGACCGGCCATTTACACTCTTTTGTGAGTG	3120
QY	3121	GAATGTCAATCAGTTAAAGTTGGGGCAGGGCATATTCACCTCTTTTGTGATTTCACTTAC	3180
Db	3121	GAATGTCAATCAGTTAAAGTTGGGGCAGGGCATATTCACCTCTTTTGTGATTTCACTTAC	3180
QY	3181	TTTCAGGCCATCTGGGGCTATATGTGCAAGTTTACAGGGAGATGCGATGGCTTGGGCT	3240
Db	3181	TTTCAGGCCATCTGGGGCTATATGTGCAAGTTTACAGGGAGATGCGATGGCTTGGGCT	3240
QY	3241	CAGAGGCTTGACAGCTACTCTGGTGGGGCCCTGGAGATGTTTGTGTCGACACTGTAT	3300
Db	3241	CAGAGGCTTGACAGCTACTCTGGTGGGGCCCTGGAGATGTTTGTGTCGACACTGTAT	3300
QY	3301	CTAGTTAAATCTAGTGGGGACGTGGAGAACCTTTTGTCTAGCTCAGAGATTTGTAAACGA	3360
Db	3301	CTAGTTAAATCTAGTGGGGACGTGGAGAACCTTTTGTCTAGCTCAGAGATTTGTAAACGA	3360
QY	3361	CCAATCAGCGCCCTGTCAAAAACAGACACTGGCTTACCAATCAGCAGATGTGGGTGG	3420
Db	3361	CCAATCAGCGCCCTGTCAAAAACAGACACTGGCTTACCAATCAGCAGATGTGGGTGG	3420
QY	3421	GGCCAGATPAAGATTAAGACAGGCGCCGACCCAGCAGCAAGTGGCAACGGGCAAGTCC	3480
Db	3421	GGCCAGATPAAGATTAAGACAGGCGCTGCCGACCCAGCAGCAAGTGGCAACGGGCAAGTCC	3480
QY	3481	CTATCCAAATATGAGGAGCTTTGTCTTTTGTGCTTTTGGCATTAATTTTCTACTGCTCG	3540
Db	3481	CTATCCAAATATGAGGAGCTTTGTCTTTTGTGCTTTTGGCATTAATTTTCTACTGCTCG	3540
QY	3541	CTTTTGGGTGCACACTGTCTTTATATGAGCTGTAACTCACACGAAAGTCTCAGCTTC	3600
Db	3541	CTTTTGGGTGCACACTGTCTTTATATGAGCTGTAACTCACACGAAAGTCTCAGCTTC	3600
QY	3601	ACTCCTGAAGCATTAAAGACACAGACGACCGGAGAGATGAAACACTCCGGGCGGCT	3660
Db	3601	ACTCCTGAAGCATTAAAGACACAGACGACCGGAGAGATGAAACACTCCGGGCGGCT	3660
QY	3661	GCTTTAAGAGTATTAACACTCAGCGGCAAGGTGTGACGTTCACTCTCTCAGCAGCGAGA	3720
Db	3661	GCTTTAAGAGTATTAACACTCAGCGGCAAGGTGTGACGTTCACTCTCTCAGCAGCGAGA	3720
QY	3721	CCACGAAACCCACAGAAAGAAAGTGCAGAACATCTGAACATCGAAGAGAAACAACCT	3780
Db	3721	CCACGAAACCCACAGAAAGAAAGTGCAGAACATCTGAACATCGAAGAGAAACAACCT	3780
QY	3781	CCAAGTGCACACTTAAAGAGCTGTAACTCACTGGGAGAGGTCCGGGGCTTCTCTTGG	3840
Db	3781	CCAAGTGCACACTTAAAGAGCTGTAACTCACTGGGAGAGGTCCGGGGCTTCTCTTGG	3840
QY	3841	AAGTCAGAGAACCAAGCACTCAGCACTTTCGGGACAGAACCCAGAGAGTTTGAATAGC	3900
Db	3841	AAGTCAGAGAACCAAGCACTCAGCACTTTCGGGACAGAACCCAGAGAGTTTGAATAGC	3900
QY	3901	CTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCGG	3960

```
|||||
Db 3901 CTGGGCAACATGATGTAATGACCTCTCTGCAAAAAAAAAAAATTAACAAAATTG6CGG 3960
QY 3961 AGCATGTGGTCCGTCCTGTGTGTCCAGTACGCGGAGGCTAAAGTGGGAGATGCT 4020
Db 3961 AGCATGTGGTCCGTCCTGTGTGTCCAGTACGCGGAGGCTAAAGTGGGAGATGCT 4020
QY 4021 TAGAGCTGGGAGGTGAAGACTGCAAGTGTGATGTTACACAGCCCTTGTAGCTGGG 4080
Db 4021 TAGAGCTGGGAGGTGAAGACTGCAAGTGTGATGTTACACAGCCCTTGTAGCTGGG 4080
QY 4081 GGACACACTGAGACCTGTTTCCCTCCGCAAAAAAATTAACAAAAGTGAATAGAGT 4140
Db 4081 GGACACACTGAGACCTGTTTCCCTCCGCAAAAAAATTAACAAAAGTGAATAGAGT 4140
QY 4141 GCGTGTATGTGCTAGGCGAGTGGCTCATGCTGTATCCACAGCTTTGGGAAGCGAG 4200
Db 4141 GCGTGTATGTGCTAGGCGAGTGGCTCATGCTGTATCCACAGCTTTGGGAAGCGAG 4200
QY 4201 GCGGGGCGGCTACCTTAAGTCAAGAGTGTGACACAGCCCTGGCCAACTGGAAGAGCC 4260
Db 4201 GCGGGGCGGCTACCTTAAGTCAAGAGTGTGACACAGCCCTGGCCAACTGGAAGAGCC 4260
QY 4261 ATCTCTTCAAAAATACAAAATTAAGCGGCTGTGGGGGCGAGTGGAGCATGCTGTAA 4320
Db 4261 ATCTCTTCAAAAATACAAAATTAAGCGGCTGTGGGGGCGAGTGGAGCATGCTGTAA 4320
QY 4321 TCCACCTACTCAGAGGCTGAGGCAAGAAATCACTTGAACCCAGAGGCGGCTTGC 4380
Db 4321 TCCACCTACTCAGAGGCTGAGGCAAGAAATCACTTGAACCCAGAGGCGGCTTGC 4380
QY 4381 AGTGACCCGAGATCGTGCCATTGCTACTCCACCACTCCAGCTTGCGGCAACAGCCAAA 4440
Db 4381 AGTGACCCGAGATCGTGCCATTGCTACTCCACCACTCCAGCTTGCGGCAACAGCCAAA 4440
QY 4441 CTCTGCTTAAAAAATAAAAAAATGCTGCTGACATATTAAGAGGTGTGCAATGCAATAG 4500
Db 4441 CTCTGCTTAAAAAATAAAAAAATGCTGCTGACATATTAAGAGGTGTGCAATGCAATAG 4500
QY 4501 TTGCGCAGGCAACATGTTTAAAGATGTGAGCTCTGCTTCATGTGCTGTTAAAAACC 4560
Db 4501 TTGCGCAGGCAACATGTTTAAAGATGTGAGCTCTGCTTCATGTGCTGTTAAAAACC 4560
QY 4561 CACCCCAAGGCCAGGTGCAAGTGGCTCATGCTATATCCACACTTTTGGAGGCGGAG 4620
Db 4561 CACCCCAAGGCCAGGTGCAAGTGGCTCATGCTATATCCACACTTTTGGAGGCGGAG 4620
QY 4621 GCGGGTGGATCACTGAGTCAAGAGTTCGAGACAGCCCTGACACCAACATGCTGAAT 4680
Db 4621 GCGGGTGGATCACTGAGTCAAGAGTTCGAGACAGCCCTGACACCAACATGCTGAAT 4680
QY 4681 CCCACCTCTAATAAATAACAAAATTAAGATGAGCATGTGTGCTGATGCTTAATCCAC 4740
Db 4681 CCCACCTCTAATAAATAACAAAATTAAGATGAGCATGTGTGCTGATGCTTAATCCAC 4740
QY 4741 CTACTTGGGAGGTGAGGCGAGAAATTAACATAGAACAGGAGCGGAGGTTTGTAGAG 4800
Db 4741 CTACTTGGGAGGTGAGGCGAGAAATTAACATAGAACAGGAGCGGAGGTTTGTAGAG 4800
QY 4801 CCGAGATCGTGCATGCACTCCAGCTGAGCAATGAGGAGGCAATCCTCATCAAAAAAAC 4860
Db 4801 CCGAGATCGTGCATGCACTCCAGCTGAGCAATGAGGAGGCAATCCTCATCAAAAAAAC 4860
QY 4861 AACACAAAAACCACTCTACTTCCAGGAGAGTGGGTACAGAGCTGGGCGCATCAGT 4920
Db 4861 AACACAAAAACCACTCTACTTCCAGGAGAGTGGGTACAGAGCTGGGCGCATCAGT 4920
QY 4921 GCAAGGTGCTGAGCCACAGAGCTTAAGCGGAGCTGCAAGACCGCGACCAAGATTAACAGT 4980
Db 4921 GCAAGGTGCTGAGCCACAGAGCTTAAGCGGAGCTGCAAGACCGCGACCAAGATTAACAGT 4980
QY 4981 TGTGAGATCAGTGTGAGATCAGAGCTCCCTGCAATGTGGTGAACACAGGGGCGCCCA 5040
|||||
Db 4981 TGTGAGATCAGTGTGAGATCAGAGCTCCCTCCATTTGCTGACACACAGGGGCGCCCA 5040
QY 5041 AGCACCAGAGATGGCCCATCCAGTCAACACATCACTTCTCATCCAGAGATGCTGTTT 5100
Db 5041 AGCACCAGAGATGGCCCATCCAGTCAACACATCACTTCTCATCCAGAGATGCTGTTT 5100
QY 5101 CTTGGCACGCTGGGGTAAATTAAGACAGAAAGTGTGAGTGTGGGTGTGTGATGAGAC 5160
Db 5101 CTTGGCACGCTGGGGTAAATTAAGACAGAAAGTGTGAGTGTGGGTGTGTGATGAGAC 5160
QY 5161 TGCCCCAGCAGGCTTGTGGCTGTGAATAAGTTTACAGGCTTAGCCCGGACAGGTGCG 5220
Db 5161 TGCCCCAGCAGGCTTGTGGCTGTGAATAAGTTTACAGGCTTAGCCCGGACAGGTGCG 5220
QY 5221 TCAGGCTGTAAATCCAGACATTTTGGAGGCGAGGCGGCTGTATCAGAGTCCAGAGA 5280
Db 5221 TCAGGCTGTAAATCCAGACATTTTGGAGGCGAGGCGGCTGTATCAGAGTCCAGAGA 5280
QY 5281 TCGTGACATCCCTGGCTAACACGCTGAAACCCGCTCTAATAAATAAATAATG 5340
Db 5281 TCGTGACATCCCTGGCTAACACGCTGAAACCCGCTCTAATAAATAAATAATG 5340
QY 5341 CCGGGCATGCTGGGCGACCTGTAGTTCAGCTACTCGGAGGCTTGAGGCAAGAGATG 5400
Db 5341 CCGGGCATGCTGGGCGACCTGTAGTTCAGCTACTCGGAGGCTTGAGGCAAGAGATG 5400
QY 5401 GCGTGAACCCGAGAGCGAGATTTGCAAGTGAAGCCAGATGCGCCACTGCATCCAGCT 5460
Db 5401 GCGTGAACCCGAGAGCGAGATTTGCAAGTGAAGCCAGATGCGCCACTGCATCCAGCT 5460
QY 5461 GGGCGACAGACGAACTCCATCTGGAATAAAGAAAAGAAAACCTTCAGGCTGAGCGAGA 5520
Db 5461 GGGCGACAGACGAACTCCATCTGGAATAAAGAAAAGAAAACCTTCAGGCTGAGCGAGA 5520
QY 5521 GGCCCAAGGCTGTAATCTGTCACTTACATGACCTTGGGCAAGGCACTTCTCCCTGGC 5580
Db 5521 GGCCCAAGGCTGTAATCTGTCACTTACATGACCTTGGGCAAGGCACTTCTCCCTGGC 5580
QY 5581 CCAGTTCAGGGGTTGGAATGCACTCCAGAGCTCCCTTCAGCATTAACGCTGATGGTTG 5640
Db 5581 CCAGTTCAGGGGTTGGAATGCACTCCAGAGCTCCCTTCAGCATTAACGCTGATGGTTG 5640
QY 5641 TAAGATGAGAAATGGGGGAGTTTCCCTCTCACCCAGCCCGGTGTCCACTTCAAGGT 5700
Db 5641 TAAGATGAGAAATGGGGGAGTTTCCCTCTCACCCAGCCCGGTGTCCACTTCAAGGT 5700
QY 5701 GAATGACACAGGAAATGCACTGTCCTCAATCCCGAGTTCCAAAGCCCTTGGGAGCCCTAC 5760
Db 5701 GAATGACACAGGAAATGCACTGTCCTCAATCCCGAGTTCCAAAGCCCTTGGGAGCCCTAC 5760
QY 5761 TGTCAAGGCTGTCACAGAGAGTGAAGGTCAAGTGAAGCCCAATCGCCTCGAAGGCTTGG 5820
Db 5761 TGTCAAGGCTGTCACAGAGAGTGAAGGTCAAGTGAAGCCCAATCGCCTCGAAGGCTTGG 5820
QY 5821 CCTCATTTGGGACAGACATCCGTTTCTGTGCTTACCGGGATTTCTAGGGCTTTAGC 5880
Db 5821 CCTCATTTGGGACAGACATCCGTTTCTGTGCTTACCGGGATTTCTAGGGCTTTAGC 5880
QY 5881 CGAATGATCATGGGGGCGGGGGGTTTCTGGGGAGTTTCCAGGCTTAATCACTTGGGA 5940
Db 5881 CGAATGATCATGGGGGCGGGGGGTTTCTGGGGAGTTTCCAGGCTTAATCACTTGGGA 5940
QY 5941 CAGGACAGCTGGAATTTGATGATGTGCTATCAAGTGTGGGTGGGCGACAGACCAA 6000
Db 5941 CAGGACAGCTGGAATTTGATGATGTGCTATCAAGTGTGGGTGGGCGACAGACCAA 6000
QY 6001 GACCCAAATGCTTAACTCAGGTAGGGGCTCAGAGAGTCTCCAGACAGGACCTTCGG 6060
Db 6001 GACCCAAATGCTTAACTCAGGTAGGGGCTCAGAGAGTCTCCAGACAGGACCTTCGG 6060
QY 6061 AGAGTTTGGGGTAGAATAAGGAGCAACAGGCTTCTTTTCTCTTAAATTTGGG 6120
|||||
Db 6061 AGAGTTTGGGGTAGAATAAGGAGCAACAGGCTTCTTTTCTCTTAAATTTGGG 6120
```


|||||
Db 920 ATCAACAGTTGGAGACCGCTGGCCAAACATAGCAAAACCCCATTTCTACTAAAAATAAA 979
Oy 961 AAAATTAGCTGGCATAGTGGTGCACACCTGTGATCCAGCTACTTGGAGGCTGAGCA 1020
Db 980 AAAATTAGCTGGCATAGTGGTGCACACCTGTGATCCAGCTACTTGGAGGCTGAGCA 1039
Oy 1021 GGAGAAATCGCTTGAACCTGGGAGCGGAGGTTGACAGTAGGCAACATATGCTCCATGAC 1080
Db 1040 GGAGAAATCGCTTGAACCTGGGAGCGGAGGTTGACAGTAGGCAACATATGCTCCATGAC 1099
Oy 1081 TCACAGCTGGGTGACAGAGTGAAGCTTCTCAACGAAAAAAGTGTAAAAAGCCAT 1140
Db 1100 TCACAGCTGGGTGACAGAGTGAAGCTTCTCAACGAAAAAAGTGTAAAAAGCCAT 1159
Oy 1141 TCCATAATTCAGTGTACATCATGTATACATACAGAGTCTGCGTACTCTGCTGTGAGCAT 1200
Db 1160 TCCATAATTCAGTGTACATCATGTATACATACAGAGTCTGCGTACTCTGCGTGTGAGCAT 1219
Oy 1201 ACCTGAGAAATGAGAGTGGCTTGTACAGAGACATACACATTTCCACATTACTAGACACT 1260
Db 1220 ACCTGAGAAATGAGAGTGGCTTGTACAGAGACATACACATTTCCACATTACTAGACACT 1279
Oy 1261 ACCAAGTTGCCATCCAAAGAGGTTTTTTTTTACAAATCTACACTCCCCCAGCAACAAT 1320
Db 1280 ACCAAGTTGCCATCCAAAGAGGTTTTTTTTTACAAATCTACACTCCCCCAGCAACAAT 1339
Oy 1321 GAGAGTACTCCAGATCCTTTACAAAGATGCTTAAGCCCATACAGATATAAACAAGA 1380
Db 1340 GAGAGTACTCCAGATCCTTTACAAAGATGCTTAAGCCCATACAGATATAAACAAGA 1399
Oy 1381 AGTGGAGGGGAAAGCTCCAGACCCCTTCTTAACATGAGAAATACCTGGTAGAGCCCTCT 1440
Db 1400 AGTGGAGGGGAAAGCTCCAGACCCCTTCTTAACATGAGAAATACCTGGTAGAGCCCTCT 1459
Oy 1441 GGATGCTGGAAGATGAATAACGGGGGCTCTGTGAGGCTGCCCCCTGTCAAGATCATGTG 1500
Db 1460 GGATGCTGGAAGATGAATAACGGGGGCTCTGTGAGGCTGCCCCCTGTCAAGATCATGTG 1519
Oy 1501 ACCTTGTAGGCTCCAGTCCAGCTGTCAACGCCCATATGTCAATGGCAGTGAATGAGCCCT 1560
Db 1520 ACCTTGTAGGCTCCAGTCCAGCTGTCAACGCCCATATGTCAATGGCAGTGAATGAGCCCT 1579
Oy 1561 CACTCTCTGTTGGCTTTATTCCTCCCATGTGGGGCTGAAGTGTGATTTGAGCCGTTAT 1620
Db 1580 CACTCTCTGTTGGCTTTATTCCTCCCATGTGGGGCTGAAGTGTGATTTGAGCCGTTAT 1639
Oy 1621 TCAGAGATGACAGCTTTCTTGACAGAAAGTAGTGTCACAGAAAAACAGAGGGGCTTGCA 1680
Db 1640 TCAGAGATGACAGCTTTCTTGACAGAAAGTAGTGTCACAGAAAAACAGAGGGGCTTGCA 1699
Oy 1681 AGATGATCTAATCGCAAAATGCTTACCTGGCTCAGGCACACCTAGTTGTGTGATCTTGAC 1740
Db 1700 AGATGATCTAATCGCAAAATGCTTACCTGGCTCAGGCACACCTAGTTGTGTGATCTTGAC 1759
Oy 1741 AAGTTTTTCACTTCTCTGAGGCCATCCCTGGCTTACACACACAGCAAGTTGGTTGACAGGA 1800
Db 1760 AAGTTTTTCACTTCTCTGAGGCCATCCCTGGCTTACACACACAGCAAGTTGGTTGACAGGA 1819
Oy 1801 TGAATGAGAGAGTCCCTTACACCTGTATTCACAGCACTTTGGAGGCAAGGCGGGTGG 1860
Db 1820 TGAATGAGAGAGTCCCTTACACCTGTATTCACAGCACTTTGGAGGCAAGGCGGGTGG 1879
Oy 1861 ATGGGCTTGAAGCTGGAAGGTGACAGCATGCGGCACTCCACAGCCCTGCTGCGTCGC 1920
Db 1880 ATGGGCTTGAAGCTGGAAGGTGACAGCATGCGGCACTCCACAGCCCTGCTGCGTCGC 1939
Oy 1921 GGGGCTCTCTGCTGGGCTCCACTTGTGGTGGGCACTTGAAGAGCCCTTCAAGCCACCG 1980
Db 1940 GGGGCTCTCTGCTGGGCTCCACTTGTGGTGGGCACTTGAAGAGCCCTTCAAGCCACCG 1999
Oy 1981 CTGCACTGTGGAGCCCTTCTGTGGGCTGGCAAGGCGAGGCGGGCTCCCTAGCTTGC 2040
|||||

Db 2000 CTGCACTGTGGGAGCCCTTCTGTGGCTTGGCCAAAGCCAGACCCGGCTCCTCAAGCTTGC 2059
Oy 2041 AGGAGGTGTGAGGAGAGGCTCAAGCAGAAACCGGGGCTGCGCACGGCTTGGCGGC 2100
Db 2060 AGGAGGTGTGAGGAGAGGCTCAAGCAGAAACCGGGGCTGCGCACGGCTTGGCGGC 2119
Oy 2101 CAGCTGGAGTTCGGGGTGGGCTGTGGGCTTGGCGGGCCGCACTGCGAGCAGCGGGCCAG 2160
Db 2120 CAGCTGGAGTTCGGGGTGGGCTGTGGGCTTGGCGGGCCGCACTGCGAGCAGCGGGCCAG 2179
Oy 2161 CCTGCGAGGCCCCGGAATGAGAGGCTTAGCAACCCGGGGCAGCGGCTGGGGAGGGTGT 2220
Db 2180 CCTGCGAGGCCCCGGAATGAGAGGCTTAGCAACCCGGGGCAGCGGCTGGGGAGGGTGT 2239
Oy 2221 ACTGGGTGCCCCAGCAGTCCAGCCCGCGGCGGTGTGCTGCTGATTTCTCATGTGGC 2280
Db 2240 ACTGGGTGCCCCAGCAGTCCAGCCCGCGGCGGTGTGCTGCTGATTTCTCATGTGGC 2299
Oy 2281 CTTAGCAGCCCTTCCCGGGGGGAGGCTGCGGGGACTGTGACGCCGCATGCTGAGCCTCC 2340
Db 2300 CTTAGCAGCCCTTCCCGGGGGGAGGCTGCGGGGACTGTGACGCCGCATGCTGAGCCTCC 2359
Oy 2341 CCTCATGGGCTCCTGTGTGGGCGCCGAGCCTCCCGAGAGCAGCACCCCTGCTCCAG 2400
Db 2360 CCTCATGGGCTCCTGTGTGGGCGCCGAGGCTCCCGAGAGCAGCACCCCTGCTCCAG 2419
Oy 2401 CGCCCATGCCATGACACAGCAGAAAGGCTGGAAGTGGGGGCGACGCGGAGCTGG 2460
Db 2420 CGCCCATGCCATGACACAGCAGAAAGGCTGGAAGTGGGGGCGACGCGGAGCTGG 2479
Oy 2461 CAGGACGCTACCCCTGCGAGCCCTGTGGGAAATCATCTGGGTGAAGCAGCTGGGCTCT 2520
Db 2480 CAGGACGCTACCCCTGCGAGCCCTGTGGGAAATCATCTGGGTGAAGCAGCTGGGCTCT 2539
Oy 2521 GAGTCTGGTGAAGACTTGGAGAACTTTATGTCTAGCTCAGAGGATCGAAATACACAAT 2580
Db 2540 GAGTCTGGTGAAGACTTGGAGAACTTTATGTCTAGCTCAGAGGATCGAAATACACAAT 2599
Oy 2581 CAGCACCTGTGTCTAGCTCAGAGGCTGTGTAATGACACAATCCACACTGTGTATCTAGCT 2640
Db 2600 CAGCACCTGTGTCTAGCTCAGAGGCTGTGTAATGACACAATCCACACTGTGTATCTAGCT 2659
Oy 2641 ACTGTGATGGGCTTGGAGAACTTTATGTCTAGCTCAGAGGATGTAAATACACAATC 2700
Db 2660 ACTGTGATGGGCTTGGAGAACTTTATGTCTAGCTCAGAGGATGTAAATACACAATC 2719
Oy 2701 GGCACCTGTATCTAGCTCAAGGTTGTAAACACACAATCAGACCCCTGTGTACTCTC 2760
Db 2720 GGCACCTGTATCTAGCTCAAGGTTGTAAACACACAATCAGACCCCTGTGTACTCTC 2779
Oy 2761 AGGGTATGTAAATGACACAATCGACAGTGTATCTGGCTACTTTCATGGGACATCCGTGT 2820
Db 2780 AGGGTATGTAAATGACACAATCGACAGTGTATCTGGCTACTTTCATGGGACATCCGTGT 2839
Oy 2821 GAAGAGACCAACCAAGGCTTGTGTGAGCAATTAAGCTTCTATCACTGGGTGCAAGT 2880
Db 2840 GAAGAGACCAACCAAGGCTTGTGTGAGCAATTAAGCTTCTATCACTGGGTGCAAGT 2899
Oy 2881 GGGCTGAGTCCGAAAAAGAGATGAGGGAAGGAGATAAAGGCTGGGGCCGTTTATAGAT 2940
Db 2900 GGGCTGAGTCCGAAAAAGAGATGAGGGAAGGAGATAAAGGCTGGGGCCGTTTATAGAT 2959
Oy 2941 TTGGGTAGGTAAAGAAAAATTACAGTCAAAAGGGGTTGTCTCTGGGGGCGAGAGTG 3000
Db 2960 TTGGGTAGGTAAAGAAAAATTACAGTCAAAAGGGGTTGTCTCTGGGGGCGAGAGTG 3019
Oy 3001 GGGGTGCAAGGTGCTCACTGGGGGCTTTTGTGACCAAGATGAGCAGAAAGAGACT 3060
Db 3020 GGGGTGCAAGGTGCTCACTGGGGGCTTTTGTGACCAAGATGAGCAGAAAGAGACT 3079
Oy 3061 TTCACAAGGTAAATGTATCAATTAAGGCAAGGACCCGCAATTTACACTCTTTTGTGGTG 3120
Db 3080 TTCACAAGGTAAATGTATCAATTAAGGCAAGGACCCGCAATTTACACTCTTTTGTGGTG 3139
|||||

QY	4201	GGGGGGGTCACCTTAAGTACAGAGTGTGAGACCAAGCTTGCCCAATGAGAAAGCC	4260
Db	4220	GGGGGGGGGTACCTTAAGTACAGAGTGTGAGACCAAGCTTGCCCAATGAGAAAGCC	4279
QY	4261	ATCTCTTAAAAAATNCAAAATTTAGCCGGCTGTGGGGGCACTGGTGGCAATGCTGTAA	4320
Db	4280	ATCTCTTAAAAAATNCAAAATTTAGCCGGCTGTGGGGGCACTGGTGGCAATGCTGTAA	4339
QY	4321	TCCCAGCTACTCAGAGGCTGAGGAGAGATCACTTGAACCCAGAGGGGGCTGTGC	4380
Db	4340	TCCCAGCTACTCAGAGGCTGAGGAGAGATCACTTGAACCCAGAGGGGGCTGTGC	4399
QY	4391	AGTGAAGCCGAGATCGTGCATTGCACTCCACCACCTCCAGCGCTGGGCAACAAGCCAAA	4440
Db	4400	AGTGAAGCCGAGATCGTGCATTGCACTCCACCACCTCCAGCGCTGGGCAACAAGCCAAA	4459
QY	4441	CTCTGTCTTAAAAAATTTAGAGTGTGACATTTAAGAGGTGTGCAATGCATAG	4500
Db	4460	CTCTGTCTTAAAAAATTTAGAGTGTGACATTTAAGAGGTGTGCAATGCATAG	4519
QY	4501	TTGGCAGGCAACATGTTTAAAGATTTGAGGCTCCGCTTCCATAGTGTCTGTAAAAAC	4560
Db	4520	TTGGCAGGCAACATGTTTAAAGATTTGAGGCTCCGCTTCCATAGTGTCTGTAAAAAC	4579
QY	4561	CACCCCTAAGGCGAGGTGCACTGGCTCATGCTATTAATCCAGCACTTTGGGAGCCGAG	4620
Db	4580	CACCCCTAAGGCGAGGTGCACTGGCTCATGCTATTAATCCAGCACTTTGGGAGCCGAG	4639
QY	4621	GGGGGTGATACACCTGAGGTGAGAGTTCGAGACCAGCTTCAACCAACATGTTGAAT	4680
Db	4640	GGGGGTGATACACCTGAGGTGAGAGTTCGAGACCAGCTTCAACCAACATGTTGAAT	4699
QY	4681	CCCAACCTTACTAAAAATACAAAAATTTAGATAGCATGGTGTGATGCTTAAATCCAC	4740
Db	4700	CCCAACCTTACTAAAAATACAAAAATTTAGATAGCATGGTGTGATGCTTAAATCCAC	4759
QY	4741	CTACTTGGGAGGCTGAGGCGAGAAATCTAGAACAGGAGGCGGAGTTGTAGTAG	4800
Db	4760	CTACTTGGGAGGCTGAGGCGAGAAATCTAGAACAGGAGGCGGAGTTGTAGTAG	4819
QY	4801	CCGAGATCGTCCANTGCACTCCAGCGCTGACCAATGAGCCAAATCTCCATCTCAAAAAAC	4860
Db	4820	CCGAGATCGTCCANTGCACTCCAGCGCTGACCAATGAGCCAAATCTCCATCTCAAAAAAC	4879
QY	4861	AACAAACAAAAACCCACTCTTACTTCCAGGAGGCTGGGTAAAGAGCTGGGCGACATAGT	4920
Db	4880	AACAAACAAAAACCCACTCTTACTTCCAGGAGGCTGGGTAAAGAGCTGGGCGACATAGT	4939
QY	4921	GCAAGGTGCTGAGCGACAGAGCTAAAGCGGAGCTGACAGAACCGCGGACACAGATAAGTG	4980
Db	4940	GCAAGGTGCTGAGCGACAGAGCTAAAGCGGAGCTGACAGAACCGCGGACACAGATAAGTG	4999
QY	4981	TGTAGATCACTGTGTGTGAGATCAACAGTCCCTGGCATTTGGTGTGTGTCACTGCAGAC	5040
Db	5000	TGTAGATCACTGTGTGTGAGATCAACAGTCCCTGGCATTTGGTGTGTGTCACTGCAGAC	5059
QY	5041	AGCACCAGAGATGGGCCCATCCAGTCAACACATCCATTCATCCAGAGATGTCTGTTT	5100
Db	5060	AGCACCAGAGATGGGCCCATCCAGTCAACACATCCATTCATCCAGAGATGTCTGTTT	5119
QY	5101	CTTGGCAGCGTGGGGTAAATTAGAGCAGAAAGTGCACAGTCTTGGGTGTGTCACTGCAGAC	5160
Db	5120	CTTGGCAGCGTGGGGTAAATTAGAGCAGAAAGTGCACAGTCTTGGGTGTGTCACTGCAGAC	5179
QY	5161	TGCCCCAGGCGAGGCTTGTGGCTGTGAAAAAGCTTAAGGCTTAAGGCCGGGCGACAGTGGC	5220
Db	5180	TGCCCCAGGCGAGGCTTGTGGCTGTGAAAAAGCTTAAGGCTTAAGGCGGCGCGACAGTGGC	5239
QY	5221	TCACGGCTGTAAATCCAGCACTTTGGGAGGCGGAGGCGGGTGTGATCAAGAGTCAAGAGA	5280
Db	5240	TCACGGCTGTAAATCCAGCACTTTGGGAGGCGGAGGCGGGTGTGATCAAGAGTCAAGAGA	5299
QY	5281	TCGAGACCATCTTGCTTAACAGGTTGAACCCGCTCTCTACTAAAAATTAACAAAAATTTGG	5340

Db 5300 TCCTGACCAATCCCTGGGTAACACAGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATTGG 5359
 QY 5341 CCGGGATGGTGGCGGGACACCTGTAGTTCAGTACTCGGAGAGGCTGAGGACAGAGATG 5400
 Db 5360 CCGGGATGGTGGCGGGACACCTGTAGTTCAGTACTCGGAGAGGCTGAGGACAGAGATG 5419
 QY 5401 GCGTGAACCCGAGAGGACAGATTTGCAAGTAGAGCCGAGATGCGCCACATGACATCCAGCCT 5460
 Db 5420 GCGTGAACCCGAGAGGACAGATTTGCAAGTAGAGCCGAGATGCGCCACATGACATCCAGCCT 5479
 QY 5461 GGGCGACAGACAGAACTCCATCTGGAAAAAGAAAAAGAAACGTTCAGGTCTGAGCCAGA 5520
 Db 5480 GGGCGACAGACAGAACTCCATCTGGAAAAAGAAAAAGAAACGTTCAGGTCTGAGCCAGA 5539
 QY 5521 GGGCCAGAGGTGTAATCTGTCTACTTACATGACCTTGGGAGGACATTCCTTCCTGCG 5580
 Db 5540 GGGCCAGAGGTGTAATCTGTCTACTTACATGACCTTGGGAGGACATTCCTTCCTGCG 5599
 QY 5581 CCAGTTCACGGGGTTGGAATCGACTCCAGAGTCCCTTCACAGCATTAACGCTGCATGGTTC 5640
 Db 5600 CCAGTTCACGGGGTTGGAATCGACTCCAGAGTCCCTTCACAGCATTAACGCTGCATGGTTC 5659
 QY 5641 TAAGATGAGAAGATGGGCGAGTTCCTCTCTACACCCGAGCCCGTCTCCACTTCAAGGT 5700
 Db 5660 TAAGATGAGAAGATGGGCGAGTTCCTCTCTACACCCGAGCCCGTCTCCACTTCAAGGT 5719
 QY 5701 GAATGACACAGGAAATGACGTGTCCTCCAAATCCCGAGTTCCAAAGCCCTTGGGACCTTAC 5760
 Db 5720 GAATGACACAGGAAATGACGTGTCCTCCAAATCCCGAGTTCCAAAGCCCTTGGGACCTTAC 5779
 QY 5761 TGTGAGGCTGTGACAGAGAGAGTGAAGTCAAGTGAAGCCATCGCTCGAAGGGCTTGG 5820
 Db 5780 TGTGAGGCTGTGACAGAGAGAGTGAAGTCAAGTGAAGCCATCGCTCGAAGGGCTTGG 5839
 QY 5821 CCTCATTCGGGACAGACATCCGGTTCCTCGGCTTACCGGGATTCATAGGGGGCTTAGC 5880
 Db 5840 CCTCATTCGGGACAGACATCCGGTTCCTCGGCTTACCGGGATTCATAGGGGGCTTAGC 5899
 QY 5881 CGAATGATCATGGGGGCGGGGGGTTTCTGGGGGAGTTCCTCCAGCTAATCAACTTGGGA 5940
 Db 5900 CGAATGATCATGGGGGCGGGGGGTTTCTGGGGGAGTTCCTCCAGCTAATCAACTTGGGA 5959
 QY 5941 CAGGACAGCTGGAACCTTGCATGTGCTTATCCAAATGTGGGGTGGGACAGACCAA 6000
 Db 5960 CAGGACAGCTGGAACCTTGCATGTGCTTATCCAAATGTGGGGTGGGACAGACCAA 6019
 QY 6001 GACCCAAATGTCTAATCTCAAGTGTGGGGTCAAGAGGTCCCGACAGAGGACGCTCCGG 6060
 Db 6020 GACCCAAATGTCTAATCTCAAGTGTGGGGTCAAGAGGTCCCGACAGAGGACGCTCCGG 6079
 QY 6061 AGAGTTTGGGGGTAGGAATGGGAGCAACAGGCTTCTTTTCTCTTGAATTTGGG 6120
 Db 6080 AGAGTTTGGGGGTAGGAATGGGAGCAACAGGCTTCTTTTCTCTTGAATTTGGG 6139
 QY 6121 GCGTTGGGGGACAGGCTTGAAGATCCCAAAGAGAGGGGCAAAAGACACTCCCCACAG 6180
 Db 6140 GCGTTGGGGGACAGGCTTGAAGATCCCAAAGAGAGGGGCAAAAGACACTCCCCACAG 6199
 QY 6181 TCTGCCAGAGGAGAGAGGAGAGACCCGAGTCACTGCCACTTCCACAGAGCCT 6235
 Db 6200 TCTGCCAGAGGAGAGAGGAGAGACCCGAGTCACTGCCACTTCCACAGAGCCT 6254

RESULT 3
 AAD17443
 ID AAD17443 standard; DNA; 6679 BP.
 AC AAD17443;
 XX
 XX 10-DEC-2001 (first entry)
 DE Human granulocyte colony stimulating factor (hucsf) fragment #1.

XX Human: mutation; homologous recombination; target sequence; gene therapy;
 KW homologous recombination-enhancing agent; non-homologous end joining;
 KM therapeutic protein; granulocyte colony stimulating factor; hucsf; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200168882-A2.
 PD 20-SEP-2001.
 XX
 PE 13-MAR-2001; 2001MO-US07870.
 XX
 PR 14-MAR-2000; 2000US-0525160.
 XX
 PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
 XX
 PI Ivanov E;
 DR WPI; 2001-582459/65.
 XX
 PT Complex or composition comprising a double stranded DNA sequence, a
 PT homologous recombination-enhancing agent, and agent inhibiting
 PT non-homologous end joining, for promoting alteration of a target
 PT sequence in a cell -
 XX
 PS Disclosure; Page 77-79; 82pp; English.
 XX
 CC The invention relates to a complex for promoting alteration of a target
 CC sequence in a cell, comprising a double stranded DNA sequence, a
 CC homologous recombination-enhancing agent and an agent inhibiting non-
 CC homologous end joining. The invention is used in gene therapy. The
 CC complex is useful for promoting an alteration at a selected site of
 CC a target sequence of a cell preferably of fungal, plant or animal
 CC origin, or of vertebrate origin which is a primary or secondary
 CC mammalian (human) cell or an immortalised mammalian (human) cell, where
 CC target sequence comprises a mutation preferably point mutation having
 CC less than 10 base pairs which differ from wild-type sequence, (selected
 CC from cystic fibrosis transmembrane regulator (CFTR) gene having mutation
 CC changes in an amino acid encoded by codon 508, beta-globin gene having
 CC mutation changes in an amino acid encoded by codon 6, Factor VIII gene
 CC having mutation changes in an amino acid encoded by codon 2209 or 2229,
 CC Factor IX gene, von Willebrand factor gene or xeroderma pigmentosa group
 CC G gene); and the DNA sequence comprises a wild-type sequence which can
 CC correct the mutation. The method further comprises introducing an agent
 CC which inhibits a mismatch-repair protein (expression), which is from
 CC Msh2, Msh6, Msh1 and PMS2, or is an anti-mismatch-repair protein
 CC antibody covalently linked to the DNA sequence, or to Rad52 protein or
 CC its fragment. The complex is useful for altering expression of a protein
 CC coding sequence of a gene in a cell. The method comprises introducing
 CC the complex into the cell, where the DNA sequence comprises a regulatory
 CC sequence, maintaining the cell under conditions which permit alteration
 CC of a targeted genomic sequence to produce a homologically recombinant
 CC cell and maintaining the homologically recombinant cell under conditions
 CC which permit expression of the protein coding sequence of the gene under
 CC control of the regulatory sequence. Homologously recombinant cell is
 CC useful as a vehicle or delivery system for therapeutic proteins, such as
 CC enzymes, hormones, cytokines, antigens, antibodies, clotting factors,
 CC anti-sense RNA, regulatory proteins, transcription proteins, receptors,
 CC structural proteins, novel (non-optimised) proteins and nucleic acid
 CC products and engineered DNA and for supplying a therapeutic protein,
 CC including erythropoietin, calcitonin, growth hormone, insulin and
 CC insulinotropin. The present sequence is human granulocyte colony
 CC stimulating factor (hucsf) fragment used in the invention.
 XX
 SQ Sequence 6679 BP; 1684 A; 1739 C; 1830 G; 1426 T; 0 other;
 Query Match 100.0%; Score 6235; DB 22; Length 6679;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATCAGCTTGAAGAGACAGTTCAGAACAGCAGCTGGGAGCATAGGAGACTGTCTACG 60

Db 20 GATCATTGAGACAGTAGTTCAAGACCAGCTGGGACATAGAGAGACTGTCTACG 79
QY 61 AAAAAATCAAAAAATTTATGGCCGGCATGTGGCTCAGCTGTATTCCTTGAACCTTTGGG 120
Db 80 AAAAAATCAAAAAATTTATGGCCGGCATGTGGCTCAGCTGTATTCCTTGAACCTTTGGG 139
QY 121 ACATCAAGGCAAGTGGATCATTGAGGTGAGAGTTCAGACTAGCTGGCCCAACATGGT 180
Db 140 ACATCAAGGCAAGTGGATCATTGAGGTGAGAGTTCAGACTAGCTGGCCCAACATGGT 199
QY 181 GAAACCCCTATCTCCACTAAAAAATACAAAAATTAGCCAGCATGGTGGCAGGACCTTGA 240
Db 200 GAAACCCCTATCTCCACTAAAAAATACAAAAATTAGCCAGCATGGTGGCAGGACCTTGA 259
QY 241 ATCCCGGCTACTCAGAGAGGTGAGGAGCAATCATTGAACCCAGAGAGGCGGAGTTG 300
Db 260 ATCCCGGCTACTCAGAGAGGTGAGGAGCAATCATTGAACCCAGAGAGGCGGAGTTG 319
QY 301 CAGTGAAGTGAATCACACCACTGCACTCCAGCCCTGGGTGACAGAGCAAGACTGTATCTC 360
Db 320 CAGTGAAGTGAATCACACCACTGCACTCCAGCCCTGGGTGACAGAGCAAGACTGTATCTC 379
QY 361 AAAAAAATAAAAAAATAAAAAATTTAGCCAGCATGGTGGTGCACACCTGTATGTCTAG 420
Db 380 AAAAAAATAAAAAAATAAAAAATTTAGCCAGCATGGTGGTGCACACCTGTATGTCTAG 439
QY 421 CTACTCAGAGAGGTGAGGTGGGAGGATCATTTGAACCTGGGGCAGTCAAGGCTACAGTGA 480
Db 440 CTACTCAGAGAGGTGAGGTGGGAGGATCATTTGAACCTGGGGCAGTCAAGGCTACAGTGA 499
QY 481 GCCAAGATCATGCCACTACCTCCAGCCCTGGGCAACAGAGAGACCCCTGTCTCTAAAAA 540
Db 500 GCCAAGATCATGCCACTACCTCCAGCCCTGGGCAACAGAGAGACCCCTGTCTCTAAAAA 559
QY 541 AATAATATATATAAAGAAAAAACAAGCTCTGTTTATGTCTCTGGTCCATCATACTACT 600
Db 560 AATAATATATATAAAGAAAAAACAAGCTCTGTTTATGTCTCTGGTCCATCATACTACT 619
QY 601 ATGTATATAGTTTGCAGAACTCAAAAGATCCAGATAGTCAATTTTTTAGGCTTGGCCGT 660
Db 620 ATGTATATAGTTTGCAGAACTCAAAAGATCCAGATAGTCAATTTTTTAGGCTTGGCCGT 679
QY 661 ATGCTCTCTGCACAACTCTGCCCTGTCTTCTAGCACAAAAAGCAGCTATAAACAT 720
Db 680 ATGCTCTCTGCACAACTCTGCCCTGTCTTCTAGCACAAAAAGCAGCTATAAACAT 739
QY 721 ACATACATGAATTTTTTATAGACATCGAGATTGAATTCATATGATTTTTACATTTTAT 780
Db 740 ACATACATGAATTTTTTATAGACATCGAGATTGAATTCATATGATTTTTACATTTTAT 799
QY 781 AAAAAATATCTTTAAAAAATTTCCCTTAACCATTTAAAAAGTAAAAAGCCGGCCAGCGC 840
Db 800 AAAAAATATCTTTAAAAAATTTCCCTTAACCATTTAAAAAGTAAAAAGCCGGCCAGCGC 859
QY 841 GCCATGCTCAGCCCTGTATTCACAGACTTTGGAGGCTGAGTGGGAGATACATTGAG 900
Db 860 GCCATGCTCAGCCCTGTATTCACAGACTTTGGAGGCTGAGTGGGAGATACATTGAG 919
QY 901 ATCAACAGTTGAGACACAGCTGGGCCAATAGCAAAACCCCATTTCTACTAAAAATAAA 960
Db 920 ATCAACAGTTGAGACACAGCTGGGCCAATAGCAAAACCCCATTTCTACTAAAAATAAA 979
QY 961 AAAAAATAGCTGGGATAGTGGTGCACACCTGTGATCCAGTACTTGGGAGGCTGAGGCA 1020
Db 980 AAAAAATAGCTGGGATAGTGGTGCACACCTGTGATCCAGTACTTGGGAGGCTGAGGCA 1039
QY 1021 GGAGAAATGCTTGAACCTGGGAAGGAGGTTGACAGTGGAGCAACATATGCACTGAC 1080
Db 1040 GGAGAAATGCTTGAACCTGGGAAGGAGGTTGACAGTGGAGCAACATATGCACTGAC 1099
QY 1081 TCCAGCCTGGGTGACAGATGAGACTTGTCTCAACGAAAAAAGTGTAAAAAGCCAT 1140
Db 1100 TCCAGCCTGGGTGACAGATGAGACTTGTCTCAACGAAAAAAGTGTAAAAAGCCAT 1159

QY 1141 TCCTAATTCAGTGTACATCAGTGTACATACACAGGCTGCGGATCTGCTGTAGGCAT 1200
Db 1160 TCCTAATTCAGTGTACATCAGTGTACATACACAGGCTGCGGATCTGCTGTAGGCAT 1219
QY 1201 ACCGTGAGAGTGTAGATGCTGTTGGTGCAGAGACATACATTTCCACATTAATAGACT 1260
Db 1220 ACCGTGAGAGTGTAGATGCTGTTGGTGCAGAGACATACATTTCCACATTAATAGACT 1279
QY 1261 ACCAAGTTCATCCATCAAGAGAGTTTTTTTTTACATCTACACTCCCCAGCACAAAAT 1320
Db 1280 ACCAAGTTCATCCATCAAGAGAGTTTTTTTTTACATCTACACTCCCCAGCACAAAAT 1339
QY 1321 GAGAGTACTCCAGATTCCTTTACAAAGATGCTCTAAGCCAGTACCAATGAAAAACAGA 1380
Db 1340 GAGAGTACTCCAGATTCCTTTACAAAGATGCTCTAAGCCAGTACCAATGAAAAACAGA 1399
QY 1381 AGTGGAGGGGAGAGTGGCCAGCCCTTCTAACCATGAAAGAAATTACCTGGTAGAGCTTCT 1440
Db 1400 AGTGGAGGGGAGAGTGGCCAGCCCTTCTAACCATGAAAGAAATTACCTGGTAGAGCTTCT 1459
QY 1441 GGATCTGGAAGATGAATTAACGGGGGTCTGTGAGCCTGCCCTGTCAATCACTGTG 1500
Db 1460 GGATCTGGAAGATGAATTAACGGGGGTCTGTGAGCCTGCCCTGTCAATCACTGTG 1519
QY 1501 ACTTGTGAGCCTCCAGTCCAGTCTCAGCCCATGTGTATGTGCGCAGTATAGACCT 1560
Db 1520 ACTTGTGAGCCTCCAGTCCAGTCTCAGCCCATGTGTATGTGCGCAGTATAGACCT 1579
QY 1561 CACTCTGTTTGGTCTTATATCTCCCATGATGGGGGTGAAGTGTGATGAGCCGTAT 1620
Db 1580 CACTCTGTTTGGTCTTATATCTCCCATGATGGGGGTGAAGTGTGATGAGCCGTAT 1639
QY 1621 TCAAGATGTACAGCTTTCTTGACAGAAAGTATGTCTCAGAGAAACAGCAGGGGCTTGCA 1680
Db 1640 TCAAGATGTACAGCTTTCTTGACAGAAAGTATGTCTCAGAGAAACAGCAGGGGCTTGCA 1699
QY 1681 AGATATATCACTGCAAAATCCACTGCTGACGCCACCAAGCTAGTTCTGTATCTTGAAC 1740
Db 1700 AGATATATCACTGCAAAATCCACTGCTGACGCCACCAAGCTAGTTCTGTATCTTGAAC 1759
QY 1741 AAGTTTCTTCACTTCTTGAGGCGCATCCCTTGGTACAAACACACAGTGTGTCACAGA 1800
Db 1760 AAGTTTCTTCACTTCTTGAGGCGCATCCCTTGGTACAAACACACAGTGTGTCACAGA 1819
QY 1801 TGAATGACGAAGTCCCTTACACCTGTATATCCACACTTTGGAGGCCAAGCGGGTGG 1860
Db 1820 TGAATGACGAAGTCCCTTACACCTGTATATCCACACTTTGGAGGCCAAGCGGGTGG 1879
QY 1861 ATGGCTTGAAGCTGAGAGGTGACACAGTCCGGGAGTCTCTACACCCCTCGTCCCTGC 1920
Db 1880 ATGGCTTGAAGCTGAGAGGTGACACAGTCCGGGAGTCTCTACACCCCTCGTCCCTGC 1939
QY 1921 GCGCGCTCTGCTGCGTGGGCTCCCACTTCGGTGGGACTTGGAGGAGCCCTTCAGCCACCG 1980
Db 1940 GCGCGCTCTGCTGCGTGGGCTCCCACTTCGGTGGGACTTGGAGGAGCCCTTCAGCCACCG 1999
QY 1981 CTGCACTGTGGAGCCCTTTCTGCGGTGGCCAAAGCCAGAGCCGGCTCCCTCAGCCTTGC 2040
Db 2000 CTGCACTGTGGAGCCCTTTCTGCGGTGGCCAAAGCCAGAGCCGGCTCCCTCAGCCTTGC 2059
QY 2041 AGGAGAGTGTGAGAGGAGAGGCTCAAGCAGAGAACCGGGGCTTCGCAAGCGGCTTGGGGC 2100
Db 2060 AGGAGAGTGTGAGAGGAGAGGCTCAAGCAGAGAACCGGGGCTTCGCAAGCGGCTTGGGGC 2119
QY 2101 CAGCTGAGATTCGCGGCTGGGCTGGGCTGGGCGGCGCCGCACTGAGAGACAGCGGGCAG 2160
Db 2120 CAGCTGAGATTCGCGGCTGGGCTGGGCTGGGCGGCGCCGCACTGAGAGACAGCGGGCAG 2179
QY 2161 CCTGCGAGGCCCGCGGCAATGAGAGGCTTAGACACCCGCGCCAGCGGCTGCGGAGGTTGT 2220
Db 2180 CCTGCGAGGCCCGCGGCAATGAGAGGCTTAGACACCCGCGCCAGCGGCTGCGGAGGTTGT 2239

QY 2221 ACTGGTGCCTCCAGAGTGGCCAGCCCGCGCGCTGTGCTCGTCGATTTTCACATGGGC 2280
|||||
Db 2240 ACTGGGTCCCCAGAGTGGCAGCCCGCGCGCTGTGCTCGTCGATTTTCACATGGGC 2299
QY 2281 CTTAGACGCTTCCCGGGGAGGGGCTCGGGACCTGCAGCCCGCATGCCGTGAGCCCTCC 2340
|||||
Db 2300 CTTAGACGCTTCCCGGGGAGGGGCTCGGGACCTGCAGCCCGCATGCCGTGAGCCCTCC 2359
QY 2341 CCTCATGGGGCTCGTGTGGGGCCGAGGCTCCCGAGACAGACACACCCCTGTCTCAGAG 2400
|||||
Db 2360 CCTCATGGGGCTCGTGTGGGGCCGAGGCTCCCGAGACAGACACACCCCTGTCTCAGAG 2419
QY 2401 CGCCAGTCCCATCGACACGCAAGGGCTGAGAAAGTGGGGCGCACGGCACCGGAGACTGG 2460
|||||
Db 2420 CGCCAGTCCCATCGACACGCAAGGGCTGAGAAAGTGGGGCGCACGGCACCGGAGACTGG 2479
QY 2461 CAGGACGTAACCCCTGCAGCCCTGTGGGAAATCACTGGGTGAAGCCAGCTGGGCTCT 2520
|||||
Db 2480 CAGGACGTAACCCCTGCAGCCCTGTGGGAAATCACTGGGTGAAGCCAGCTGGGCTCT 2539
QY 2521 GAGTCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCCGTAATACACCAAT 2580
|||||
Db 2540 GAGTCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCCGTAATACACCAAT 2599
QY 2581 CAGCACCTGTGTCTACCTCAGGGTCTGTGAATGCACCAATCCACACTCTGTATCTAGCT 2640
|||||
Db 2600 CAGCACCTGTGTCTACCTCAGGGTCTGTGAATGCACCAATCCACACTCTGTATCTAGCT 2659
QY 2641 ACTGTGATGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATTTTAAATACACCAATC 2700
|||||
Db 2660 ACTGTGATGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATTTTAAATACACCAATC 2719
QY 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCTGTGTAGCTC 2760
|||||
Db 2720 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCTGTGTAGCTC 2779
QY 2761 AGGTAATGTGAATCACCATTCAGACGTCGTGTATCTGGCTACTTTCATGGGCATCCGCT 2820
|||||
Db 2780 AGGTAATGTGAATCACCATTCAGACGTCGTGTATCTGGCTACTTTCATGGGCATCCGCT 2839
QY 2821 GAAGAGACCAACCAAGGGCTTTGTGAGCAATTAAGCTTCTATCACCTGGGTGCGAGCT 2880
|||||
Db 2840 GAAGAGACCAACCAAGGGCTTTGTGAGCAATTAAGCTTCTATCACCTGGGTGCGAGCT 2899
QY 2881 GGGCTGAGTCCGAAAAGAGATCAGCAGAGGAGATTAAGGTGGGGCGCTTTTATAGAT 2940
|||||
Db 2900 GGGCTGAGTCCGAAAAGAGATCAGCAGAGGAGATTAAGGTGGGGCGCTTTTATAGAT 2959
QY 2941 TTGGGTAGGTAAAGAAAATTACAGTCAAAAGGGGTTTGTCTCTGGCGGCGAGAGTGG 3000
|||||
Db 2960 TTGGGTAGGTAAAGAAAATTACAGTCAAAAGGGGTTTGTCTCTGGCGGCGAGAGTGG 3019
QY 3001 GGGGTGCAGAGTGTGCTAGTGGGGGTCTTTTGAAGCAGAGATGAGCAGAAAAGAGACT 3060
|||||
Db 3020 GGGGTGCAGAGTGTGCTAGTGGGGGTCTTTTGAAGCAGAGATGAGCAGAAAAGAGACT 3079
QY 3061 TTCACAAAGTAATGTCACTAATTAAAGCAAGAACCCGCATTACACCTCTTTTGTGTG 3120
|||||
Db 3080 TTCACAAAGTAATGTCACTAATTAAAGCAAGAACCCGCATTACACCTCTTTTGTGTG 3139
QY 3121 GAATGTCAATCACTTAAGTTGGGCGAGGGCATTTCACTCTTTTGTGATTTCTCAAGTTAC 3180
|||||
Db 3140 GAATGTCAATCACTTAAGTTGGGCGAGGGCATTTCACTCTTTTGTGATTTCTCAAGTTAC 3199
QY 3181 TTCAGGCCAATCTGGGGGTATATGTGCAAGTTACAGGGGATGCATGGCTTGGGCT 3240
|||||
Db 3200 TTCAGGCCAATCTGGGGGTATATGTGCAAGTTACAGGGGATGCATGGCTTGGGCT 3259
QY 3241 CAGAGGCTTGACAGCTACTCTGTGGGGCTTGGAGAAATGTTGTGCGACACTCTGTAT 3300
|||||
Db 3260 CAGAGGCTTGACAGCTACTCTGTGGGGCTTGGAGAAATGTTGTGCGACACTCTGTAT 3319
QY 3301 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTCTAGCTCAGGGAATTTGAACGCA 3360

|||||
Db 3320 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTAGCTCAGGATTTGAACGCA 3379
QY 3361 CCAATCAGCGCCCTGTCAAAAACAGACACTGGGGCTTACCAATCAGCAGATGTGGGGG 3420
|||||
Db 3380 CCAATCAGCGCCCTGTCAAAAACAGACACTGGGGCTTACCAATCAGCAGATGTGGGGG 3439
QY 3421 GGCAGATTAAGAAATAAAGCAGGGCTCCGAGCAGCAGTGGCAACGCCAGAGTCC 3480
|||||
Db 3440 GGCAGATTAAGAAATAAAGCAGGGCTCCGAGCAGCAGTGGCAACGCCAGAGTCC 3499
QY 3481 CTATCCAAATATAGGAGCTTTGTCTTTTGTCTGTTCGATTAATCTTGTCTACTGCTG 3540
|||||
Db 3500 CTATCCAAATATAGGAGCTTTGTCTTTTGTCTGTTCGATTAATCTTGTCTACTGCTG 3559
QY 3541 CTTTTGGGTCACACTGCTTTTATGAGCTTAACACTCAGCAGGAAGGTGTGACGATC 3600
|||||
Db 3560 CTTTTGGGTCACACTGCTTTTATGAGCTTAACACTCAGCAGGAAGGTGTGACGATC 3619
QY 3601 ACTCTGAAGCCTTAAGACAGAGCCACCGGAGAGATGAACAACTCCGGCGGCT 3660
|||||
Db 3620 ACTCTGAAGCCTTAAGACAGAGCCACCGGAGAGATGAACAACTCCGGCGGCT 3679
QY 3661 GCCTTAAGAGCTATTAACACTCAGCGGAGGCTGCAAGCTCACTCCAGCCAGCGAGA 3720
|||||
Db 3680 GCCTTAAGAGCTATTAACACTCAGCGGAGGCTTGCAGGCTTCACTCCAGCCAGCGAGA 3739
QY 3721 CCACGAACCCACGAAAGGAAGAACTGCGAACAATCTGAAATCAGAAAGAACAACT 3780
|||||
Db 3740 CCACGAACCCACGAAAGGAAGAACTGCGAACAATCTGAAATCAGAAAGAACAACT 3799
QY 3781 CCAAGTGCACCACTTAAGAGCTTAACACTCAGCGAGGCTCCGGGCTTCTTCTTG 3840
|||||
Db 3800 CCAAGTGCACCACTTAAGAGCTTAACACTCAGCGAGGCTCCGGGCTTCTTCTTG 3859
QY 3841 AAGTCAATGAGACCAACCACTCAGCAGTTTGGGACACAAAGCCAGAGTTGAGATCAGC 3900
|||||
Db 3860 AAGTCAATGAGACCAACCACTCAGCAGTTTGGGACACAAAGCCAGAGTTTGAATCAGC 3919
QY 3901 CTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAAAATTAACAAAATTTGGCGG 3960
|||||
Db 3920 CTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAAAATTAACAAAATTTGGCGG 3979
QY 3961 AGCATGGTGGTCCGCTGGCTGTGTCGACGCTACCCGGGAGGCTTAAATGGAGATGCT 4020
|||||
Db 3980 AGCATGGTGGTCCGCTGGCTGTGTCGACGCTACCCGGGAGGCTTAAATGGAGATGCT 4039
QY 4021 TGAACCTGGGAGGTGAAGACTGCAAGCTGTGATTTGTACCAAGCCCTCTAGGCTGGG 4080
|||||
Db 4040 TGAACCTGGGAGGTGAAGACTGCAAGCTGTGATTTGTACCAAGCCCTCTAGGCTGGG 4099
QY 4081 GGCACAGCTGAGACCTGTTTCCCTCCGAAAAAAAATTGACAAAAGTGAATTAAGAGT 4140
|||||
Db 4100 GGCACAGCTGAGACCTGTTTCCCTCCGAAAAAAAATTGACAAAAGTGAATTAAGAGT 4159
QY 4141 GCGTGAATATGGCTAGGGGCGAGTGGCTCATGCTGTATATCCACAGCTTTGGGAAGCCGAG 4200
|||||
Db 4160 GCGTGAATATGGCTAGGGGCGAGTGGCTCATGCTGTATATCCACAGCTTTGGGAAGCCGAG 4219
QY 4201 GCGGGGCGGTACACTAAGGTCAAGAGTGTGAGACAGCAGCTGGGCAACATGGAAGAACCC 4260
|||||
Db 4220 GCGGGGCGGTACACTAAGGTCAAGAGTGTGAGACAGCAGCTGGGCAACATGGAAGAACCC 4279
QY 4261 ATCTCTTAAAAAATACAAAATTAGCCGGCTGTGGGGCGAGTGTGGAGCATGCTGTAA 4320
|||||
Db 4280 ATCTCTTAAAAAATACAAAATTAGCCGGCTGTGGGGCGAGTGTGGAGCATGCTGTAA 4339
QY 4321 TCCACAGCTACTCAGAGGCTGAGGCGAGGAGATCACTTGAACCCAGAGGCGCGGTTGC 4380
|||||
Db 4340 TCCACAGCTACTCAGAGGCTGAGGCGAGGAGATCACTTGAACCCAGAGGCGCGGTTGC 4399
QY 4381 AGTGAACCGGAGATCGGCAATTGCCACTCCACCCACTCAGCTGGGCAACAGAGCCAAA 4440
|||||

Db 4400 AGTGAGCCGAGATGCTGCCATTGCACTCCACCCTCCAGCCTGGGCAACAGACCCAAA 4459
Oy 4441 CTCTGCTTTAAAAAAGGAGGCGCTGACATATAGAGGCTGCAATGCAATAG 4500
Db 4460 CTCTGCTTTAAAAAAGGAGGCGCTGACATATAGAGGCTGCAATGCAATAG 4519
Oy 4501 TTGGCAGGCAACATGTTAAGATGAGAGCTCTGCTTCATGCTCTGTTAAAAAC 4560
Db 4520 TTGGCAGGCAACATGTTAAGATGAGAGCTCTGCTTCATGCTCTGTTAAAAAC 4579
Oy 4551 CACCTCAAGGCAAGGCTGCAAGTGGCTCATGCTTATATCCAGCACTTTGGAGGCGGAG 4620
Db 4580 CACCTCAAGGCAAGGCTGCAAGTGGCTCATGCTTATATCCAGCACTTTGGAGGCGGAG 4639
Oy 4621 GGGGCTGATCACTGAGTCAAGGCTGAGAGCCAGCCTGACCAACATGGTGAAT 4680
Db 4640 GGGGCTGATCACTGAGTCAAGGCTGAGAGCCAGCCTGACCAACATGGTGAAT 4699
Oy 4681 CCCACCTTACTAAAAATACAAAATTAGATGAGCATGGTGGTGCATGCTGTAATCCAC 4740
Db 4700 CCCACCTTACTAAAAATACAAAATTAGATGAGCATGGTGGTGCATGCTGTAATCCAC 4759
Oy 4741 CTACTGGAGGCTGAGGCAAGAAATCATAAGAACAGGAGGCGGAGGTTGTAGTAG 4800
Db 4760 CTACTGGAGGCTGAGGCAAGAAATCATAAGAACAGGAGGCGGAGGTTGTAGTAG 4819
Oy 4801 CCGAGATGCTGCCATGTCACCTGACCTGAGCAATGAGCAAGAACTTCATCAAAAAAC 4860
Db 4820 CCGAGATGCTGCCATGTCACCTGAGCTGACCAATGAGCAAGAACTTCATCAAAAAAC 4879
Oy 4861 AACAAACAAAACCCACTCTACTCCAGGAGCTGGGTACAGAGCTGGGCGACATCACT 4920
Db 4880 AACAAACAAAACCCACTCTACTCCAGGAGCTGGGTACAGAGCTGGGCGACATCACT 4939
Oy 4921 GCAAGGCTCTAGGCAAGCACTAAGGCGAGCTGACAGACCGCGGACAGATAACAGTG 4980
Db 4940 GCAAGGCTCTAGGCAAGCACTAAGGCGAGCTGACAGACCGCGGACAGATAACAGTG 4999
Oy 4981 TGTAGATCAGTGTGTAGATCAGACCTCCCTGCCATGCTGTGACCAACAGGAGGCGCCCA 5040
Db 5000 TGTAGATCAGTGTGTAGATCAGACCTCCCTGCCATGCTGTGACCAACAGGAGGCGCCCA 5059
Oy 5041 AGCAGCAGATGAGCCCATCCAGTACACACATCCACTTCATCCAGAGATGTGTGT 5100
Db 5060 AGCAGCAGATGAGCCCATCCAGTACACACATCCACTTCATCCAGAGATGTGTGT 5119
Oy 5101 CTGGCAGCCTGGGGTAATTAAGACAGAGGTGACAGCTTGGGTGTGTGTCAGACAG 5160
Db 5120 CTGGCAGCCTGGGGTAATTAAGACAGAGGTGACAGCTTGGGTGTGTGTCAGACAG 5179
Oy 5161 TGCCCCAGGCAAGGCTTGTGGCTGTAGAAAACTTCAGGCTTAGGCGGCGACGCTGGC 5220
Db 5180 TGCCCCAGGCAAGGCTTGTGGCTGTAGAAAACTTCAGGCTTAGGCGGCGACGCTGGC 5239
Oy 5221 TCAGGCTGTATATCCAGCATTTGGAGGCGGAGGCGGAGTACAGAGTCCAGAGA 5280
Db 5240 TCAGGCTGTATATCCAGCATTTGGAGGCGGAGGCGGAGTACAGAGTCCAGAGA 5299
Oy 5281 TCGTGACCATCTGGCTAACAAGGTGAACCCCGCTCTCTACTAAAAATACAAAAATGG 5340
Db 5300 TCGTGACCATCTGGCTAACAAGGTGAACCCCGCTCTCTACTAAAAATACAAAAATGG 5359
Oy 5341 CCGGGCATGTTGGGGGCACTGTAGTTCAGCTACTGGAAGGCTGAGGAGAGGAATG 5400
Db 5360 CCGGGCATGTTGGGGGCACTGTAGTTCAGCTACTGGAAGGCTGAGGAGAGGAATG 5419
Oy 5401 GCGTGAAACCCGAGAGGCAAGATTTGAGTGAGCCGAGATCCGCACTGCACTCCAGCT 5460
Db 5420 GCGTGAAACCCGAGAGGCAAGATTTGAGTGAGCCGAGATCCGCACTGCACTCCAGCT 5479
Oy 5461 GGGGCAAGCAAGCAAGTCCATCTGAGAAAGAAAAAGAAAGCTTCAGGCTTGAGCCAGA 5520
Db 5480 GGGGCAAGCAAGCAAGTCCATCTGAGAAAGAAAAAGAAAGCTTCAGGCTTGAGCCAGA 5539

Oy 5521 GGGCCAGGCTGTAAATTCGTCACTTACATGACCTTGGGCAAGGCACTTCTCCCTGGC 5580
Db 5540 GGGCCAGGCTGTAAATTCGTCACTTACATGACCTTGGGCAAGGCACTTCTCCCTGGC 5599
Oy 5581 CCAGTTCAGGAGGTTGATTCAGTCCAGAGTCCCTTCAGCATTAAGCTCATGTTTC 5640
Db 5600 CCAGTTCAGGAGGTTGATTCAGTCCAGAGTCCCTTCAGCATTAAGCTCATGTTTC 5659
Oy 5641 TAAAGTGAAGATGGGGAGTTTCCCTCTCTACCCAGCCGCTGTCACACTTAAGT 5700
Db 5660 TAAAGTGAAGATGGGGAGTTTCCCTCTCTACCCAGCCGCTGTCACACTTAAGT 5719
Oy 5701 GAATGACAGGGAATTCACGCTGCCAATCCCGCAGTTCCAAAGCCCTGGGAGCCATC 5760
Db 5720 GAATGACAGGGAATTCACGCTGCCAATCCCGCAGTTCCAAAGCCCTGGGAGCCATC 5779
Oy 5761 TGTCAAGGCTGTGACAGAGAGTGAAGTCAAGTCAAGTCAAGTCAAGGCTCTTG 5820
Db 5780 TGTCAAGGCTGTGACAGAGAGTGAAGTCAAGTCAAGTCAAGTCAAGGCTCTTG 5839
Oy 5821 CCTCATTCGGGACAGACATCCGTTTCTCTGCTCTACCCGGAATTAAGGGCTTTAGC 5880
Db 5840 CCTCATTCGGGACAGACATCCGTTTCTCTGCTCTACCCGGAATTAAGGGCTTTAGC 5899
Oy 5881 CGAATGAGTCAATGGGGGGGGGGGGTTCCTGGGGAAGTCCACATTAATCACTTGGGA 5940
Db 5900 CGAATGAGTCAATGGGGGGGGGGGGTTCCTGGGGAAGTCCACATTAATCACTTGGGA 5959
Oy 5941 CAGGACAGCCTGAATCTTCATGGTGCCTATCCAAAGTGTGGGTCAGACAGCCAA 6000
Db 5960 CAGGACAGCCTGAATCTTCATGGTGCCTATCCAAAGTGTGGGTCAGACAGCCAA 6019
Oy 6001 GACCAATGCTCTTATCTCAGTAGGGCTCAGAGTCTCCAGACAGGACCTCCGG 6060
Db 6020 GACCAATGCTCTTATCTCAGTAGGGCTCAGAGTCTCCAGACAGGACCTCCGG 6079
Oy 6061 AGAGTTTGGGGTGAAGATGGAGACACAGGCTCTTTTCTCTCTTAATAATTTGGG 6120
Db 6080 AGAGTTTGGGGTGAAGATGGAGACACAGGCTCTTTTCTCTCTTAATAATTTGGG 6139
Oy 6121 GGCTTGGGGGACGCTTGAAGATCCCAAGGAGAGGGAAGGACATCCGCCACAAG 6180
Db 6140 GGCTTGGGGGACGCTTGAAGATCCCAAGGAGAGGGAAGGACATCCGCCACAAG 6199
Oy 6181 TCTGCCAGAGCAGAGAGGAGACCCGCACTGAGTGCATCTTCCCAAGGCT 6235
Db 6200 TCTGCCAGAGCAGAGAGGAGACCCCGCACTGAGTGCATCTTCCCAAGGCT 6254

RESULT 4
AADI7447
ID AADI7447 standard; DNA; 6753 BP.
XX
AC AADI7447;
XX
XX 10-DEC-2001 (first entry)
DE
XX Human Interferon alpha2 (huIFNalpha2) fragment #4.
KW Human; mutation; homologous recombination; target sequence; gene therapy;
KW homologous recombination-enhancing agent; non-homologous end joining;
KW therapeutic protein; Interferon alpha2; huIFNalpha2; ds.
OS Homo sapiens.
XX
XX
XX W0200168882-AZ.
PN
XX
PD 20-SEP-2001.
XX
XX 13-MAR-2001; 2001WO-0507870.
PF
XX
XX 14-MAR-2000; 2000US-0525160.

XX (TRAN-) TRANSKARYOTIC THERAPIES INC.
XX Ivanov E:
XX WPI: 2001-582459/65.
XX
PT Complex or composition comprising a double stranded DNA sequence, a
PT homologous recombination-enhancing agent, and agent inhibiting
PT non-homologous end joining, for promoting alteration of a target
PT sequence in a cell
XX
XX
XX Disclosure; Page 80-82; 82pp; English.

XX The invention relates to a complex for promoting alteration of a target
CC sequence in a cell, comprising a double stranded DNA sequence, a
CC homologous recombination-enhancing agent and an agent inhibiting non-
CC homologous end joining. The invention is used in gene therapy. The
CC complex is useful for promoting an alteration at a selected site of
CC a target sequence of a cell preferably of fungal, plant or animal
CC origin, or of vertebrate origin which is a primary or secondary
CC mammalian (human) cell or an immortalised mammalian (human) cell, where
CC target sequence comprises a mutation preferably point mutation having
CC less than 10 base pairs which differ from wild-type sequence, (selected
CC from cystic fibrosis transmembrane regulator (CFTR) gene having mutation
CC changes in an amino acid encoded by codon 508, beta-globin gene having
CC mutation changes in an amino acid encoded by codon 6, Factor VIII gene
CC having mutation changes in an amino acid encoded by codon 2209 or 2229,
CC Factor IX gene, von Willebrand factor gene or xeroderma pigmentosa group
CC G gene); and the DNA sequence comprises a wild-type sequence which can
CC correct the mutation. The method further comprises introducing an agent
CC which inhibits a mismatch-repair protein (expression), which is from
CC Msh2, Msh6, Msh3, Mlh1 and PMS2, or is an anti-mismatch-repair protein
CC antibody covalently linked to the DNA sequence, or to Rad52 protein or
CC its fragment. The complex is useful for altering expression of a protein
CC coding sequence of a gene in a cell. The method comprises introducing
CC the complex into the cell, where the DNA sequence comprises a regulatory
CC sequence, maintaining the cell under conditions which permit alteration
CC of a targeted genomic sequence to produce a homologously recombinant
CC cell and maintaining the homologously recombinant cell under conditions
CC which permit expression of the protein coding sequence of the gene under
CC control of the regulatory sequence. Homologously recombinant cell is
CC useful as a vehicle or delivery system for therapeutic proteins, such as
CC enzymes, hormones, cytokines, antigens, antibodies, clotting factors,
CC anti-sense RNA, regulatory proteins, transcription proteins, receptors,
CC structural proteins, novel (non-optimised) proteins and nucleic acid
CC products and engineered DNA and for supplying a therapeutic protein,
CC including erythropoietin, calcitonin, growth hormone, insulin and
CC (human) fragment used in the invention.
CC
XX
XX Sequence 6753 BP; 2096 A; 1477 C; 1573 G; 1607 T; 0 other;

Query Match 59.78; Score 3725; DB 22; Length 6753;
Best Local Similarity 99.94; Pred. No. 0;
Matches 3728; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2218 TGTACTGGGTGCGCCAGCAGTGCAGCGCGCGGTGTCGTCGATTTCTACTG 2277
DB 1738 TATACGTGGGTGCGCCAGCAGTGCAGCGCGCGGTGTCGTCGATTTCTACTG 1797
QY 2278 GGCCTTAGCAGCCTTCCGCGGGGCAAGGGCTCGGAGCTCAGCCGCCATGCTGAGCC 2337
DB 1798 GGCCTTAGCAGCCTTCCGCGGGGCAAGGGCTCGGAGCTCAGCCGCCATGCTGAGCC 1857
QY 2338 TCCCTTCATGAGCTCTGTGCGGCCCGAGCCTTCCCGAGAGCAGCAGCCCTGCTGCA 2397
DB 1858 TCCCTTCATGAGCTCTGTGCGGCCCGAGCCTTCCCGAGAGCAGCAGCCCTGCTGCA 1917
QY 2398 CAGCGCCAGTGCATCGACGACGCAAGGGCTGAGAGTGGGGCGAGCGGACGAC 2457
DB 1918 CAGCGCCAGTGCATCGACGACGCAAGGGCTGAGAGTGGGGCGAGCGGACGAC 1977

QY 2458 TGGCAGCAGCTACCCCTCGACGCCCTGTGCGGAATCACTGGGTGAGCCAGCTGGGCT 2517
DB 1978 TGGCAGCAGCTACCCCTCGACGCCCTGTGCGGAATCACTGGGTGAGCCAGCTGGGCT 2037
QY 2518 CCTGAGTCTGATGAGAGCTTGGAGAACTTATGCTAGCTCAGGAGATCGTAATACACC 2577
DB 2038 CCTGAGTCTGATGAGAGCTTGGAGAACTTATGCTAGCTCAGGAGATCGTAATACACC 2097
QY 2578 AATCAGCAGCCCTGTGTCTAGCTCAGGAGTGTGTAATGACCAATCCACACTGTATCTA 2637
DB 2098 AATCAGCAGCCCTGTGTCTAGCTCAGGAGTGTGTAATGACCAATCCACACTGTATCTA 2157
QY 2638 GCTACCTGATGGGCGCTTGGAGAACTTATGCTAGCTCAGGAGATGTAATACCA 2697
DB 2158 GCTACCTGATGGGCGCTTGGAGAACTTATGCTAGCTCAGGAGATGTAATACCA 2217
QY 2698 ATCGGCACTGTATCTAGCTCAGGAGTGTGTAATGACCAATCAGCAGCCCTGTCTAG 2757
DB 2218 ATCGGCACTGTATCTAGCTCAGGAGTGTGTAATGACCAATCAGCAGCCCTGTCTAG 2277
QY 2758 CTCAGGATATGTAATGACCAATCAGCAGCTGTATCTGAGCTACTTTCATGGGCATCCG 2817
DB 2278 CTCAGGATATGTAATGACCAATCAGCAGCTGTATCTGAGCTACTTTCATGGGCATCCG 2337
QY 2818 TGTGAAGAGACCAACCAAGGCTTGTGAGCAATTAAGCTTCTACCTGGGGTCA 2877
DB 2338 TGTGAAGAGACCAACCAAGGCTTGTGAGCAATTAAGCTTCTACCTGGGGTCA 2397
QY 2878 GGTGGGCTGATCCGAAAGAGATCAGCAAGGAGATTAAGGTTGGGCGCTTTATAG 2937
DB 2298 GGTGGGCTGATCCGAAAGAGATCAGCAAGGAGATTAAGGTTGGGCGCTTTATAG 2457
QY 2938 GATTTGGGTAGTAAAGAAATTTACAGTCAAAAGGGGTTTCTCTGGCGGACAGAG 2997
DB 2458 GATTTGGGTAGTAAAGAAATTTACAGTCAAAAGGGGTTTCTCTGGCGGACAGAG 2517
QY 2998 TGGGGGCTCCCAAGGCTCAGTGGGGGCTTTTATAGCAGAGATGAGCAGAAAG 3057
DB 2518 TGGGGGCTCCCAAGGCTCAGTGGGGGCTTTTATAGCAGAGATGAGCAGAAAG 2577
QY 3058 ACTTTCAGAGTATGATCATTAATTAAGCAGAGCCGCATTTACCTCTTTGTG 3117
DB 2578 ACTTTCAGAGTATGATCATTAATTAAGCAGAGCCGCATTTACCTCTTTGTG 2637
QY 3118 GTGAATGATCATTAATTAAGTGGGAGGAGCAATCACTCTTTGATCTTCACT 3177
DB 2638 GTGAATGATCATTAATTAAGTGGGAGGAGCAATCACTCTTTGATCTTCACT 2697
QY 3178 TACTTCAAGGCATCTGGGCTATATGTGCAAGTTACAGGGATGCGATGGCTGGCTTG 3237
DB 2698 TACTTCAAGGCATCTGGGCTATATGTGCAAGTTACAGGGATGCGATGGCTGGCTTG 2757
QY 3238 GCTCAGAGCTTGAACACTACTGCTGGGCGCTTGGAGAAATGTTGTGCACTCTG 3297
DB 2758 GCTCAGAGCTTGAACACTACTGCTGGGCGCTTGGAGAAATGTTGTGCACTCTG 2817
QY 3298 TATCTAGTATATAGTGGGAGCTGAGAACTTGTCTGCTCAGGAGATGTAAC 3357
DB 2818 TATCTAGTATATAGTGGGAGCTGAGAACTTGTGTGCTCAGGAGATGTAAC 2877
QY 3358 GCAACATACAGCCCTGTGCAAAAGAGACACTCGGCTTACCAATCAGCAGATGAGG 3417
DB 2878 GCAACATACAGCCCTGTGCAAAAGAGACACTCGGCTTACCAATCAGCAGATGAGG 2937
QY 3418 TGGGGCCAGATTAAGAAATTAAGAGAGCTGCCCCAGACAGAGTGGCAAGCGCACAG 3477
DB 2938 TGGGGCCAGATTAAGAAATTAAGAGAGCTGCCCCAGACAGAGTGGCAAGCGCACAG 2997
QY 3478 TCCCTATCCCAATATGAGAGCTTTGTTCTTTTGTGCTTGTGCAATTAATTTCTACTGC 3537
DB 2998 TCCCTATCCCAATATGAGAGCTTTGTTCTTTTGTGCTTGTGCAATTAATTTCTACTGC 3057
QY 3538 TCGCTTTTGGTTCACACTGCTTTTATGAGTGTAACTACACAGAAAGTGTGAGC 3597

```
Db 3058 TCGCTTTTGGGTCACACTGCTTTATGAGCTGTAACTCACCAGCAAGGTCGTGCAGC 3117
OY 3598 TTCACCTCCGGAAGCCACTTAAGACACAGAGCCACCGGGGAGATGAACACTCCGGCCGC 3657
Db 3118 TTCACCTCCGGAAGCCACTTAAGACACAGAGCCACCGGGGAGATGAACACTCCGGCCGC 3177
OY 3658 GCTGCTTTAAGAGCTATAACACTCAACCGGAGGTCGTGAGCTTCACTCCTCAGCCAGGC 3717
Db 3178 GCTGCTTTAAGAGCTATAACACTCAACCGGAGGTCGTGAGCTTCACTCCTCAGCCAGGC 3237
OY 3718 AGACCAAGAACCCACAGAGAGAGAACTCGAAACATCTGAACATCAGAGAAACAA 3777
Db 3238 AGACCAAGAACCCACAGAGAGAGAACTCGAAACATCTGAACATCAGAGAAACAA 3297
OY 3778 ACTCAGATGCACACCTTAAGAAGCTGTAACTCACTGCGAGGTCGCCGCTTCCTTC 3837
Db 3298 ACTCAGATGCACACCTTAAGAAGCTGTAACTCACTGCGAGGTCGCCGCTTCCTTC 3357
OY 3838 TTGAAGTCAGTGAACCAAGCACTCACCAGTTTGGACACAGCCAGAGTTTGATGC 3897
Db 3358 TTGAAGTCAGTGAACCAAGCACTCACCAGTTTGGACACAGCCAGAGTTTGATGC 3417
OY 3898 AGCCTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAATTTACAAAAATTGG 3957
Db 3418 AGCCTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAATTTACAAAAATTGG 3477
OY 3958 CGGAGCATGTGTGTCCTGCTGCTGTGCTCCAGCTACGCGGAGGCTAAAGTGGAGATC 4017
Db 3478 CGGAGCATGTGTGTCCTGCTGCTGTGCTCCAGCTACGCGGAGGCTAAAGTGGAGATC 3537
OY 4018 GCTTGAAGCTGGAGGTGAAGCTGAGCTGAGCTGAGTGAACACAGCCCTTAAGCT 4077
Db 3538 GCTTGAAGCTGGAGGTGAAGCTGAGCTGAGTGAACACAGCCCTTAAGCT 3597
OY 4078 GGGGACAGACTGAGACCTGTTTCCCTCCGCAAAAAAATTGACAAAAAGTTAATA 4137
Db 3598 GGGGACAGACTGAGACCTGTTTCCCTCCGCAAAAAAATTGACAAAAAGTTAATA 3657
OY 4138 GGTGCTGATATGCTAGGCGCAGTGCTCATGCTGTAACTCCAGCACTTTGGAGGC 4197
Db 3658 GGTGCTGATATGCTAGGCGCAGTGCTCATGCTGTAACTCCAGCACTTTGGAGGC 3717
OY 4198 GAGGCGGGGGGTCACTAAGGTGAGGTGAGACAGCAAGCCCTGGCCAACTGAGAAAG 4257
Db 3718 GAGGCGGGGGGTCACTAAGGTGAGGTGAGACAGCAAGCCCTGGCCAACTGAGAAAG 3777
OY 4258 CCCATCTCTTAAATAATACAAATTAAGCCGCTGTGGGCGAGTGTGACATGCTG 4317
Db 3778 CCCATCTCTTAAATAATACAAATTAAGCCGCTGTGGGCGAGTGTGACATGCTG 3837
OY 4318 TAACTCCAGACTACTCAGAGGCTGAGGAGAAATCACTTGAAACCCAGAGCGCGGT 4377
Db 3838 TAACTCCAGACTACTCAGAGGCTGAGGAGAAATCACTTGAAACCCAGAGCGCGGT 3897
OY 4378 TGCAGTGAAGGAGATGCTGCATGCTGCACTCAGCCACTCCAGCTGGGCAACAAGGC 4437
Db 3898 TGCAGTGAAGGAGATGCTGCATGCTGCACTCAGCCACTCCAGCTGGGCAACAAGGC 3957
OY 4438 AAACCTGCTTAAATAAAAAAAGTGCATATATTAAGAGGTGCATGCA 4497
Db 3958 AAACCTGCTTAAATAAAAAAAGTGCATATATTAAGAGGTGCATGCA 4017
OY 4498 TAGTTCGACGCAACATGTTTAAGAATGGAAGTCTCGCCCTTCATGCTCTGTTAAA 4557
Db 4018 TAGTTCGACGCAACATGTTTAAGAATGGAAGTCTCGCCCTTCATGCTCTGTTAAA 4077
OY 4558 ACCCAGCTCAAGGCGAGGTGAGTGCATGCTCATATATCCAGCACTTTGGAGGC 4617
Db 4078 ACCCAGCTCAAGGCGAGGTGAGTGCATGCTCATATATCCAGCACTTTGGAGGC 4137
OY 4618 GAGGCGGTGATCACTGAGGTGAGATTCGAGACAGCCCTGACCAACATGTTGA 4677
Db 4138 GAGGCGGTGATCACTGAGGTGAGATTCGAGACAGCCCTGACCAACATGTTGA 4197
OY 4678 AATCCCACTCTAATAAATAATAGATGAGCATGTGTGTCATGCTGTATCC 4737
Db 4198 AATCCCACTCTAATAAATAATAGATGAGCATGTGTGTCATGCTGTATCC 4257
OY 4738 CACCTACTTTGGAGGCTGAGGAGAAATCACTAGAACAGAGAGCGGAGTTTGTAGT 4797
Db 4258 CACCTACTTTGGAGGCTGAGGAGAAATCACTAGAACAGAGAGCGGAGTTTGTAGT 4317
OY 4798 GAGCCGAGATGCTGCATTGTCATCCAGCTGAGCAATGAGGAAATCCTATCTCAAAA 4857
Db 4318 GAGCCGAGATGCTGCATTGTCATCCAGCTGAGCAATGAGGAAATCCTATCTCAAAA 4377
OY 4858 AACCAACAAAAAACCACCTCTCTACTCCAGAGGACTGGTACAGAGCTGGGCCATC 4917
Db 4378 AACCAACAAAAAACCACCTCTCTACTCCAGAGGACTGGTACAGAGCTGGGCCATC 4437
OY 4918 AGTGCAGGTCGAGCCACAGAGCTAAAGCGGAGCTGACAGACCGGAGCATTAACA 4977
Db 4438 AGTGCAGGTCGAGCCACAGAGCTAAAGCGGAGCTGACAGACCGGAGCATTAACA 4497
OY 4978 GTGTGTGATCATAGTGTGATCATCAGAGCTCCCTGCATTTGGTGAACACAGGGGCC 5037
Db 4498 GTGTGTGATCATAGTGTGATCATCAGAGCTCCCTGCATTTGGTGAACACAGGGGCC 4557
OY 5038 CCAAGCACCAGAGATGGCCCATCCAGTACACACATCCACTCTCAACAGAGATGTG 5097
Db 4558 CCAAGCACCAGAGATGGCCCATCCAGTACACACATCCACTCTCAACAGAGATGTG 4617
OY 5098 TTTCTTGGACAGCTGGGTAATTAAGACAGAAAGTGAACAGTGGGTGCTACGTA 5157
Db 4618 TTTCTTGGACAGCTGGGTAATTAAGACAGAAAGTGAACAGTGGGTGCTACGTA 4677
OY 5158 GACTGCCAGGAGGAGCTTGTGCTGTAGAAAAGCTTCAGGCGTCAAGCGCGGACGGT 5217
Db 4678 GACTGCCAGGAGGAGCTTGTGCTGTAGAAAAGCTTCAGGCGTCAAGCGCGGACGGT 4737
OY 5218 GGTCAAGCTGTATCCAGACATTTGGAGGCGGAGGCGGTGATCAGAGGTGAG 5277
Db 4738 GGTCAAGCTGTATCCAGACATTTGGAGGCGGAGGCGGTGATCAGAGGTGAG 4797
OY 5278 AGATGTCACATCCGTCGTAAACAGGTCAAACCCGCTCTAATAAATAACAAAAAT 5337
Db 4798 AGATGTCACATCCGTCGTAAACAGGTCAAACCCGCTCTAATAAATAACAAAAAT 4857
OY 5338 TGGCGGAGATGTGGCGGACCTGTAGTTCAGCTACTCGGAGGCTGAGAGCAGAGA 5397
Db 4858 TGGCGGAGATGTGGCGGACCTGTAGTTCAGCTACTCGGAGGCTGAGAGCAGAGA 4917
OY 5398 ATGGCGTGAACCCGAGAGGAGAGTTGCAGTGAGCCGAGATCGGCCACTGCATCCAG 5457
Db 4918 ATGGCGTGAACCCGAGAGGAGAGTTGCAGTGAGCCGAGATCGGCCACTGCATCCAG 4977
OY 5458 CCTGGGCGCAGACAGAACTCTCTGAAAAAAGAAAAAGTTTGAAGTGTGAGGC 5517
Db 4978 CCTGGGCGCAGACAGAACTCTCTGAAAAAAGAAAAAGTTTGAAGTGTGAGGC 5037
OY 5518 AGAGGCCAGGCTGTAAATCTGTCACTTCACTGACATGACCTTGGGCAAGGCACTTCCT 5577
Db 5038 AGAGGCCAGGCTGTAAATCTGTCACTTCACTGACATGACCTTGGGCAAGGCACTTCCT 5097
OY 5578 GGCCAGTTTCACGGGGTTGGAATCGATCCAAAGTCCCTTCAGCATTAACGCTGCATG 5637
Db 5098 GGCCAGTTTCACGGGGTTGGAATCGATCCAAAGTCCCTTCAGCATTAACGCTGCATG 5157
OY 5638 TTCTAAGATGAGAAATGGGCGAGTTTCCCTCTCTCACGCCAGCCGCTGCATTCAA 5697
Db 5158 TTCTAAGATGAGAAATGGGCGAGTTTCCCTCTCTCACGCCAGCCGCTGCATTCAA 5217
OY 5698 GGTGAATGACAGGGAAGTCACTGTCCAAATCCGCAAGTTCCAAAGCCCTTGGGAGCC 5757
Db 5218 GGTGAATGACAGGGAAGTCACTGTCCAAATCCGCAAGTTCCAAAGCCCTTGGGAGCC 5277
```


QY 2910 GGGAGATAGGGTGGGGCGTTTATAGATTGGTAGTAAAGAAAATTACAGTCAA 2969
 |||||||
 Db 1021 GGGAGATAGGGTGGGGCGTTTATAGATTGGTAGTAAAGAAAATTACAGTCAA 1080
 QY 2970 AGGGGGTTTGTCTCTGGCGGGCAGAGTGGGGGGTCCCAAGTCTCAGTGGGGTCT 3029
 |||||||
 Db 1081 AGGGGGTTTGTCTCTGGCGGGCAGAGTGGGGGGTCCCAAGTCTCAGTGGGGTCT 1140
 QY 3030 TTTTGGAGCAGAGTGGAGCCAGAAAAGCATTTTCAAGTAAATCTCATTTAAGCA 3089
 |||||||
 Db 1141 TTTTGGAGCAGAGTGGAGCCAGAAAAGCATTTTCAAGTAAATCTCATTTAAGCA 1200
 QY 3090 AGGAGCCGCGATTTACCTCTTTTGTGGTGAATGATCATGATTAGTGGGGAGGGC 3149
 |||||||
 Db 1201 AGGAGCCGCGATTTACCTCTTTTGTGGTGAATGATCATGATTAGTGGGGAGGGC 1260
 QY 3150 ATATTCACTCTTTTGTGATTTCTTCAGTTACTTTCAGGCCATCTGGGCGTATATGCAAG 3209
 |||||||
 Db 1261 ATATTCACTCTTTTGTGATTTCTTCAGTTACTTTCAGGCCATCTGGGCGTATATGCAAG 1320
 QY 3210 TTACAGGGGATGCGATGCTTGGCTTGGGCTCAGAGGCTTGACAGCTTCTGTGGGGC 3269
 |||||||
 Db 1321 TTACAGGGGATGCGATGCTTGGCTTGGGCTCAGAGGCTTGACAGCTTCTGTGGGGC 1380
 QY 3270 CTGGAGAAATGTTTGTGCAACCTGTATCTATCTAATCTAATCTAATCTAATCTAATCT 3329
 |||||||
 Db 1381 CTGGAGAAATGTTTGTGCAACCTGTATCTAATCTAATCTAATCTAATCTAATCTAATCT 1440
 QY 3330 CTTTGTCTAGCTCAGGAGATTGTAAACGCAATCAGCGCCGTGCAAAACAGACAC 3389
 |||||||
 Db 1441 CTTTGTCTAGCTCAGGAGATTGTAAACGCAATCAGCGCCGTGCAAAACAGACAC 1500
 QY 3390 TCGGCTCTACCAATCAGAGATGTGGTGGGGCCAGATTAAGAAATAAACAGAGCTGC 3449
 |||||||
 Db 1501 TCGGCTCTACCAATCAGAGATGTGGTGGGGCCAGATTAAGAAATAAACAGAGCTGC 1560
 QY 3450 CCGAGCCAGAGTGGGCAACGGGCAAGCCCTATCCCAATATGAGAGCTTGTCTTT 3509
 |||||||
 Db 1561 CCGAGCCAGAGTGGGCAACGGGCAAGCCCTATCCCAATATGAGAGCTTGTCTTT 1620
 QY 3510 TGTCTTTTGCATTAATCTTGTCTACCTGCTTTTGGTGCACACTCTTTTATGAGC 3569
 |||||||
 Db 1621 TGTCTTTTGCATTAATCTTGTCTACCTGCTTTTGGTGCACACTCTTTTATGAGC 1680
 QY 3570 TGTAACTCTACACGAAAGTCTGCACTCTGCTGAAAGCCACTTAAGACAGAGCC 3629
 |||||||
 Db 1681 TGTAACTCTACACGAAAGTCTGCACTCTGCTGAAAGCCACTTAAGACAGAGCC 1740
 QY 3630 ACCGGGAGGATGAACAACCTCGGCGGCTCTTAAGAGCTATTAACCTACCGCGAA 3689
 |||||||
 Db 1741 ACCGGGAGGATGAACAACCTCGGCGGCTCTTAAGAGCTATTAACCTACCGCGAA 1800
 QY 3690 GGTGCGAGCTTCACTCTCAGCGAGACCAAGAACCCGCAAGGAAGAAACTGC 3749
 |||||||
 Db 1801 GGTGCGAGCTTCACTCTCAGCGAGACCAAGAACCCGCAAGGAAGAAACTGC 1860
 QY 3750 GAACACATCTGAACATCAGAAAGAACAACTCCAGATGACACCTTAAGAGCTGTAA 3809
 |||||||
 Db 1861 GAACACATCTGAACATCAGAAAGAACAACTCCAGATGACACCTTAAGAGCTGTAA 1920
 QY 3810 CTCACCTGCGAGGGTCCGGGCTTCTTGTGAAGTCACTGAGACCAAGCCTCACCACT 3869
 |||||||
 Db 1921 CTCACCTGCGAGGGTCCGGGCTTCTTGTGAAGTCACTGAGACCAAGCCTCACCACT 1980
 QY 3870 TCGGACACAAAGCCAGAGTTGAGATCAGCTGGGCAACATGATGAATGCGCTCTG 3929
 |||||||
 Db 1981 TCGGACACAAAGCCAGAGTTGAGATCAGCTGGGCAACATGATGAATGCGCTCTG 2040
 QY 3930 CAAAAAATTTACAAAAATTTGGCGAGCATGTGTCCGTGCTGTGCTCCAG 3989
 |||||||
 Db 2041 CAAAAAATTTACAAAAATTTGGCGAGCATGTGTGCTGCTGTGCTCCAG 2100

QY 3990 CTACGGGGAGGCTAAATGGGAGATGCTTGAACCTGGAGTGAAGACTGACGTAG 4049
 |||||||
 Db 2101 CTACGGGGAGGCTAAATGGGAGATGCTTGAACCTGGAGTGAAGACTGACGTAG 2160
 QY 4050 CTGTATTTTACACAGCCCTCTAGCTGGGGGACAGACTGACCTGTTTCCCTCCG 4109
 |||||||
 Db 2161 CTGTATTTTACACAGCCCTCTAGCTGGGGGACAGACTGACCTGTTTCCCTCCG 2220
 QY 4110 CAAAAAATTTGCAAAAAGTAAATGAAGTCCCTGATATGCTAGGGGCGAGTGCAT 4169
 |||||||
 Db 2221 CAAAAAATTTGCAAAAAGTAAATGAAGTCCCTGATATGCTAGGGGCGAGTGCAT 2280
 QY 4170 GCTGTAAATCCAGACTTTGGGAAGCCGAGGCGGGGCTACCTTAAGTACAGAGTGT 4229
 |||||||
 Db 2281 GCTGTAAATCCAGACTTTGGGAAGCCGAGGCGGGGCTACCTTAAGTACAGAGTGT 2340
 QY 4230 GAGACAGCCTGGCCAACTGAGAAAGCCATCTCTTAAATAATACAAAATTAGCCGG 4289
 |||||||
 Db 2341 GAGACAGCCTGGCCAACTGAGAAAGCCATCTCTTAAATAATACAAAATTAGCCGG 2400
 QY 4290 CTGTGGGGGACATGTTGGAGCATGCTGTAAATCCAGACTACAGAGGCTGAGCAGGA 4349
 |||||||
 Db 2401 CTGTGGGGGACATGTTGGAGCATGCTGTAAATCCAGACTACAGAGGCTGAGCAGGA 2460
 QY 4350 GAATCACTTGAACCCAGAGGAGGCGGCTTGCAGTGAGCCGAGATGTCGATTCACCTCC 4409
 |||||||
 Db 2461 GAATCACTTGAACCCAGAGGAGGCGGCTTGCAGTGAGCCGAGATGTCGATTCACCTCC 2520
 QY 4410 ACCCACTCAGCCTGGGCAACAAGAGCCAACTGTCTTAAATAATTAATAATTAATTAAT 4469
 |||||||
 Db 2521 ACCCACTCAGCCTGGGCAACAAGAGCCAACTGTCTTAAATAATTAATAATTAATTAAT 2580
 QY 4470 CCTGACATTAAGAGTGTGCAATGATGTCAGAGCAACATGTTAAATATGTGA 4529
 |||||||
 Db 2581 CCTGACATTAAGAGTGTGCAATGATGTCAGAGCAACATGTTAAATATGTGA 2640
 QY 4530 GCTCGCTTCCATGATGCTCTGTAAATAACCCACCTCAAGGCGAGTGCAGTGCAT 4589
 |||||||
 Db 2641 GCTCGCTTCCATGATGCTCTGTAAATAACCCACCTCAAGGCGAGTGCAGTGCAT 2700
 QY 4590 GCCTATTAATCCAGACTTTGGAGGCGGAGGCTGATCACTGAGTCAAGAGTTC 4649
 |||||||
 Db 2701 GCCTATTAATCCAGACTTTGGAGGCGGAGGCTGATCACTGAGTCAAGAGTTC 2760
 QY 4650 GAGACAGCCTGACACCAACATGCTGAATCCACCTTACTATAAATACAAATTAGA 4709
 |||||||
 Db 2761 GAGACAGCCTGACACCAACATGCTGAATCCACCTTACTATAAATACAAATTAGA 2820
 QY 4710 TGAGCATGGTGTG 4723
 |||||||
 Db 2821 TGAGCATGGTGTG 2834
 |||||||
 RESULT 6
 AAD17444
 ID AAD17444 standard; DNA; 2515 bp.
 XX
 AC AAD17444;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human granulocyte colony stimulating factor (hugCSF) fragment #2.
 XX
 KW Human; mutation; homologous recombination; target sequence; gene therapy;
 KW homologous recombination-enhancing agent; non-homologous end joining;
 KW therapeutic protein; granulocyte colony stimulating factor; hugCSF; ds.
 OS Homo sapiens.
 OS
 PN WO200168882-A2.
 XX
 PD 20-SEP-2001.
 XX

Db 1261 ACCAAGTGGCCATCCAGAGAGGTTTATTTTATCAATCTACACTCCCGCCAGCAAAAT 1320
 QY 1321 GAGAGTTACTCCAGATCCCTTACAAAGATGCTCTAAGCCAGTACCAAGATGAAGAAACGGA 1380
 Db 1321 GAGAGTTACTCCAGATCCCTTACAAAGATGCTCTAAGCCAGTACCAAGATGAAGAAACGGA 1380
 QY 1381 AGTGGAGGGGGAAGCTGCGCCAGCCCTTCTAACCATGAAGAAATACCTGGTAGAGCCCTCT 1440
 Db 1381 AGTGGAGGGGGAAGCTGCGCCAGCCCTTCTAACCATGAAGAAATACCTGGTAGAGCCCTCT 1440
 QY 1441 GGATGCTGGAGAGATGAATACGAGGGGCTCTGAGAGCTCCCTGTCAGATCATCTGTG 1500
 Db 1441 GGATGCTGGAGAGATGAATACGAGGGGCTCTGAGAGCTCCCTGTCAGATCATCTGTG 1500
 QY 1501 ACTTGTAGCCCTCCAGCCAGTCCAGCCCATGTGTGACAGGCGAGTGAATAGAGCCCT 1560
 Db 1501 ACTTGTAGCCCTCCAGCCAGTCCAGCCCATGTGTGACAGGCGAGTGAATAGAGCCCT 1560
 QY 1561 CACTCTCTGTTGGTCTTTATTCCTCCCATGTGGGCTGAAGTCTGAGTTCAGCCCTTAT 1620
 Db 1561 CACTCTCTGTTGGTCTTTATTCCTCCCATGTGGGCTGAAGTCTGAGTTCAGCCCTTAT 1620
 QY 1621 TCAAGATGTACACTTTCTTGACAGGAAATAGTGTACAGAAACAGCAGGGGCTTGGA 1680
 Db 1621 TCAAGATGTACACTTTCTTGACAGGAAATAGTGTACAGAAACAGCAGGGGCTTGGA 1680
 QY 1681 AGATGATCTACGCAATCTCTACCTGCTCAGCCACCCACTAGTCTGTGATCTTGAAC 1740
 Db 1681 AGATGATCTACGCAATCTCTACCTGCTCAGCCACCCACTAGTCTGTGATCTTGAAC 1740
 QY 1741 AAGTTTTTCACTTCTCTGAGGCCATCCCTGGCTACACACACACACAGATTTGATCAGGA 1800
 Db 1741 AAGTTTTTCACTTCTCTGAGGCCATCCCTGGCTACACACACACACAGATTTGATCAGGA 1800
 QY 1801 TGAATAGACAGATCCCTTACACCTGTATCCACAGACTTTGGAGGCCAAGCGGGTGG 1860
 Db 1801 TGAATAGACAGATCCCTTACACCTGTATCCACAGACTTTGGAGGCCAAGCGGGTGG 1860
 QY 1861 ATGGCTTGAAGCCGAGAGGTGACAGATGCGGCGAGTCCCTCACAAGCCCTGCTGCTC 1920
 Db 1861 ATGGCTTGAAGCCGAGAGGTGACAGATGCGGCGAGTCCCTCACAAGCCCTGCTGCTC 1920
 QY 1921 GGGGCTCTCTGCTGAGGCTCCACTTGGTGGCACTTGAAGAGCCCTTCAAGCCACG 1980
 Db 1921 GGGGCTCTCTGCTGAGGCTCCACTTGGTGGCACTTGAAGAGCCCTTCAAGCCACG 1980
 QY 1981 CTGCACTGTGGAGAGCCCTTCTGAGGCTGGCAAGGCCAGAGCCGCTCCCTCAGCTTGC 2040
 Db 1981 CTGCACTGTGGAGAGCCCTTCTGAGGCTGGCAAGGCCAGAGCCGCTCCCTCAGCTTGC 2040
 QY 2041 AGGGAGGTGTGGAGGAGAGGCTCAAGCAGGAACCGGGGCTGGCGACGGGCTTGGCGGC 2100
 Db 2041 AGGGAGGTGTGGAGGAGAGGCTCAAGCAGGAACCGGGGCTGGCGACGGGCTTGGCGGC 2100
 QY 2101 CAGCTGAGGTTCGGGGTGGGCTGGGCTGGGCGGCCCGCACTCGAGAGAGGGGCGAG 2160
 Db 2101 CAGCTGAGGTTCGGGGTGGGCTGGGCTGGGCGGCCCGCACTCGAGAGAGGGGCGAG 2160
 QY 2161 CCCTGCGAGGCGCCGGGCAATGAGAGGCTTAGCACCAGCGGCGCTCGAGAGGGTGT 2220
 Db 2161 CCCTGCGAGGCGCCGGGCAATGAGAGGCTTAGCACCAGCGGCGCTCGAGAGGGTGT 2220
 QY 2221 ACTGGGTGCC 2230
 Db 2221 CAGGACAGCC 2230

RESULT 7
 AA229174
 ID AA229174 standard; DNA: 1252 BP.
 XX
 AC AA229174;
 XX

DT 21-FEB-2000 (first entry)
 XX
 DE Targeting sequence-2 homologous to part of 5' non-coding region of G-CSF.
 KW Granulocyte colony stimulating factor; G-CSF; genomic sequence;
 KW translation start site; 5' non-coding sequence; DNA construct; downstream;
 KW targeting sequence-2; regulatory region; marker gene; selection;
 KW homologous recombination; gene therapy; delivery system; CMV promoter;
 KW haematopoietic progenitor cell; chemotherapy-induced neutropenia;
 KW bone marrow transplantation; congenital neutropenic disorder;
 KW chronic idiopathic disorder; plasmid pGcl3; neomycin resistance gene; ds.
 XX
 OS Homo sapiens.
 PN
 XX W09957291-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-US09924.
 XX
 PR 07-MAY-1998; 98US-0084649.
 XX
 PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
 XX
 PI Treco DA, Hartlehn MW, Selden RF;
 XX
 DR WPI: 2000-072235/06.
 XX
 PT Novel genomic sequences used for treating human diseases and disorders
 PS
 XX Disclosure; Fig 7; 58bp; English.
 XX
 CC The present DNA sequence is the second targeting sequence that
 CC corresponds to nucleotides 4728-5979 of the human genomic sequence from
 CC a region relative to the translation start site of granulocyte colony-
 CC stimulating factor (G-CSF). A DNA construct comprising this targeting
 CC sequence is cloned into the plasmid pGcl3, downstream of a CMV promoter
 CC and neomycin resistance gene, that functions as the transcriptional
 CC regulatory sequence and as selectable marker respectively. Homologous
 CC recombination of this construct into the host cells, can be used to
 CC modify the expression of G-CSF. These recombinant cells which express
 CC G-CSF are useful for in vitro production of the protein and gene therapy.
 CC Such cells may also be used in a delivery system for stimulating the
 CC proliferation and differentiation of haematopoietic progenitor cells, or
 CC for other conditions that can be treated with G-CSF, like chemotherapy-
 CC induced neutropenia, to treat patients undergoing bone marrow
 CC transplantation, chronic idiopathic and congenital neutropenic disorders.
 XX
 SO Sequence 1252 BP; 300 A; 337 C; 372 G; 243 T; 0 other;
 Query Match 20.1%; Score 1252; DB 21; Length 1252;
 Best Local Similarity 100.0%; Pred. No. 5.5e-271;
 Matches 1252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4728 CTTGTAATCCACCTACTTGGAGAGCTGAGGAGGAAATCTAGTAACAGGAGGCGG 4787
 Db 1 CTTGTAATCCACCTACTTGGAGAGCTGAGGAGGAAATCTAGTAACAGGAGGCGG 60
 QY 4788 AGGTGTAGTGGAGCGGAGATCGTGCATCTCCAGCCCTGAGCATGAGCGGAAATCC 4847
 Db 61 AGGTGTAGTGGAGCGGAGATCGTGCATCTCCAGCCCTGAGCATGAGCGGAAATCC 120
 QY 4848 ATCTCAAAAAAACAACAACCAACCACTCTCTACCTCCAGGAGGCTGGTACAGAGCT 4907
 Db 121 ATCTCAAAAAAACAACAACCAACCACTCTCTACCTCCAGGAGGCTGGTACAGAGCT 180
 QY 4908 GGGCCACATCAGTGCAGAGGTCTGAGGCACAGAGCTTAAGCGGAGCTGCAGAGACCGCGGA 4967
 Db 181 GGGCCACATCAGTGCAGAGGTCTGAGGCACAGAGCTTAAGCGGAGCTGCAGAGACCGCGGA 240
 QY 4968 CCAAGTAAACAGTGTGAGATCAAGTGTGTAGATCAAGCTCCCTGCATTTGGTACAC 5027

D	b		241	CCAGATTAACAGTGTGTGAGATCAGTGTGTGAGATCAGACGTCCTCCATTTGGTGAACC	300
O	y		5028	CAGGGGGCCCCCAAGCACACAGATATGGCCCCCATCCAGTCCACACATCCACTTTCATCCA	5087
D	b		301	CAGGGGGCCCCCAAGCACACAGATATGGCCCCCATCCAGTCCACACATCCACTTTCATCCA	360
O	y		5088	GAGATGTCTGTTTCTTGGCACGCTGGGGTAAATTAGACAGAGGTGACAGTCTTGGGTG	5147
D	b		361	GAGATGTCTGTTTCTTGGCACGCTGGGGTAAATTAGACAGAGGTGACAGTCTTGGGTG	420
O	y		5148	TGGTCAGTCAACATGCCCCCAGGACAGGCTTGTGGCTGTAGAAAAAGCTTCAGGCTTAGC	5207
D	b		421	TGGTCAGTCAACATGCCCCCAGGACAGGCTTGTGGCTGTAGAAAAAGCTTCAGGCTTAGC	480
O	y		5208	CGGCGACGGTGGCTCACGCTGTATATCCACACACTTGTGGAGGCGGAGGCGGTGATCA	5267
D	b		481	CGGCGACGGTGGCTCACGCTGTATATCCACACACTTGTGGAGGCGGAGGCGGTGATCA	540
O	y		5268	CGAGGTCAAGAGATCTGTACCATCTCTGGCTAAACAGGTGAACCCCGTCTTACTAAAAA	5327
D	b		541	CGAGGTCAAGAGATCTGTACCATCTCTGGCTAAACAGGTGAACCCCGTCTTACTAAAAA	600
O	y		5328	TACAAAAAATTTGGCCGGGCATGTGTGGCGGCACCTGTATGTTCCAGCTACTCGGAGCTG	5387
D	b		601	TACAAAAAATTTGGCCGGGCATGTGTGGCGGCACCTGTATGTTCCAGCTACTCGGAGCTG	660
O	y		5388	AGGCAGAGGAATGGGTGTACCCCGGAGGACAGATGTTGCACGTGAGCGCAGATCGCGCAC	5447
D	b		661	AGGCAGAGGAATGGGTGTACCCCGGAGGACAGATGTTGCACGTGAGCGCAGATCGCGCAC	720
O	y		5448	TGCATCTCAGGCTGGGCGACAGAGCAGACATCTCTGGAAAGAAAAAGAAACGTTCA	5507
D	b		721	TGCATCTCAGGCTGGGCGACAGAGCAGACATCTCTGGAAAGAAAAAGAAACGTTCA	780
O	y		5508	GGTCTGAGCCAGAGGCCCAAGGCTGTAAATTCTGTCACTTACATGACCTTGGGCAAGCAC	5567
D	b		781	GGTCTGAGCCAGAGGCCCAAGGCTGTAAATTCTGTCACTTACATGACCTTGGGCAAGCAC	840
O	y		5568	TTCCCTCCCTGGCCAGTTCAACGGGGTGGAAATGACATCCAAAGGCCCTTCAGACATTAA	5627
D	b		841	TTCCCTCCCTGGCCAGTTCAACGGGGTGGAAATGACATCCAAAGGCCCTTCAGACATTAA	900
O	y		5628	CGCTGCATGTTCTTAAGATGAGAAAGATGGGCAATTTCCCTCTCTCACCCAGCCGTG	5687
D	b		901	CGCTGCATGTTCTTAAGATGAGAAAGATGGGCAATTTCCCTCTCTCACCCAGCCGTG	960
O	y		5688	TCCACTTAAAGTGAATGACCAAGGAAATCACTGTGCCAATCCCGCATTTCCAAAGCC	5747
D	b		961	TCCACTTAAAGTGAATGACCAAGGAAATCACTGTGCCAATCCCGCATTTCCAAAGCC	1020
O	y		5748	TTGGGGACCTTACTGTCAAGGTCGTCGACAGAGGAGTGAAGGTGACGTGAGCCAAATGCGC	5807
D	b		1021	TTGGGGACCTTACTGTGTCAAGGTCGTCGACAGAGGAGTGAAGGTGACGTGAGCCAAATGCGC	1080
O	y		5808	TCGAAGGCTTGTGCTCATTTGGGACACACATCCGGTTTCCCTGTGGCTCTACCGGATTC	5867
D	b		1081	TCGAAGGCTTGTGCTCATTTGGGACACACATCCGCTTCCCTGTGGCTCTACCGGATTC	1140
O	y		5868	TAGGGGCTTTAGCCGAATGAGTCAATGGGGGCGGGGGGTTCTGTGGGGAATTCACACT	5927
D	b		1141	TAGGGGCTTTAGCCGAATGAGTCAATGGGGGCGGGGGGTTCTGTGGGGAATTCACACT	1200
O	y		5928	AATCAACTTTGGGACAGGACACGCTTGAATTCGATGTGCTATCCAAAGTG	5979
D	b		1201	AATCAACTTTGGGACAGGACACGCTTGAATTCGATGTGCTATCCAAAGTG	1252
RESULT 8					
AAA96363/C					
ID AAA96363 standard; DNA: 50000 BP.					
AC AAA96363;					
XX					

DT	08-FEB-2001	(first entry)
DE	Polymorphic repeat microsatellite sequences present in the CTLA4 locus.	
XX		
XX		
XX	Autoimmune disease: polymorphic microsatellite repeat: PMR: CD28 gene;	
KM	ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CTLA; lupus;	
KM	Insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;	
KM	Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma;	
KM	thyroiditis; postpartum thyroiditis; rheumatoid arthritis;	
KM	Hashimoto's disease; coeliac disease; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	satellite	5722..5746
FT		/*tag= a
FT	satellite	/note= "sara41/42 microsatellite repeat"
FT		6550..6597
FT		/*tag= b
FT	satellite	/note= "sara43/44 microsatellite repeat"
FT		1991..19956
FT		/*tag= c
FT	satellite	/note= "PW210/211 microsatellite repeat"
FT		23904..23957
FT		/*tag= d
FT	satellite	/note= "sara45/46 microsatellite repeat"
FT		27689..27780
FT		/*tag= e
FT	satellite	/note= "sara17/18 microsatellite repeat"
FT		30766..30801
FT		/*tag= f
FT	satellite	/note= "sara19/20 microsatellite repeat"
XX		
PN	WO200056856-A2.	
XX		
PD	28-SEP-2000.	
XX		
PF	24-MAR-2000; 2000WO-US07938.	
XX		
PR	25-MAR-1999; 99US-0126215.	
XX		
PA	(GENY) GENETICS INST INC.	
PI	Ling V, Wu P, Gray GS;	
XX	WPI: 2000-628257/60.	
DR		
PT	Determining predisposition of humans to develop autoimmune disease	
PT	Involves detecting polymorphic microsatellite repeat sequence within	
PT	human costimulatory receptor gene locus -	
XX		
PS	Claim 2; Page 67-82; 160pp: English.	
XX		
XX	Two human bacterial artificial chromosome (BAC) clones that included	
CC	and flanked the human CTLA-4 locus were cloned and sequenced. The	
CC	sequence data was assembled into a contiguous sequence that is presented	
CC	in AA96363-68. AA96363-64 comprises BAC clone 22700, and AA96365-68	
CC	comprise BAC clone 22608. The sequences contain polymorphic	
CC	microsatellite repeat (PMR) sequences. The specification describes a	
CC	method for determining the predisposition of a human subject to develop	
CC	autoimmune disease. The method comprises detecting a PMR sequence in the	
CC	CD28, ICOS gene or CTLA4 gene of the human costimulatory receptor gene	
CC	locus (HCCR). PMR sequences vary in length among individuals and can be	
CC	amplified to generate products that differ in size. These products can	
CC	then be detected by rapid and convenient high resolution processes. The	
CC	method is useful for determining the predisposition of insulin-dependent	
CC	diabetes mellitus (IDDM), Addison's disease, Graves disease, autoimmune	
CC	hypothyroidism, myasthenia gravis, thymoma, lupus, thyroiditis,	
CC	postpartum thyroiditis, rheumatoid arthritis, Hashimoto's disease,	
CC	coeliac disease and leprosy. PMR sequences within HCCR are useful as	
CC	markers in a variety of assays and in the field of forensic medicine,	
CC	disease diagnosis and human genome mapping.	
XX		

Db 74236 TTAGAGGTGACAGCTGTGGCAGTCTTCAGAGCCCTGCTGTCTAGCACCTCTCT 74177
Qy 1933 GCCTGGGCTCCCACTTCGGTGGCACTTTAGAGAGCCCTTCAGAGCCCAACCCGCTGACCTGTGG 1992
Db 74176 GCGTGGGCTCCCACTTTGGCGGCACTTTAGAGAGCCCTTCAGAGCCCAACCTGACCTGTGG 74117
Qy 1993 AGCCCCCTTTCGGGCTGGCCAAAGCCAGAGCCGGCTCCCTCAGCTTTCAGAGGAGGTGG 2052
Db 74116 AGCCCCCTTTCGGGCTGGCCAAAGGCTGGAGCCCACTCCCTCAGCTTTCAGAGGAGGTGG 74057
Qy 2053 AGGGAGAGGCTCAACAGAGAACCGGGGCTGGCGACAGGGGCTTGGCGGCGACGTGTGAGTTTC 2112
Db 74056 AGGGAGAGGCGCGAGCGGGAACTGGGGCTGCTCGAGGCGCTTGGCGGCGAGGTGAGTTTC 73997
Qy 2113 CGGGGCGGCTGGGGCTTGGGGGCGCCGCACTCGAGAGAGCGGGGCGAGCCCTGCGAGGCG 2172
Db 73996 CGGGGCGGCTGGGGCTTGGGGGCGCCGCACTCGAGAGAGCGGGGCGAGCCCTG-CTGGCG 73938
Qy 2173 CCGGGCAATYAGAGGCTTACACACCGGGGCGAGCGGGCTGCGAGGAGGTGACTGGGTGCC 2232
Db 73937 CGGGGCAATYAGAGGCTTACACACCGGGGCGAGCGGGCTGCGAGGAGGTGACTGGGTGCC 73878
Qy 2233 AGCAGTGGCAGCGCCCGCGCGCTGTGCTGCTCGATTTCTCAGTGGGCTTACAGGCTT 2292
Db 73877 AGCAGTGGCAGCGCCCAACCGGCACTGT- -GCTCAATTTCTCACCGGGGCTTACGCTGCTT 73822
Qy 2293 CCGCGGGGCGAGGGCTCGGGACCTGACAGCCCGCACTGGCTGAGCT- -CCCTCCAT 2347
Db 73821 CCGCGGGGCGAGGGCTCGGGACCTGACAGCCCGCACTGGCTGAGCTTCCACCCCTCCAT 73762
Qy 2348 GGGCTCTGTGGGCGCCGAGGCTCCCGAGAGACACACACCCCTGCTCCACAGCGCCAG 2407
Db 73761 GGGCTCTGTGGGCGCCGAGGCTCCCGAGAGACACACACCCCTGCTCCACAGCGCCAG 73702
Qy 2408 TCCCATTCACACGAGAGGCTGAGAAAGTGGGGGCGACAGCGAGCGGCACTGGCGAGCGAG 2467
Db 73701 TCCCATTCACACACGAGAGGCTGAGAAAGTGGGAGAGCGACAGCGC- -GAGAGACTGGCGAG 73643
Qy 2468 CTACCCCTGCAAGCCCTGTGGGAAATTCACACTGGTGAAGCAGTGGGCTCTGTAGTCTG 2527
Db 73642 CTCACCTGCAAGCCCTGTGGGAAATTCACACTGGTGAAGCAGCTGGGCTCTGTAGTCTG 73583
Qy 2528 GTGAGACTTGGAGAACCTTATGTCTAGCTCAGGAGATCTTAATATACCAATCAGCAAC 2587
Db 73582 GTGGGAGATGGAGAGCTTATATCTAGCTCAGGAGATGTAACACCAATCAGCAAC 73523
Qy 2588 CTGTGTC- - - - -TAGTCAAGGTC 2606
Db 73522 CTGTGTCAGCTCAGGAGTTTGTAGTGCACCAATCAGCAACCTGTGTAGCTCAGGCTT 73463
Qy 2607 TGTGAATGCACCAATTCACACTCTGTATCTAGCTACTGTGATGGGCTTGGAGAACCTT 2666
Db 73462 TGTGAATGCACCAATTCACACTCTGTATCTAGCTCTGTGGGGGCTTGGAGAACCTT 73403
Qy 2667 TATGCTAGCTCAGGAGATGTAATATACCAATCGGCACTGTATCTAGCTCAAGTTT 2726
Db 73402 TATGCTAGCTCAGGAGATGTAATATACCAATCGGCACTGTATCTAGCTCAAGTTT 73343
Qy 2727 GTAAACACACCAATCAGCAACCTGTGTAGCTCAGGATGTGAATGCACCAATCGCA 2786
Db 73342 GTAAATACACCAATCAGCACTGTGTCTAATCTCAGGATTTGTGTGATGCACCTAATCGCA 73283
Qy 2787 GTCTGTATCTGGCTACTTTCATYGGGCACTCGGTGTAAGAGACACCAAAAGGCTTGTG 2846
Db 73282 CTCTGTATCT- - - - - 73273
Qy 2847 TGAGCAATAAAGCTTCTATCACTGGGTGTCAGAGTGGGCTGAGTCCGAAAAGAGACTAGC 2906
Db 73272 - - - - - 73273
Qy 2907 GAAGGAGATAAAGGTGGGCGCTTTTATAGGATTTGGGTAGCTAAAGAAATTTACACT 2966

Db 73272 - - - - - 73273
Qy 2967 CAAGGGGAGTTTGTCTCTGGCGGCGAGAGTGGGGGTGCGAAGTGTCTCAGTGGGGT 3026
Db 73272 - - - - - 73273
Qy 3027 GCTTTTGGAGCGAGATGAGCCAGAAAAGACTTTCACMAGTAATCATCAATTAAG 3086
Db 73272 - - - - - 73273
Qy 3087 GCAGAGACCGGCAATTTACACTCTTTGTGTGTGAATGTCAATCAATTAAGTGGGCGAG 3146
Db 73272 - - - - - 73273
Qy 3147 GGCATATTCATCTTTTGTGATTTCTCAGTTTACAGGCCATCTGGCGTATATGTGC 3206
Db 73272 - - - - - 73273
Qy 3207 AAGTTACAGGGAGTCGATGGCTTGGGCTCGAGAGCTTACAGCTACTGTGGTGG 3266
Db 73272 - - - - - 73259
Qy 3267 GGCCTTGGAGATTTTGTGTGACACTGTATCTAGTTATCTAGTGGGAGCTGGAG 3326
Db 73258 GGCCTTGGAGAACCTGTGTGTGAAAACCTGTATCTACTAATCTGATGGGAGCTGGAG 73199
Qy 3327 AACCTTGTGTCTACCTCAGGAGTTGTAACGCAACCAATCAGCGCCCTGTCAAAACAGAC 3386
Db 73198 AACCTTGTGTCTACCTCAGGAGTTGTAACGCAACCAATCAGCTGCCCTGACAAAAGGCG 73139
Qy 3387 CACTGGCTCTACCAATCAGCAGAGATGGGTGGGGCGAGATTAAGAAATTAAGCAGGC 3446
Db 73138 CACTGGCTCTACCAATCAGCAGAGATGGGTGGGGCGAGATTAAGAAATTAAGCAGGC 73079
Qy 3447 TGCCCGAGCAGACATGGGCAAGCGGACAGGTCCCTATCAACAATATGGCAGCTTGTTC 3506
Db 73078 TGCCCGAGCAGACATGGGTAACCCGCTGGGCTCCCTTCACGCTGTGGAACTTGTTC 73019
Qy 3507 TTTTGTCTGTGCAATTAATCTGTGACAGCTCGGCTTTTGGGTCCACACTCTTTTATG 3566
Db 73018 TTTTGTCTGTGCAATTAATCTGTGACAGCTCTGCTACTGCTACTCTTTTGGGTCCACACTCTTTATG 72959
Qy 3567 ACCTGTAACTCACCAGCAAGGCTGTGACGCTTCACTCTCTGAAGCCACTAAGACACAGAG 3626
Db 72958 ACCTGTAACTCACCAGCAAGGATCTGACGCTTCACTCTCTGAAGCCAGAGACACAGAG 72899
Qy 3627 CCCACCGGAGAAATGAACAATCCGGGCGGCGCTCTTAAGAGCTATTAACCTACGCG 3686
Db 72898 CCCACCGGAGGAAACGAACTCCAGAGCGGCTCTTAAGAGCTATTAACCTACGCG 72839
Qy 3687 GAAGGTCTGACGCTTCACTCTCAGCCAGCGAGACACGAAACCCAGAAAGAAAGAAAC 3746
Db 72838 GAAGGTCTGTAACCTCAGCTCTGAGACA- -GAGACACAGAAACCCAGAAAGAAAGAAAC 72781
Qy 3747 TGCGAACATCTGAACATCAGAGAGAAACAAATCTCAGATGACCACTTAAGACTGTA 3806
Db 72780 TCCGAACATCTGAACATCAGAAAGAAACAGACTCAGAGCGGCCCACTTAAGACTGTA 72721
Qy 3807 ACACATCAGTGGAGGCTCGGGGCTTCTCTGTAAGTGTAGAGACCAAGACATCAGCA 3866
Db 72720 ACACATCAGTGGAGGCTCGAGGCTTCAAGCTTCACTTGAAGTGTAGAGCAAGAAACCAACA 72661
Qy 3867 GTTTCGAGCACAAAGCCAGAGTTTGAATCAGCTGGGCAACATGATGAATGCGCTCT 3926
Db 72660 ATTCTGACATTAATAATACATGCTTAAGAAATTAATTAAGTATTTGAAGAACTAAGCGCTGT 72601
Qy 3927 CTGCAAAAAAAA 3939
Db 72600 ATATTAAATGAAA 72588

RESULT 10
ABS56564/c

ID	AB556564 standard; DNA: 260209 BP.
AC	AB556564;
XX	
DT	27-JAN-2003 (first entry)
XX	
DE	Human SULF2 genomic DNA sequence.
XX	
KW	SULF2; ds: glucosamine-6-sulphatase; cancer; Ischaemia; human;
KW	tumour; angiogenesis; coronary; carotid; arterial occlusive disease;
KW	peripheral arterial disease; atherosclerosis; myointimal hyperplasia;
KW	thromboangitis obliterans; thrombotic disorder; vasculitis;
KW	heart attack; myocardial infarction; vascular death; inflammation;
KW	rheumatoid arthritis; asthma; adult respiratory distress syndrome;
KW	sarcoidosis; hypersensitivity pneumonitis; multiple sclerosis;
KW	allergic rejection; lymphoma; thrombosis; sulphatase;
KW	chromosome 20q12-13.2.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	misc.feature
FT	184020..184561
FT	/tag- a
FT	/note- "This sequence represents 540
FT	nucleotides not shown in the specification
FT	as the result of a printing error"
XX	
PN	W0200259327-A2.
XX	
PD	01-AUG-2002.
XX	
PE	26-DEC-2001; 2001WO-US649793.
XX	
PR	27-DEC-2000; 2000US-258577P.
PR	09-FEB-2001; 2001US-267831P.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Rosen SD, Hemmerich S, Tomita M, Palmeri D;
DR	WPI; 2002-636541/68.
XX	
PT	New sulfatase polypeptides having glucosamine-6-sulfatase activity,
PT	useful in screening, discovery and preparation of diagnostic and
PT	therapeutic agents for treating cancer, ischemic conditions,
PT	inflammation, or thrombosis
XX	
PS	Disclosure; Page 180-248; 293pp; English.
XX	
CC	This invention relates to the DNA and protein sequences of a novel
CC	polypeptide having glucosamine-6-sulphatase activity. The sulphatases of
CC	are useful in screening, discovery and preparation of diagnostic and
CC	therapeutic agents for treating cancer, ischemic conditions,
CC	inflammation, or thrombosis. The nucleic acids are useful in preparing
CC	the sulfatase polypeptides, identifying the expression of genes in a
CC	biological specimen, or generating transgenic non-human animals or
CC	site-specific gene modification in cell lines. The host cells are
CC	useful in replicating and/or expressing the polynucleotides or nucleic
CC	acids. The agents are useful in treating the disorders cited above by
CC	reducing tumour growth, inflammation, and thrombosis, or increasing
CC	angiogenesis, e.g. by treating coronary, carotid, or arterial occlusive
CC	disease, peripheral arterial disease, atherosclerosis, myointimal
CC	hyperplasia, thromboangitis obliterans, thrombotic disorders,
CC	vasculitis; or preventing ischemic conditions, heart attack (myocardial
CC	infarction), or other vascular death. The sulphatases and/or agents are
CC	also useful in treating rheumatoid arthritis, asthma, adult respiratory
CC	distress syndrome, sarcoidosis, hypersensitivity pneumonitis, multiple
CC	sclerosis, allergic rejection, and spread of lymphomas to cutaneous
CC	sites. The present sequence represents the human SULF2 genomic DNA
CC	sequence of the invention. This gene maps to human chromosome
CC	20q12-13.2.
XX	
50	Sequence 260209 BP; 78471 A; 51945 C; 51242 G; 77701 T; 850 other;

Query Match Similarity		11.9%	Score 744.8	DB 24	Length 260209	
Best Local Similarity		69.6%	Pred. No. 2.4e-156			
Matches 1399		Conservative	0	Mismatches 243	Indels 369	Gaps 14
QY	1875	AGAGGTGACAGCATCCCGGACAGTCTCTCAACAGCCCTGTGTGCTCTGGGCTCTCTCTGC	1934			
Db	222481	AGTGTGACAGAGGTGTGTGGACATCTCTACAGAGCCCTGTGTGCTCTCGGCGCTCTCTGC	222422			
QY	1935	CTGGGCTCCCACTTGTGTGGACACTTGAGAGAGCCCTTCA - GCCACCCGTGCACTGTGGGA	1993			
Db	222421	GTAGGCTCTCCACTTTTGGGGGCACTTGTAGAGAGCCCTTCTGNGGCCCGCGTGTGCACTGTGGGA	222362			
QY	1994	GGCCCTTCTGTGGGCTGGCCAAAGGCCAGAGCCGGCTCCCTCACTTGTCCAGAGAGTGTGA	2053			
Db	222361	GGCCCTTCTGTGGCTGGCCAAAGGCCAGAGTCCGAGCTCCCTCACTTGTCCAGAGAGTGTGA	222302			
QY	2054	GGGAGAGCTCTAAGAGAGAAACGGGGGCTCGAGAGCGCTTTCGGGGCACTGTGAATTC	2113			
Db	222301	GGGAGAGCGCCGAATGTGAAGAACGGGGCTGCTGCGGTCTTTCGGGGCACTGTGAATTC	222242			
QY	2114	GGGTGGGCGTGGGCTTGTGGGGGCCCGGCACCTGGAGACAGGGGCAAGCCCTGCCAGGCC	2173			
Db	222241	GGATGGGCGTGGGCTTGTGGCTGGCCCACTCGAGAGAGCGGGCGGCGCCCTTGC - GGCC	222183			
QY	2174	CGGGCAATATGAGAGCTTAGCACCCGGGCCAGGGGCGCTGGCGGAGAGGTACTGGGTGCCCA	2233			
Db	222182	CGGGAGATGAGGGGGCTTAGCACCCGGGCCAGGGGCGCTGGCGGAGAGGTACTGGGTGCCCA	222135			
QY	2234	GCAGTGCAGACCCGCGCGGGGCTGTGTGCTCTCGATTTCTCACTGGGGCTTAGACGCTTC	2293			
Db	222134	GCAGTATCCAGGCCCCACCGGCGCTG - GCCTGATTTCTTCAACGGGCTTAGTGGCTTC	222079			
QY	2234	CGCGGGGCGAGGCTTCGGGACCTGCAAGCCCGCATGCTAGAGCTCC - CTCATG	2348			
Db	222078	CGCGAGGCGAGGCTTCGGGGA - CTGAGCCCGCATGCTAGAGCTCCACCCACTCATG	222020			
QY	2349	GGCTGCTGTGGGGCCCCGAGACCTCCCGAAGAGACACACCCCTGCTGCACAGGCCCAAT	2408			
Db	222019	GGCTGCTGTGACGCCCGAGCCCTCCCGAGAGCACACCCCTGCTGTATGGCTCCAGT	221960			
QY	2409	CCCATTCGACACAGCAAGGGCTGAGAAATCGGGGCGACAGCGACCCGGGACTGGCAGGACAG	2468			
Db	221959	CCCATTCGACACCCCAAGGGCTATGAGATGTGAGAGTGTGAGAGCGCATATGGC - GCGGGACTGGCAGAGCGG	221901			
QY	2469	TACCCCTGCAGCCCTGTGTGCGGAATCCACTGGGTGAAGCCAGCTGGGCTCTGAGTCTGG	2528			
Db	221900	TCCACTCTGGAGCCCTGTGTGCGGAATCCACTAATGTGAAGCAGGTGGGCTCTGAGTCTGG	221841			
QY	2529	TGGAGACTTGGAGAACTTTATGTCTAGCTCAAGGGATGCTAAATATACCAATATGACACCC	2588			
Db	221840	TGGGAGACGTGGAG - TCTTTATGTCTAGCTCAAGGGATGCTAAACACCAATATGACATCC	221783			
QY	2589	TGTGTCTAGCTCAGGGTCTGTGTAATATGACCAATCCACACTGTGTATCTAGTACTGTGAT	2648			
Db	221782	TGTGTGTAGCTCAAGGTTGTGTATGTGACACCAATTGACACTGTGTATGTAGCTGTGTGAT	221723			
QY	2649	GGGGGCTTGGAGAACCTTATGTCTAGCTCAGGAGATGTAAATATACCAATGCGGCACTCT	2708			
Db	221722	GGGGGCTTGGAGAACCTTATGTCTAGCTCAGGAGATGTAAATATACCAATGCGGCACTCT	221688			
QY	2709	GTATCTAGCTCAAGGTTTGTAAACACACCAATACAGACCCCTGTGTCTAGCTCAGGGTATG	2768			
Db	221687	-----TTGTAACACACCAATACAGACCCCTGTGTATTTAATTCAGGTTTG	221644			
QY	2769	TGAATGACCAATGACAGAGTCTGTATCTGGCTACTTTCATGGGCAATCCGTGTGAAGAGAC	2828			
Db	221643	TGACTGACCAATGACAG - CTGTATCTAGCTGCTGTGTGG -	221603			
QY	2829	CACCAAAAGGCTTGTGTGTGAGCAATAAAGCTTTATATCACTGTGGGTGAGGTGGGCTGAG	2888			
Db	221602	-----	221603			

```
QY 2889 TCCGAAAAGAGAGTCAGCGAAGAGAGATTAAGGTGGGGCGTTTTATAGATTTGGGTAG 2948
Db 221602 -----GCTTTGGAGAAC 221591
QY 2949 GTAAAGAAAATTACAGTCAAAAGGGGTTGTCTGTGGCGGAGAGAGTGGGGGTGCG 3008
Db 221590 CTTTATGTCTAGCTCAGGGATTTGTAATACACATTTCAC-----221551
QY 3009 AAGTGTCAAGTGGGGGTCTTTTGAAGCCAGATGAGCCAGAAAGACTTTCACAG 3068
Db 221550 -----ACTGTATCTAG 221540
QY 3069 GTAATGTATCAATTAAGGAGAGACCCGCAATTTACACTCTTTTGTGGTGAATGCA 3128
Db 221539 CTCAAGGTTTGTAAACACACAAATCAGACCCCTGTGTAGCTCAAGGTTTGGCAATGCA 221480
QY 3129 TCAATTAGTTGGGGCAGGGCATATTCATCTTTTGTGATTTCACTTACTTCAAGGCC 3188
Db 221479 CCAATTCGA-----221472
QY 3189 ATCTGGGCGTATATGTGCAAGTTACAGGGATGCGATGGCTTGGCTTCAGAGGCT 3248
Db 221471 -----CACTCTGT 221464
QY 3249 TGACAGCTACTGTGGGGCTTGAGAAATGTTTGTGACACTGTATATCTAGTTAA 3308
Db 221463 ATCTAGCTGTCTGTGGGGCTTGAGAAACCTGTGTCTCAAACTCTGTACTACTTAA 221404
QY 3309 TCTAGTGGGAGCTGTGAACCTTTGTCTAGCTCAGGGATTTGAAACGCACCAATCAG 3368
Db 221403 TCTGATGGGAGAGTGAGAACTTTGTATCTAGCTCAGGGATTTGAAATGACCAATCAG 221344
QY 3369 CGGCCCTGCAAAACAGACCTGGCTCTACCAATCAGCAGAGATGTGGGTGGCCAGAT 3428
Db 221343 CACCTGTCAAAACAGGCTCCTGCTCTACCAATCAGCAGAGATGTGGGTGGCCAGAT 221284
QY 3429 AAGGATTAAGAGAGGCTCCGAGCAGAGATGAGCAACGCGACAGCCCTTATCAC 3488
Db 221283 AAGGATTAAGAGAGGCTCCGAGCAGAGATGAGCAATCTGCTGGTCCCTTCCAC 221224
QY 3489 AATATGGACCTTTTGTCTGTGTTGCGATTAATCTGTACTGCTCGCTTTTGG 3548
Db 221223 ACTGTGGAAGCTCCGTTCTTGTGCTCTTGCATTAATTAATCTGTACTGCTCTTGG 221164
QY 3549 GTCCACACCTCTTTTATGACTGTAACTCAGCAGCAAGGTCTGACGTTCACTCTGA 3608
Db 221163 GTCCACGCGCTTTTATGACTGTAACTCAGCAGCAAGATCTGTACTCTCTGA 221104
QY 3609 AGCCACTAAGACACGAGCCGAGGAGATGAATGAACGTCGCGCGCGCTGCTTAAG 3668
Db 221103 GCCCAGGAGACACAGGCCACTGGAGGAGAAAGAACCTCCAGACGCGCTGCTTAAG 221044
QY 3669 AGCTAATACACTGACCGGAGGTCTGACGTTCACTCTCAGCCAGCAGACACAGAAC 3728
Db 221043 AGCTGTAACTCA-CGCGAAGGTCTGCACTTCACTGAGCGAGCAGACAGCAAC 220985
QY 3729 CCACCAAGAAAGAAACTCGAAACACATCTGAACATCAGAAGAACAACTCCAGATGC 3788
Db 220984 CCACCAAGAAAGAAACTCGAAACACATCTGAACATCAGAAGAACAGACTCCAGATGC 220925
QY 3789 ACCACCTTAAGACTGTAACTCAGTGAAGGTCGCGGGCTTCTCTTGAAGTCACT 3848
Db 220924 GCCACCTTAAGACTGTAACTCAGTGAAGGTCGCGGGCTTCTCTTGAAGTCACT 220865
QY 3849 GAGACCAAGCACTCAGCAGTTTGGACACAA 3879
Db 220864 GAGACCAAGAACCCACCAATTTGTGACACAA 220834
```

```
RESULT 11
AB088143
ID AB088143 standard; cDNA; 121724 BP.
XX
```

```
AC AB088143;
DT 18-SEP-2002 (first entry)
XX
DE Human osteoblast differentiation related cDNA SEQ ID NO 50.
XX
KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW osteoporosis; osteopathic; ss.
XX
OS Homo sapiens.
XX
PN WO200250301-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-US48276.
XX
PR 18-DEC-2000; 2000US-255882P.
XX
PR 24-APR-2001; 2001US-285691P.
XX
PA (GENE-) GENE LOGIC INC.
PA (PROC ) PROCTER & GAMBLE CO.
PI JI D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI Mertz L;
DR WPI: 2002-557663/59.
XX
XX Use of genes and their expression profiles associated with osteoblast
XX differentiation for screening modulators bone formation for diagnosing
XX or treating e.g. osteoporosis, or as markers for the differentiation
XX process.
XX
XX Claim 1: SEQ ID NO 50; 78pp + Sequence Listing; English.
XX
XX The invention relates to genes and their expression profiles are used
XX for:
XX (a) screening modulators of precursor stem cell differentiation into
XX osteoblasts, or bone tissue deposition;
XX (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
XX osteoblast formation or osteoporosis; or
XX (c) treating or monitoring treatment of the conditions cited in (b), or
XX monitoring the progression of bone tissue deposition.
XX Specific conditions include postmenopausal osteoporosis, glucocorticoid
XX osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
XX drug-induced abnormalities in bone formation or bone loss, conditions
XX that involve altered bone metabolism (e.g. idiopathic juvenile
XX osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
XX Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
XX osteoblast differentiation associated cDNA marker of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 121724 BP; 33146 A; 25480 C; 26645 G; 36453 T; 0 other;
XX
XX Query Match 11.8%; Score 733.2; DB 24; Length 121724;
XX Best Local Similarity 90.1%; Pred. No. 7.5e-154;
XX Matches 856; Conservative 0; Mismatches 78; Indels 16; Gaps 6;
XX
QY 1867 TGACCTGAGAGGTGACAGCATGCGGCGAGTCTCAGACGCTGTGCTGCGGCC 1926
Db 4692 TGCACATGAGAGGTGAGACAGCTGTGCTCCACAGCGCGCTGCGGCAC 4751
QY 1927 TCCCTGCGCTGGGCTCCACTTGGTGGCACTTGAGAGAGCCCTTACAGCCAGCGCTGCAC 1986
Db 4752 TCCCTGCGCTGGGCTCCACTTGGTGGCACTTGAGAGAGCCCTTACAGCCAGCGCTGCAC 4811
QY 1987 TGTGGAGCCCTTTCTGGGCTGAGCCAGAGAGCGGCTCCTCAGCTTGCAGAGAG 2046
Db 4812 TGTGGAGCCCTTTCTGGGCTGAGCCAGAGAGCGGCTCCTCAGCTTGCAGAGAG 4871
QY 2047 GTGTGAGGAGAGGCTCAAGAGAAACGGGGCTGCGCAAGGCGCTTGGCGGCGACGCTG 2106
```


Db	4872	GTGTGGAGGAAGAGCGCGCGCCGCGAACC	GGGGGTGCBCCGCGGCTTGC	GGCCAGCTG	4931
OY	2107	GAGTTCCGGGTGGGCGTGGCTTGGCGGGCCCG	CCACACTCGGAGCAGCGCGCCAGCCCTGC		2166
Db	4932	GAGCTCGGGGCGTGGGCTTGGCGGGCCCCCG	ACACTCGGAGCAGCGCGCGTCCCTGC		4991
OY	2167	CAGGCCCCGGGCANAGNAGAGGCTTAGCACC	CGGGGCGCAGCGGCTCGCGAGGGTGTACTGGG		2226
Db	4992	C-GGCCCCGGGCANATGAAGAGCTTAGCACC	CGGGGCGCAGCAGCTCGGAGAGTGTACTGGG		5050
OY	2227	TGCCCCAGCAATGCGCAGCGCCCGCGCGCTGT	GTCTCGCTCATTTCTCACTGGGCGCTTAGC		2286
Db	5051	TCCTCCAGCAATGCGCAGCGCCCGCGCGCTG---	CGCTCGATTTCTCGCGCGCGCTTAGC		5106
OY	2287	AGCCTTCCCGCGGGGCGAGGCTCGGGACCTG	CAGCCCGGCATGCTGAGCT----	CCC	2341
Db	5107	TGCCTTCCCGCGGGGCGAGGCGCTTGGAAACC	CGCACCGCCGCTATGCTGAGCTTCCACCCC		5166
OY	2342	CTTCATGGGCTCTCTGTGGGGCCGACAGCTCC	CCGACGAGCACACCCTCTCTCACAGC		2401
Db	5167	CTCGGTGGGCTCTCTGTGGGGCCGACAGCTCC	CCGACGTAGCGCCACACCTCTCTCACAGC		5226
OY	2402	GCCCAATGCCATGACCAACGCAAGGCGCTGAG	AGATGCGGGCGACAGCGCACCGGACCTGGC		2461
Db	5227	GCCCCAGTCCCATGCACCAACCAAGGCGTGA	AAATGTCGGGGCGCAAG---CGGAGCTAGC		5283
OY	2462	AGGAGCTACCCCTGCGACGCCCTGGTGGGGAT	TCACATGGGTGAAGCCAGCTGGGCTCCTG		2521
Db	5284	AGGAGGCTCCACCTGCGACGCGCT-GTGGGGG	ATTCATGTAGGTGAAGCCACGCTGGGCTCCTG		5342
OY	2522	AGCTGTGGTGGAGACTTGGAGAACCTTTATGT	CTAGCTCAGAGGATCTGTAATATACCAATC		2581
Db	5343	AGTGGGGGGGAGAGTGGAGAACTTTATGTAG	CTAGCTCAGGAGTTGTAAATATACCAATC		5402
OY	2582	AGCACCTGTGTCTAGCTCAGGGGTCTGTGAAT	GCACCAATCCACACTCTGTATCTAGCTA		2641
Db	5403	AGCACCTGTGTCTAGCTCAGGGGTCTGTGAAT	GCACCAATCTGACA---CTGTATCTAGCTA		5460
OY	2642	CTCTGATGGGGGCTTTGGAGAACCTTTATGT	CTACTCAGGGATGTGTAATATACCAATCG		2701
Db	5461	CTCTGATGGGGGCTTTGGAGAACCTTTATGT	CTACTCAGGGATGTGTAATATACCAATCG		5520
OY	2702	GCACCTGTATCTAGCTCAGAGTTTGTAAACAC	ACCAATCAGCACCTGTGTAGCTCA		2761
Db	5521	GCACCTGTATCTAGCTCAGAGTTTGTAAACAC	ACCAATCAGCACCTGTGTAGCTCA		5580
OY	2762	GGGATGTGAATGACCAATCGAAGCTGTATCT	GTACTCTTCAATGGG		2811
Db	5581	GGGATGTGAATGACCAATCGAAGCTGTATCT	GTACTCTCTCGGTGGG		5630

RESULT 12	
AAZ23901	
ID	AAZ23901 standard; DNA; 49999 BP.
XX	
AC	AAZ23901;
XX	
DT	25-JAN-2000 (first entry)
XX	
DE	Human LOBO homologue genomic DNA fragment 3.
XX	
KW	LOBO; long bones; bone development; bone extension; skull; osteopathic;
KW	diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;
KW	spondyloepiphyseal dysplasia; achondroplasia; human; ds.
XX	
OS	Homo sapiens.
XX	
PN	MO9950284-A2.
XX	
PD	07-OCT-1999.
XX	
PF	26-MAR-1999; 99WO-EP02055.

```

XX      27-MAR-1998;    96DE-1013799.
PR
XX
PA      (ROSE/) ROSENTHAL A.
XX
XX      Rosenthal A, Rump A, Hess J, Aligner T, Wirth T;
PI      WPT, 1999-601320/51.
XX
XX      Nucleic acids encoding proteins which influence bone development,
PT      useful for treating and studying bone disorders .
XX
PS      Example 3: Page 272-300, 391pp; German.
XX

CC      This invention describes novel nucleic acids (I; designated LOBO (long
CC      bones)) encoding proteins influencing bone development in mammals. The
CC      proteins of the invention reduce and/or inactivate bone extension (i.e.
CC      development), with exception of the skull and have osteopathic activity.
CC      The nucleic acid molecules, proteins and antibodies can be used in
CC      diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods
CC      and nucleic acid molecules, etc. are useful for production of transgenic
CC      animals, especially a transgenic mouse for the study of diseases
CC      associated with bone development, e.g. spondyloepiphyseal dysplasia and
CC      achondroplasia. This sequence encodes a human LOBO protein described
CC      in the method of the invention.
CC
SQ      Sequence 49999 BP; 12607 A; 13453 C; 13304 G; 10635 T; 0 other;

Query Match          11.4%; Score 710.8; DB 20; Length 49999;
Best Local Similarity 87.8%; Pred.No. 5,9e-149;
Matches 864; Conservative 0; Mismatches 67; Indels 53; Gaps 6;

```

Query Match	11.4%	Score 710.8	DB 20	Length 49999
Best Local Similarity	87.8%	Pred. No.5.9e-149		
Matches	864	Conservative	0	Mismatches 67; Indels 53; Gaps 6;
QY	1873	TGAGAGGTGACAGATGCCGGCAGTCCCTCAAG-CCCTCGTTCCTCTCGCGCCTCTC	1931	
Db	30814	TGAGAGGTGACAGGTGCTGTGGCAGTCCCTCAAGGCCCTCGCTTCCTCGCACCTCCTC	3087	
QY	1932	TGCTTGGGCTCCACTTGTGGTGCATTGAGAGCCCTTACGCCAACCCTGTGCACCTGTG	1991	
Db	30874	TGCTTGGTCTCCCACTTGGGGGTCACTTGAAGAACCCCTTCGGCCACACCGCTGCACCTGTG	3093	
QY	1992	GAGCCCCCTTGTGGGCTGGCCAAAGCCAGACCGGCTCCCTCAGCTTGCAGAGGAGGTG	2051	
Db	30934	GAGCCCCCTTGTGGGCTGGCCAAAGCCAGACCCCACTCCTCAGCTTGCAGAGGAGGTG	3099	
QY	2052	GAGGAGAGGCTCAAGCAGAAACCGGGGCTGGCAGCGGCTTCGGGGCCAGCTGAGATT	2111	
Db	30994	GAGGAGAGGCGCGACGAGCCAGGACTTCGGGCGGAGGCTTCGGGCCAGCTGAGATT	3105	
QY	2112	CGGGTGGGCGTGGGGCTTGGCGGGCCCCCGCACTCGAAGACCGGGCCAGCCCTGCGAGG	2171	
Db	31054	CGGGTGGGCGTGGGGCTTGGCAGGCCCCCGCACTTGAAGACAGGCGGGCCGGCCCTTCC-GGC	3111	
QY	2172	CCCGGGCAATGAGAGGCTTACACCCGGGCGAGGGCTGCGGAGGGTGTACTGGGGTCCC	2231	
Db	31113	CCCGGGCAATGAGGGGCTTACACCCGGGCGAGGGCTGAGAGGGTGTACTGGGGTCCC	3117	
QY	2232	CAGCAGTCCACCCCGCGGGCTGTGCTGCTTGATTTCTACATGGGCTTACACACT	2291	
Db	31173	CAGCAGTCCACAGACCACCGGGCTG---CGCTGATTTCTACCCGGGCGCTTACTCTCT	3122	
QY	2292	TCCCGGCGGCGAGGGCTTCGGGACCTTGACCCCGCATGCTCGAGGCT-----CCCTTCA	2346	
Db	31229	TCCCGGCGGCGAGGGCTTCGGGACCTTGACCCCGCATGCTCGAGGCTTCCACCCCTTCA	3128	
QY	2347	TGGGCTCTGTGCGGCCGAGCTTCGCCGAGACACCCTCTCTCCACAGCGCCA	2406	
Db	31289	TGGGCTCTGTGCGGCCGAGCTTCGCCGATGAGACCGCACCCCTCTCTCCATGCGGCCA	3134	
QY	2407	GTCCCATCGACAGCAAGGGCTAGAAAGTCCGGGGCGAAGCGACCGGAACTGGCAGGCA	2466	
Db	31349	GTCCCATTCACCCACCAAGGGCTTAAGCGTSCGGGGCGACGG-GGGGGACTTGGCAGGCA	3140	
QY	2467	GCTACCCCTGCGAGCGTGTGCGAATTCACATGGGTGAAGCAGCTGGGCTCTCGAGACT	2526	

Db 31408 GCTCCACCTGCAGACCCCGGTCGGAAATCCACTGAGTGAACGCACTGGGCTCCTGAGTCT 31467
QY 2527 GGTGGAGACTTGGAGAACTTTATGCTAGCTCAGGAGGTGAATACAC----- 2576
Db 31468 GGTGGGGCGCTGGAGAACTTTATGCTAGCTCAGGAGTGTGAATACACCAATCGGCAC 31527
QY 2577 -----CAATCAGCACCTGTGTCTAGCTCAGGCT 2605
Db 31528 TCTGTATCTAGCTCAAGGTTTGAACACAGCACTGACACCCCTGTCTAGCTCAGGCT 31587
QY 2606 CTGTGAATGCACCAATTCACACTGTATCTAGCTAGTATGATGGGCTTGGAGACCT 2665
Db 31588 TTGTGAATGCACCACTGACACTGTATCTAGCTGCTGTGGGCTTGGAGAACT 31647
QY 2666 TTATGCTAGCTCAGGAGTTTGAATACACCAATCGGCACACTGTATCTAGCTCAAGTT 2725
Db 31648 TTATGCTAGCTCAGGAGTTTGAATACCAATCGGCACACTGTATCTAGCTCAAGTT 31707
QY 2726 TGTAAACACACCAATGCACACCTGTGTCTAGCTCAGGAGTATGTGAATGCACCAATGCAC 2785
Db 31708 TGTAAACACACCAATGCACACCTGTGTCTAGCTCAGGAGTTTGAATGCACCAATGCAC 31767
QY 2786 AGTCTGTATCTGCTACTTTCATG 2809
Db 31768 ACTCTGTATCTAGCTGCTGTGGTG 31791

RESULT 13
AAK67426
ID AAK67426 standard; DNA; 55235 BP.

AC AAK67426;

DT 06-NOV-2001 (first entry)

DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:22238.

KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;

XX Cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

PN MO200157182-A2.

PD 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

PF 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184564.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0198874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 14-AUG-2000; 2000US-0226279.
PR 18-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227909.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244644.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.

PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251038.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0251719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure: SEQ ID NO 22238; 3071bp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytoskeletal
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK7694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 55235 BP; 16593 A; 12467 C; 11660 G; 14515 T; 0 other;

Query Match

11.4%; Score 708.4; DB 22; Length 55235;

Best Local Similarity 86.9%; Pred. No. 2,1e-148;
 Matches 857; Conservative 0; Mismatches 76; Indels 53; Gaps 5;

1872 CTGAGAGTGACAGATGCCGAGTCTCTACAGCCCTGTTGCTCTGCGGCGCTCTC 1931
 |||||
 45538 CTGAGAGTGACAGATGCCGAGTCTCTACAGCCCTGTTGCTCTGCGGCGCTCTC 45597
 |||||
 1932 TGCCTGGGCTCCCACTCTGCGGACATTAGAGAGCCCTTACGCCACCCCTGACATGTGG 1991
 |||||
 45598 TGCCTGGGCTCCCACTCTGCGGACATTAGAGAGCCCTTACGCCACCCCTGACATGTGG 45657
 |||||
 1992 GAGCCCTTCTGGGCTGAGCAGAGGCGAGGCGGCTCCCTGAGCTTGTGAGGAGGTGG 2051
 |||||
 45658 GAGCCCTTCTGGGCTGAGCAGAGGCGAGGCGGCTCCCTGAGCTTGTGAGGAGGTGG 45717
 |||||
 2052 GAGGAGAGGCTCAAGCAGGAACCGGGCTGCGACAGCGCTTGGCGGCGAGCTGAGATT 2111
 |||||
 45718 GAAGAGAGTGGCGTGAACCGGGGCTGCGTGTGAGCTTGGCGGCGAGTGAATT 45777
 |||||
 2112 CCGGCTGGGCTGGGCTTGGGCGGCGGCTGCGACCTGAGAGAGGCGGCGGCTGCGAGGC 2171
 |||||
 45778 CCGGCTGGGCTGGGCTTGGGCGGCGGCTGCGACCTGAGAGAGGCGGCGGCTGCGAGGC 45835
 |||||
 2172 CCCGGCAATGAGAGGCTTGAACCGGCGGCGGCTGCGAGGCTGAGGCTGAGGCTG 2231
 |||||
 45836 CCCGGCAATGAGAGGCTTGAACCGGCGGCGGCTGCGAGGCTGAGGCTGAGGCTG 45895
 |||||
 2232 CAGCAGTGCAGCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2291
 |||||
 45896 CAGCAGTGCAGCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 45951
 |||||
 2292 TCCCGCGGCGGCGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTG 2346
 |||||
 45952 TCCCGCGGCGGCGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTG 46011
 |||||
 2347 TGGGCTCTGCTGCGGCGGCGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTG 2406
 |||||
 46012 TGGGCTCTGCTGCGGCGGCGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTG 46071
 |||||
 2407 GTCCCATGACACCAAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2466
 |||||
 46072 GTCCCATGACACCAAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 46130
 |||||
 2467 GCTACCCCTGACGCGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2526
 |||||
 46131 GCTACCCCTGACGCGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 46190
 |||||
 2527 GGTGAGACTTGGAGAACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2572
 |||||
 46191 GGTGAGACTTGGAGAACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 46250
 |||||
 2573 -----ACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605
 |||||
 46251 TGTGATCTAGTCAAGGTTTGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTG 46310
 |||||
 2606 CTGTGATCTAGTCAAGGTTTGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTG 2665
 |||||
 46311 TGTGATCTAGTCAAGGTTTGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTG 46370
 |||||
 2666 TGTGATCTAGTCAAGGTTTGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTG 2725
 |||||
 46371 TGTGATCTAGTCAAGGTTTGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTG 46430
 |||||
 2726 TGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2785
 |||||
 46431 TGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 46490
 |||||
 2786 AGTGTGATCTAGTCAAGGTTTGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTG 2811
 |||||
 46491 AGTGTGATCTAGTCAAGGTTTGTAAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTG 46516
 |||||

RESULT 14

FT	repeat_unit	/tag- j 866..906
FT	repeat_unit	/tag- k 907..943
FT	repeat_unit	/tag- l 944..984
FT	repeat_unit	/tag- m 985..1027
FT	repeat_unit	/tag- n 1028..1066
FT	repeat_unit	/tag- o 1067..1102
FT	repeat_unit	/tag- p 1116..1152
FT	repeat_unit	/tag- q 1153..1193
FT	promoter	/tag- r 1194..1322
FT	misc_feature	/tag- s 1322..1380
FT	misc_feature	/tag- t /note= "U3 R region" 1381..1680
FT	misc_feature	/tag- u /note= "U5 region" 1380..1680
FT	repeat_region	/tag- v /rpt_type= DISPERSED /note= "3 repeats of 70 bases" 1380..1452
FT	repeat_unit	/tag- w 1481..1552
FT	repeat_unit	/tag- x 1609..1680
FT	repeat_unit	/tag- y complement (595..616)
FT	primer_bind	/tag- z /note= "primer of AAA27496 and AA295045" 1677..1694
FT	primer_bind	/tag- aa /note= "primer of AAA27497" 1700..1726
FT	primer_bind	/tag- ab /note= "primer of AA295046" complement (1349..1373)
FT	primer_bind	/tag- ac /note= "primer of AA295047" 1807..1831
FT	primer_bind	/tag- ad /note= "primer of AA295048" 1695..1698
FT	LTR	/tag- ae
FN		
PN	MO200023606-A1.	
PD	27-APR-2000.	
XX	21-OCT-1999;	99MO-US24646.
XX	22-OCT-1998;	98US-0105256.
PR	(MED1-) MEDICAL COLLEGE GEORGIA INST INC.	
PA	Tuan D, Long Q, Bengra C;	
PX	WPI; 2000-339704/29.	
DR	Retroviral U3 long terminal repeat expression control sequences useful	
PT	for controlling target gene expression, e.g. for gene therapy -	
PS	Claim 1; Fig 2A-B; 76pp; English.	
CC	The present sequence is that of a solitary endogenous retrovirus 9	

(ERV-9) long terminal repeat (LTR) from the boundary area of the human beta-globin locus control region. This ERV-9 LTR contains an unusual U3 enhancer region comprised of 14 tandem repeats with recurrent GATC, CACCC and CCAAT motifs (see also AAA27488-92). The LTR is conserved in human and gorilla. In both recombinant constructs and the endogenous human genome, the LTR enhancer and promoter activate the transcription of cis-linked DNA preferentially in erythroid cells. The U3 enhancer, insulator and promoter regions can be used to control expression of any desired gene of interest and used in any vector for this purpose. The enhancer can be used to replace the LTR in retroviral vectors to avoid transcriptional silencing of transgenes and to boost the transcription of a therapeutic transgene in erythroid progenitor cells. The insulators can be used to insulate expression cassettes, especially those to be inserted in the genome of a host cell, from the transcriptional interference and silencing of the flanking host sequences. Thus, the disclosed transcription control elements are preferably used in retroviral vectors to obtain expression in mammalian cells, and especially to express genes in cells in, or to be introduced into, animals (including humans) for gene therapy. They can be also be used in conjunction with any other control sequences and/or vectors.

Query Match	10.7%	Score 669.2;	DB 21;	Length 1831;
Best Local Similarity	68.0%;	Prod. No. 4.1e-140;		
Matches 196;	Conservative	0;	Mismatches 248;	Indels 408; Gaps 17;
QY	1873	TGAGAGCTGACAGCATGCGCGCAGACCTCCACAGCCCTGTTGCGCTCTGCGGCGCCCTCT	19323	
Db	5	TGAGAGGTGACAGCGGTGCTGGCAGTCCCTCACAGCCCTGCTCGCTCTTGCGGCGCCCTCT	64	
QY	1933	GCTTGCGCTCCCACTTCCGCTGGCAGCTTGAGAGCCCTTCAGCCCAACCGCTGCATCTG	19922	
Db	65	GCTTGCGCTCCCACTTGGTGGCACTTGAGAGCCCTTCAGCCCGCCCTCTCACTGTG	124	
QY	1993	AGCCCTTTCTGGGCTTGCGCAAGGCGCAGCGCGGCTCCCTCAGCTTGAGGAGAGGTGG	20522	
Db	125	AGCCCTTTCTTGCGGCTGGCGCAAGCGCAGAGCCGCGCTCCCTCAGCTTGCCAGAGAGTGTG	184	
QY	2053	AGGAGAGGCTCAAGCAGAGAACCGGGGCTGCGCAGCGGCTTGCGGCGCAGCTGAGTTT	21122	
Db	185	AGGCGACACCCCGGCGCAGAGAAC-GGCGTGTGCGCGCTGTGTGAG-----GGAGTTT	235	
QY	2113	CGGGGCGGCGTGGGCTTGCGGGGCGCGCAGCTCGAGAGGCGGCGCAGCCCTGCGAGGCC	21727	
Db	236	CGGGTGGCGATGGGCTCCGAGAGACCCCGCAGCTCGAGGCGCGCAGCGGCCACCC	294	
QY	2173	CGGGCAATGAGAGGCTTAGCACC CGGCGCAGCGGCTTCGAGAGGGTACTAGGGTGC	22322	
Db	295	GCGGGCACTGAGGGGCTTAGCACC TGGCGCAGCAGCTGCTG-----	335	
QY	2233	AGCAGTGCACACCCCGCGCGCTGTGCTCGCTGCTCATTTCTACATGGGCTTAGCAGCTT	22922	
Db	336	-----TGTCTAATTTCTGCGGGGCTTAGTGCTT	367	
QY	2293	CCCGCGGGGCGAGGCTCGGAGCTTGACACCCCGCATGCTTAGAGCTCT--CTCTCATGG	23492	
Db	368	CCGTGGGGGCGAGGCTCGGAGCTTGACAGCGCGCATGCTTAGGCTCCCACTTCAATG	427	
QY	2350	GCTCTGTGCGGCGCGGAGCTTCCCGAGAGACACCAACCCTGCTCCACAGCGCCAGTC	24092	
Db	428	GCTCTGTGCGGCGCGGAGCTTGCAGAGAGAGCGCGCCCTGTCTCAGGCGACCAAGTC	487	
QY	2410	CCATTCGACACGACGAAGGCTGAGAAATGTGCGGGCGCAGCGCAGCGGATGCGACAGCACT	24692	
Db	488	CCATTCGACACCAAGGCTGAAATGTGCGGGCGC-CAGCAAGGAGACTGGCAGGCACT	546	
QY	2470	ACCCCTGACGCTGTGTGCGGAATCCATGGGTGAAAGCAGCTGGGCTCTGACTGTGT	25292	
Db	547	CCCCCTGAGCCAGTGTGCGGAGTACCTAGGTGTAAACCGGCTAG--TCTGAAATTTGCT	605	

OY	2530	GGAGACCTTGGGAACCTTTATGTCTAGTCTGGGATCGTAAT-----	2572
Db	606	GGGGATGCGAAGAACCTTATGTCTAGTTAAGGGATTGTAAATACACCAATTGGCACTCT	665
OY	2573	-----ACACCAATCAGACACCCTGTCTAGTCTCAGAGGCTG	2608
Db	666	GTATCTAGCTCAAGGTTTGTAAACACACCAATCAGACACCCTGTCTAGTCTCAGAGTTTG	725
OY	2609	TGAATGCACCAATCCACACTCTGTATCTAGTCTGTGATGGGACCTTGGAAACCTTTA	2668
Db	726	TGAATGCACCAATCAACACTC--TATCTAGTACTCTGTGGGACCTTGGAAACCTTTA	783
OY	2669	TGCTAGTCTCAGGATTTGTAAATACACCAATCCGAGCACTCTATCTAGCTAAGTTTGT	2728
Db	784	TGCTAGTCTCAGGATTTGTAAATACACCAATCCGAGCACTCTATCTAGCTAAGTTTGT	843
OY	2729	AAACACACCAATCAGACACCCTGTCTAGTCTCAGAGGTATGTGAATGCACCAATGACAGT	2788
Db	844	AAACACACCAATCAGACACCCTGTCTAGTCTCAGAGGTATGTGAATGCACCAATCAACCT	903
OY	2789	CTGTATCTGGCTACTTTCATGAGGACCTCCGTGTGAAGAGACCACCAACAGGCTTGTGTG	2848
Db	904	CTGTATCTAGTACTCT-----	920
OY	2849	AGCAATAAAGCTTTATCACCCTGGGTGACAGGTGGGCTGATGCCAAGAAAGAGCTACGCA	2908
Db	921	-----	920
OY	2909	AGGAGATAAAGGTGGGGCGCTTTTATAGATTTTGGGTAGGTAAAGGAAATTCACGTCA	2968
Db	921	-----GGTGGGACGTGGAGAACCTTTATGTCTAGCTCAGAGGTATGTAAATACA	969
OY	2969	AAGGGGTGTGTCTCTGGCGGCGCAGAGAGTGGGGGTGCAAGAGTGTCAAGTGGGGTGC	3028
Db	970	-----	969
OY	3029	TTTTTGAGCCAGGATGAGCCAGAAAAGACTTTACAGATTAATGTCAATTAAGGC	3088
Db	970	-----CCACCTGGCAGAGTCTGTATCTAGCTCAAGGTTTGTAAACACAC	1011
OY	3089	AAGGACCGCATTTTACACCTCTTTGGTGGGAGATGTCAATCAATTAAGTTGGGGCAGGG	3148
Db	1012	CAATCAGACACCTGTGTCTAGCTCAGAGTTTGTGAATGCACCAATACAA-----	1059
OY	3149	CATATTCACCTCTTTTGTGATTTCTCAGTTACTTCAGGCGCATCTGGGGGTATGTGCAA	3208
Db	1060	-----	1059
OY	3209	GTTACAGGGGATGCGATGGCTTGGCTTGGGCTCAGAGGCTTGACAGCTACTCTGTGGGG	3268
Db	1060	-----CACTGTGATCTAGTACTCTGTGT--GGG	1086
OY	3269	CCTTGGAGAAATGTTGTGTGCACACTGTGATTCATGTAATCTAGTGGGGAGCGTGGAGAA	3328
Db	1087	ACTTGGAGAACTTTGTGTGCACACTGTGATTCATGTAATCTAGTGGGGAGCGTGGAGAA	1146
OY	3329	CCTTTGTGTAGCTCAGGATTTGTAAACGACCAATCAGGCGCCTGTCAAAACAGACCA	3388
Db	1147	CCTTTGTGTAGCTCAGGATTTGTAAATGACCAATCAGTGGCCCTGTCAAAACAGACCA	1206
OY	3389	CTCGG--CTCTACCAATCAGCAGATGTGGTGGGGCCAGATTAAGAGATTAAGCAGGC	3446
Db	1207	CTGGGCTCTCTACCAATCAGCAGATGTGGTGGGGCCAGATTAAGAGATTAAGCAGGC	1266
OY	3447	TGCCCGAGCCAGAGTGGCAACGGGCAAGGTCCCTTACCAATATAGGCGCTTGTTC	3506
Db	1267	TGCCCGAGCCAGAGTGGCAACCCGCTGGGTCCCTTCACACTGTGGAGAGCTTTGTTC	1326
OY	3507	TTTTTGCTGTGTGCAATAATCTTGTCTACTGTCTCTTTTGGGTCCACACAGCTTTTATG	3566
Db	1327	TTTTTGCTGTGTGCAATAATCTTGTCTGTCTGTCTCTTTTGGGTCTACACAGCTTTTATG	1386
OY	3567	AGCTGTACACTCACCACGAAAGTCTCGAGCTTCACTCTGTGAAGCCACTAAGACACGAG	3626

Db	1387	AGCTGTAAAGCTTCAACCGGGAAGGCTCTGACGCTTCACTCTTGAAGCCAGCGAGACACAGAA	1446
QY	3627	CCCAACCGGGAAGATGAACAATCCCGGCGCGCTGCCTTAAAGACTATTAACACTACCGC	3686
Db	1447	CCCCACG- GGAAGAACGAACAACCTCCAGAGGCGCG- CTTAAGAGCTGGAACGTTCACACTGT	1504
QY	3687	GAAGGTCTGCAGCTTCACTCTCTCAGCCACGACGACACAGAACCCACCAAGAAAGAAAGAAC	3746
Db	1505	GAAAGGTCTGCAGCTTCACTCTCTTGAGCCACGACGACACAGAACCCATCAGAAAGAAAGAA- -	1562
QY	3747	TGCGAACACATCTGAACATCAGAAAGAACAAATCCAGATGCACACCTTAAGAGCTGTA	3806
Db	1563	CTCGAACACATCCAAACATCTGGAAGCAAGAACAACTCCACACAGCAGCCTTTAAGAACTGTA	1622
QY	3807	ACACTCACTGCGAGGGTCCGCGGCTTCTTTGAAGTCACTGAGACCAAGCACTCACC	3866
Db	1623	ACACTCAACAGAGGGTCCCGGCTTCACTTTGTAAGTCACTGAAACCAAGAACCAACCA	1682
QY	3867	GTTTCGACAC	3878
Db	1683	ATTCCGACAC	1694

Search completed: August 16, 2003, 16:00:37
Job time : 1037 secs

Job time : 1037 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2003, 13:22:16 ; Search time 272 Seconds
(without alignments)
10117.735 Million cell updates/sec

Title: US-09-845-020A-5
Perfect score: 6235
Sequence: 1 gatcacttgagagacagtagt.....tgcacttccccacagcct 6235

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PCrUS.COMB.seq: *
6: /cgn2_6/ptodata/2/1na/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6235	100.0	6235	US-09-305-384-5	Sequence 5, Appl1
2	6235	100.0	6235	US-09-525-160B-6	Sequence 6, Appl1
3	6235	100.0	6679	US-09-305-384-1	Sequence 1, Appl1
4	6235	100.0	6679	US-09-525-160B-5	Sequence 5, Appl1
5	2834	45.5	2834	US-09-305-384-6	Sequence 6, Appl1
6	1252	20.1	1252	US-09-305-384-7	Sequence 7, Appl1
7	669.2	10.7	1831	US-09-422-576D-1	Sequence 1, Appl1
8	563.8	9.0	9704	US-09-814-951A-3	Sequence 3, Appl1
9	462.2	7.4	1091	US-09-422-576D-5	Sequence 5, Appl1
10	442.4	7.1	1165	US-09-422-576D-25	Sequence 25, Appl1
11	439.6	7.1	801	US-09-422-576D-7	Sequence 7, Appl1
12	426.4	6.6	1043	US-09-422-576D-6	Sequence 6, Appl1
13	413.8	6.6	80246	US-09-078-294-4	Sequence 4, Appl1
14	412.2	6.6	80595	US-09-078-294-3	Sequence 3, Appl1
15	401.8	6.4	43950	US-09-735-934A-3	Sequence 3, Appl1
16	401.8	6.4	43950	US-10-060-332-3	Sequence 3, Appl1
17	389.8	6.3	31571	US-08-323-443B-1	Sequence 1, Appl1
18	389.8	6.3	53526	US-08-658-136-2	Sequence 2, Appl1
19	389.8	6.3	53577	US-08-658-136-1	Sequence 1, Appl1
20	381.4	6.1	45716	US-08-965-048-5	Sequence 5, Appl1
21	381.4	6.1	45989	US-08-965-048-6	Sequence 6, Appl1
22	377	6.0	59065	US-09-813-817-3	Sequence 3, Appl1
23	377	6.0	59065	US-09-978-197-3	Sequence 3, Appl1
24	376.2	6.0	51719	US-09-918-686-2	Sequence 2, Appl1
25	376.2	6.0	92139	US-09-918-686-1	Sequence 1, Appl1
26	375.6	6.0	14796	US-08-975-080-35	Sequence 35, Appl1
27	375.6	6.0	14796	US-09-630-706-10	Sequence 10, Appl1

C	28	375.6	6.0	14796	4	US-09-496-694B-3	Sequence 3, Appl1
C	29	366.2	5.9	3885	1	US-08-688-145-1	Sequence 1, Appl1
C	30	366.2	5.9	64467	4	US-09-803-671B-3	Sequence 3, Appl1
C	31	361	5.8	62804	4	US-09-800-960-3	Sequence 3, Appl1
C	32	354.4	5.7	36159	4	US-09-749-588-3	Sequence 3, Appl1
C	33	354.4	5.7	99500	4	US-09-798-096-10	Sequence 10, Appl1
C	34	352.6	5.7	1351	4	US-09-205-258-104	Sequence 10, Appl1
C	35	350.6	5.6	14747	4	US-09-608-285A-42	Sequence 42, Appl1
C	36	350.6	5.6	14747	4	US-09-557-800C-42	Sequence 42, Appl1
C	37	349.4	5.6	15977	4	US-09-608-285A-59	Sequence 59, Appl1
C	38	349.2	5.6	11811	3	US-09-078-294-7	Sequence 7, Appl1
C	39	346.4	5.6	55298	4	US-09-491-356C-1	Sequence 1, Appl1
C	40	341.8	5.5	2713	2	US-08-916-901-6	Sequence 6, Appl1
C	41	341.8	5.5	2713	4	US-09-154-602-6	Sequence 6, Appl1
C	42	340.2	5.5	63588	4	US-09-873-404-3	Sequence 3, Appl1
C	43	338.8	5.4	33060	3	US-08-814-095-7	Sequence 7, Appl1
C	44	338.2	5.4	162450	4	US-09-345-882-1	Sequence 1, Appl1
C	45	336.8	5.4	162450	4	US-09-345-882-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-305-384-5
Sequence 5, Application US/09305384
Patent No. 6242218
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Seiden, Richard F.
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/017001
CURRENT APPLICATION NUMBER: US/09/305,384
EARLIER FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: fastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 6235
TYPE: DNA
ORGANISM: Homo sapiens
US-09-305-384-5

Query Match 100.0%; Score 6235; DB 3; Length 6235;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GATCCTTGAGAGACAGTACTTCACAGACCGCTGGGACGATAGGAGACTCTCTACG	60
DB	1	GATCCTTGAGAGACAGTACTTCACAGACCGCTGGGACGATAGGAGACTCTCTACG	60
QY	61	AAAAATCAAAAAATATATGCGCGGCGATGTCACGTCGTATATCCCTGAACCTTGGG	120
DB	61	AAAAATCAAAAAATATATGCGCGGCGATGTCACGTCGTATATCCCTGAACCTTGGG	120
QY	121	ACATCAGGCAAGTGTACCTGAGTGTGAGAGTTCAGACTACCTGGCCACATGCT	180
DB	121	ACATCAGGCAAGTGTACCTGAGTGTGAGAGTTCAGACTACCTGGCCACATGCT	180
QY	181	GAACCCATATCTCCACTTAAAAATATACCAAGCATGTGTGGCAGGACACTCTA	240
DB	181	GAACCCATATCTCCACTTAAAAATATACCAAGCATGTGTGGCAGGACACTCTA	240
QY	241	ATCCCGGCTACTCAGAGAGCTGAGGACAGAGATACCTGAACCCAGAGGCGAGGTTG	300
DB	241	ATCCCGGCTACTCAGAGAGCTGAGGACAGAGATACCTGAACCCAGAGGCGAGGTTG	300
QY	301	CAGTGAAGTGAATCACCACCTGCATCTCCAGCTGGGTGACAGACAAGACTTATCTC	360
DB	301	CAGTGAAGTGAATCACCACCTGCATCTCCAGCTGGGTGACAGACAAGACTTATCTC	360

QY	361	AAAAAAATTAATAAAATTAATAAAATTAAGCCAGCGATGGTAGTCACACCTCTAGTCTGAG	420
Dd	361	AAAAAAAAATTAATAAAATTAATAAAATTAAGCCAGCGATGGTAGTCACACCTCTAGTCTGAG	420
QY	421	CTACTCAGAGGCTGAGGCGGAGGATGACCTTGAACCTGGGGCAGTCAAGGCTACAGTGA	480
Dd	421	CTACTCAGAGGCTGAGGCTGGGAGATACCTTGAACCTGGGGCAGTCAAGGCTACAGTGA	480
QY	481	GCCAAAGATCATGCCACTACACTCCAGCCTGGGCAACAGAGAGACCCGTCTTCAAAAA	540
Dd	481	GCCAAAGATCATGCCACTACACTCCAGCCTGGGCAACAGAGAGACCCGTCTTCAAAAA	540
QY	541	AATATATATATTAAGAAAAAACAAGCTGTTATGTCTCTCTGGTCCATACATCTACT	600
Dd	541	AATATATATATTAAGAAAAAACAAGCTGTTATGTCTCTCTGGTCCATACATCTACT	600
QY	601	ATGTATATAGTTTGGCAAACTCAAAAGATCAGATAGTCAATTTTATAGGCTTGTGGCCGT	660
Dd	601	ATGTATATAGTTTGGCAAACTCAAAAGATCAGATAGTCAATTTTATAGGCTTGTGGCCGT	660
QY	661	ATGGCTCTGTACACATCAGCTGTGCCCTCTTCTTACACAAAAAGCAGCTATTAACAAT	720
Dd	661	ATGGCTCTGTACACATCAGCTGTGCCCTCTTCTTACACAAAAAGCAGCTATTAACAAT	720
QY	721	ACATACATGAATTTTATAGACATCGAGATTGAAATTCATATGATTTTACATTTAT	780
Dd	721	ACATACATGAATTTTATAGACATCGAGATTGAAATTCATATGATTTTACATTTAT	780
QY	781	AAAAATACCTTTTAAAAATTTTCCCTTACCATTTAAAAAGTGTAAAAAGCGGCGACGCC	840
Dd	781	AAAAATACCTTTTAAAAATTTTCCCTTACCATTTAAAAAGTGTAAAAAGCGGCGACGCC	840
QY	841	GCCATCTGTACAGCGCTGTAAATTCAGACACTTTTGGAGGCTGAGAGTGGCGAGATCACTTGA	900
Dd	841	GCCATCTGTACAGCGCTGTAAATTCAGACACTTTTGGAGGCTGAGAGTGGCGAGATCACTTGA	900
QY	901	ATCAACAATTTGAGACGACGCGTGGCCAAATAGCAAAAACCCATTCTACTAAAAATAAA	960
Dd	901	ATCAACAATTTGAGACGACGCGTGGCCAAATAGCAAAAACCCATTCTACTAAAAATAAA	960
QY	961	AAAAATACCTGGGCAATGTGGTGACACACTGTGATCCGAGCTACTGGGAGCTGAGCA	1020
Dd	961	AAAAATACCTGGGCAATGTGGTGACACACTGTGATCCGAGCTACTGGGAGCTGAGCA	1020
QY	1021	GGAGATGCGCTTGAACCTGGGAGGAGGAGTTCGAGTGAAGCCATATCGCACTGGCAC	1080
Dd	1021	GGAGATGCGCTTGAACCTGGGAGGAGGAGTTCGAGTGAAGCCATATCGCACTGGCAC	1080
QY	1081	TCGACGCTGGGGAGACAGAGTGAATCTGTGCACAGAAAAAATAAGCTATTAAGCCAT	1140
Dd	1081	TCGACGCTGGGGAGACAGAGTGAATCTGTGCACAGAAAAAATAAGCTATTAAGCCAT	1140
QY	1141	TCCTAATTCAGTTCATCAGTGTACATACTCAGGCTGCGTACTCCTCTGAGGCAT	1200
Dd	1141	TCCTAATTCAGTGTACATCAGTGTACATACTCAGGCTGCGTACTCCTCTGAGGCAT	1200
QY	1201	ACCGGAGAAAGTAACTGTGCTGTGACAGGACATCAATTTCCACATTAACTAGACACT	1260
Dd	1201	ACCGTGAAGTAACTGTGCTGTGACAGGACATCAATTTCCACATTAACTAGACACT	1260
QY	1261	ACCAAGTTCGCATCCAAAGAGGTTTTTTTTTATACAATACACTCCCCCAGCAACAAT	1320
Dd	1261	ACCAAGTTCGCATCCAAAGAGGTTTTTTTTTATACAATACACTCCCCCAGCAACAAT	1320
QY	1321	GAGAGTTACTCCAGATCCTTTACAAAGATGCTCTAAGCCAGTACCAATGAACAACAGGA	1380
Dd	1321	GAGAGTTACTCCAGATCCTTTACAAAGATGCTCTAAGCCAGTACCAATGAACAACAGGA	1380
QY	1381	AGTGGAGAGGGAAGCTGCGACGCCCTTAACGATGAAGAAATACCTGCTAGAGCTTCT	1440
Dd	1381	AGTGGAGAGGGAAGCTGCGACGCCCTTTAACCATGAAGAAATACCTGCTAGAGCTTCT	1440
QY	1441	GGATGCTGGAAGATGAATTAACGGGGGCTCTGAGAGCCTGACCCCTGTCAATCACTGTG	1500

Db	1441	GGATGCTGGAGGAGGAATTAACGGGGGGCTCTGGAGCCTGCCCTGTCAATCACTGTG	1500
Qy	1501	ACCTGTGAGCCGCCATGCAGTCTGAGCCCATGTGATGAGCCAGTATATGAGCCCT	1560
Db	1501	ACTTTGAGCCTCCAGTCCAGTCTGAGCCCATGTGTATGTAGCCAGTATATGAGCCCT	1566
Qy	1561	CACCTCTGTTTGGTCTTATTTCTTCCCATGTGGGGGCGAAGTCTGATAGCCGTAT	1620
Db	1561	CACCTCTGTTTGGTCTTATTTCTTCCCATGTGGGGGCGAAGTCTGATAGCCGTAT	1620
Qy	1621	TCAGATGTACAGCTTTCTTGACAGAAAGTAGTCTACAGAAACGACAGGGGCTTGGCA	1688
Db	1621	TCAGATGTACAGCTTTCTTGACAGAAAGTAGTCTACAGAAACGACAGGGGCTTGGCA	1688
Qy	1681	AGATGATCTAACTGCAAAATCCATACCTGGCTAGCCAGCCAGGTAGTCTGTATCTTGAC	1740
Db	1681	AGATGATCTAACTGCAAAATCCATACCTGGCTAGCCAGCCAGGTAGTCTGTATCTTGAC	1740
Qy	1741	AAGTTTTTTCACCTTCTTGAGGCCATCCCTTGGCTACACACACACAGTTGGTTGACAGA	1800
Db	1741	AAGTTTTTTCACCTTCTTGAGGCCATCCCTTGGCTACACACACACAGTTGGTTGACAGA	1800
Qy	1801	TGAATGACGAAGTCCCTTACACCGTATATCCACAGCACTTGGGAGGCCAGAGGGGTGG	1866
Db	1801	TGAATGACGAAGTCCCTTACACCGTATATCCACAGCACTTGGGAGGCCAGAGGGGTGG	1866
Qy	1861	ATGGCTTAGCCTTGAGAGGTGACAGCATGCCGGCAGTCTTACAGACCTCTGTGGCTCTC	1920
Db	1861	ATGGCTTAGCCTTGAGAGGTGACAGCATGCCGGCAGTCTTACAGACCTCTGTGGCTCTC	1920
Qy	1921	GGCGCCTCTGTGCTTGCGGTGGGCTCCCACTTGGGTGAGCACTTGAAGAGCCCTTGAGCCACG	1988
Db	1921	GGCGCCTCTCTGTGCTTGCGGTGGGCTCCCACTTGGGTGAGCACTTGAAGAGCCCTTGAGCCACG	1988
Qy	1981	CTGCACGTGSGAGGCCCTTCTTGGGGCTGGGCCAAGGCCAGCGGGCTCCCTCAACCTTGC	2040
Db	1981	CTGCACGTGSGAGGCCCTTCTTGGGGCTGGGCCAAGGCCAGCGGGCTCCCTCAACCTTGC	2040
Qy	2041	AGGAGGTGTGAGAGGAGAGGCTCAAGAGGAAOCGGGGGCGAGCCAGCGGGCTTGGCGGGC	2100
Db	2041	AGGAGGTGTGAGAGGAGAGGCTCAAGAGGAAOCGGGGGCGAGCCAGCGGGCTTGGCGGGC	2100
Qy	2101	CAGCTGAGTTCCGGGTGGGCTTGGGCTTGGCGGGCCCGCACTCGAGCAGCGGGCCAG	2166
Db	2101	CAGCTGAGTTCCGGGTGGGCTTGGGCTTGGCGGGCCCGCACTCGAGCAGCGGGCCAG	2166
Qy	2161	CCGTGCCAGGGCCCGGGGCAATGAGAGGTTTGAACCCCGGGGCAAGCGGTGGGGAGGGT	2220
Db	2161	CCGTGCCAGGGCCCGGGGCAATGAGAGGTTTGAACCCCGGGGCAAGCGGTGGGGAGGGT	2220
Qy	2221	ACTGGGTGCCAGCAGTGCACGCCGCGGGCGGTGCTGCTCGATTTCTCACTGGGC	2288
Db	2221	ACTGGGTGCCAGCAGTGCACGCCGCGGGCGGTGCTGCTCGATTTCTCACTGGGC	2288
Qy	2281	CTTAGCAGCCTTCCCGGGGGGAGGGGCTTCGGGACCTGACAGCCCGCATGCTGAGCCTCC	2340
Db	2281	CTTAGCAGCCTTCCCGGGGGGAGGGGCTTCGGGACCTGACAGCCCGCATGCTGAGCCTCC	2340
Qy	2341	CCTCCATGGGGCTCGTGTGCGGCGCGAGGCTCCCGAGACAGACACCCCTGTCTCAGAG	2400
Db	2341	CCTCCATGGGGCTCGTGTGCGGCGCGAGGCTCCCGAGACAGACACCCCTGTCTCAGAG	2400
Qy	2401	CGCCAGTCCCATGCAGCACGCAAGGGCTGAGAAGTGGGGGCGCAGCGCACCGGAGCTGG	2460
Db	2401	CGCCAGTCCCATGCAGCACGCAAGGGCTGAGAAGTGGGGGCGCAGCGCACCGGAGCTGG	2460
Qy	2461	CAGGAGGTACCCCTGCAAGCCCTGTGGGGAATCACTGGGTGAAGGCAGCTGGGGCTCT	2520
Db	2461	CAGGAGGTACCCCTGCAAGCCCTGTGGGGAATCACTGGGTGAAGGCAGCTGGGGCTCT	2520
Qy	2521	GAGTGTGTTGAGACTTGGAAACCTTATGTAGCTACAGAGATCTAAATACCAAT	2580

Dh 2521 GAGTCTGTGGAGACTTGGAGACCTTTATGTCTAGCTCAGGATCGTAATAACCAAT 2580
Qy 2581 CAGACCCCTGTGTAGCTCAGGCTCTGTGTGAATGCACCAATCCACACTCTGTATCTACT 2640
Dh 2581 CAGACCCCTGTGTAGCTCAGGCTCTGTGTGAATGCACCAATCCACACTCTGTATCTACT 2640
Qy 2641 ACTGTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGATGTGAATACACCAATC 2700
Dh 2641 ACTGTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGATGTGAATACACCAATC 2700
Qy 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGCACCCTGTGTCTAGCTC 2760
Dh 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGCACCCTGTGTCTAGCTC 2760
Qy 2761 AGGCTATGTGAATGCACCAATGCACAGCTCTATCTGTGCTACTTTCATGGGCTCCGCT 2820
Dh 2761 AGGCTATGTGAATGCACCAATGCACAGCTCTATCTGTGCTACTTTCATGGGCTCCGCT 2820
Qy 2821 GAAGAGACACCAACAGGCTTGTGTGAGCAATTAAGCTCTATCACCCTGGTGCAGCT 2880
Dh 2821 GAAGAGACACCAACAGGCTTGTGTGAGCAATTAAGCTCTATCACCCTGGTGCAGCT 2880
Qy 2881 GGGCTGAGTCCGAAAGAGAGTCAAGCAAGGAGATTAAGGTGGGCGCTTTTATAGAT 2940
Dh 2881 GGGCTGAGTCCGAAAGAGAGTCAAGCAAGGAGATTAAGGTGGGCGCTTTTATAGAT 2940
Qy 2941 TTGGGTAGTAAAGAAATTTACAGTCAAAAGGGGTTTCTCTGGGCGGAGAGTGG 3000
Dh 2941 TTGGGTAGTAAAGAAATTTACAGTCAAAAGGGGTTTCTCTGGGCGGAGAGTGG 3000
Qy 3001 GGGGTCCCAAGCTCTCAGTGGGGGTCTTTTGGAGGAGATGAGCCAGGAAAGAGCT 3060
Dh 3001 GGGGTCCCAAGCTCTCAGTGGGGGTCTTTTGGAGGAGATGAGCCAGGAAAGAGCT 3060
Qy 3061 TTCAACAAGTAAATGTCATCAATTAAGGCAAGACCCGCAATTAACCTCTTTTGTG 3120
Dh 3061 TTCAACAAGTAAATGTCATCAATTAAGGCAAGACCCGCAATTAACCTCTTTTGTG 3120
Qy 3121 GAATGTCAATCAGTTAAGTTGGGCGAGGCAATTAATCACTCTTTTGTGATTTTCA 3180
Dh 3121 GAATGTCAATCAGTTAAGTTGGGCGAGGCAATTAATCACTCTTTTGTGATTTTCA 3180
Qy 3181 TTCAAGGCATCTGGGCGTAATGTGTGCAATTAAGGGAATGCAATGGTGTGGCT 3240
Dh 3181 TTCAAGGCATCTGGGCGTAATGTGTGCAATTAAGGGAATGCAATGGTGTGGCT 3240
Qy 3241 CAGAGGCTTGAACACTCTCTGTGGGGCTTGGAGAAATGTTGTGTGACACTCTGTAT 3300
Dh 3241 CAGAGGCTTGAACACTCTCTGTGGGGCTTGGAGAAATGTTGTGTGACACTCTGTAT 3300
Qy 3301 CTAGTAAATCTAGTGGGAGCTGGAGAACCTTTGTCTAGCTCAGGATGTGAAGCA 3360
Dh 3301 CTAGTAAATCTAGTGGGAGCTGGAGAACCTTTGTCTAGCTCAGGATGTGAAGCA 3360
Qy 3361 CCAATTCAGGCGCTGTCAAAAACAGACACTGGCTTAACCAATCAGCAGATGTGGG 3420
Dh 3361 CCAATTCAGGCGCTGTCAAAAACAGACACTGGCTTAACCAATCAGCAGATGTGGG 3420
Qy 3421 GGCAGATTAAGAGAAATAAAGCAGGCTGCCGAGCAGCAGTGGCAACGCGCACAGTCC 3480
Dh 3421 GGCAGATTAAGAGAAATAAAGCAGGCTGCCGAGCAGCAGTGGCAACGCGCACAGTCC 3480
Qy 3481 CTATCCACAATATGGCAGCTTTGTCTTTTGTCTGTGGCATTAATCTTGTCTAGCTCCG 3540
Dh 3481 CTATCCACAATATGGCAGCTTTGTCTTTTGTCTGTGGCATTAATCTTGTCTAGCTCCG 3540
Qy 3541 CTTTGTGGTCCACACTGCTTTTATAGCTTAACACTCAACGAGAGGTGTGAGCTTC 3600
Dh 3541 CTTTGTGGTCCACACTGCTTTTATAGCTTAACACTCAACGAGAGGTGTGAGCTTC 3600
Qy 3601 ACTCTGAAGCCTAAGACAGCAGCCAGCGGAGAGATGAACAATCCGCGCGCT 3660
Dh 3601 ACTCTGAAGCCTAAGACAGCAGCCAGCGGAGAGATGAACAATCCGCGCGCT 3660

Qy 3661 GCGTTAAGAGGTATTAACACTCAGCGGAGAGGTCTGACCTTCACTCTCAGCAGCAGAG 3720
Dh 3661 GCGTTAAGAGGTATTAACACTCAGCGGAGAGGTCTGACCTTCACTCTCAGCAGCAGAG 3720
Qy 3721 CCAGCAACCCACAGAGAGAAAGAACTCGAACATCTGAACATCAGAGAACAACT 3780
Dh 3721 CCAGCAACCCACAGAGAGAAAGAACTCGAACATCTGAACATCAGAGAACAACT 3780
Qy 3781 CCAGATGCACCACTTAAGAGCTGTAACTCTGCGAGGGTCCGGGCTTCTCTTGTG 3840
Dh 3781 CCAGATGCACCACTTAAGAGCTGTAACTCTGCGAGGGTCCGGGCTTCTCTTGTG 3840
Qy 3841 AAGTATGAGAGCAGAGACTCAGAGTTTGGACACAAAGCCAGAGTTTGAATGATGAC 3900
Dh 3841 AAGTATGAGAGCAGAGACTCAGAGTTTGGACACAAAGCCAGAGTTTGAATGATGAC 3900
Qy 3901 CTGGCAACATGATGAATGCGCTCTCTGCAAAAAAATAAATAAATAAATTTACAAAA 3960
Dh 3901 CTGGCAACATGATGAATGCGCTCTCTGCAAAAAAATAAATAAATAAATTTACAAAA 3960
Qy 3961 AGCATGTGTCCGTGCTGTGTCCAGCTACGCGGAGGCTAAATGTGGAGATCCCT 4020
Dh 3961 AGCATGTGTCCGTGCTGTGTCCAGCTACGCGGAGGCTAAATGTGGAGATCCCT 4020
Qy 4021 TGAAGCTGGAGGTAAAGACTGACAGCTGTGTATTTACACACAGCCCTTAGCTGG 4080
Dh 4021 TGAAGCTGGAGGTAAAGACTGACAGCTGTGTATTTACACACAGCCCTTAGCTGG 4080
Qy 4081 GGACAGACTGAGACCTGTTTCCCTCCGCAAAAAAATAAAGTAAATAGAGAT 4140
Dh 4081 GGACAGACTGAGACCTGTTTCCCTCCGCAAAAAAATAAAGTAAATAGAGAT 4140
Qy 4141 GCGTGTATGTGCTAGGCGCAGTGGCTCATGTGCTGTATCCAGCACTTTGGGAAGCCGAG 4200
Dh 4141 GCGTGTATGTGCTAGGCGCAGTGGCTCATGTGCTGTATCCAGCACTTTGGGAAGCCGAG 4200
Qy 4201 GCGGCGGGGTCACTTAAGCTCAGAGGTGTGAGACCGCTGGCAACATGTGGAAGCC 4260
Dh 4201 GCGGCGGGGTCACTTAAGCTCAGAGGTGTGAGACCGCTGGCAACATGTGGAAGCC 4260
Qy 4261 ATCTCTTAAATAAATAAATAATTAAGCGGCTGTGGGAGAGTGGAGCATGCTGTAA 4320
Dh 4261 ATCTCTTAAATAAATAAATAATTAAGCGGCTGTGGGAGAGTGGAGCATGCTGTAA 4320
Qy 4321 TCCAGACTACTCAGAGGCTGAGCAGAGAAATCACTTGAACCCAGAGGCGGCTTGC 4380
Dh 4321 TCCAGACTACTCAGAGGCTGAGCAGAGAAATCACTTGAACCCAGAGGCGGCTTGC 4380
Qy 4381 AGTGAAGCGAGATGTGCTGCAATTCACCTCAGGCTGGGCAACAGAGCCAAA 4440
Dh 4381 AGTGAAGCGAGATGTGCTGCAATTCACCTCAGGCTGGGCAACAGAGCCAAA 4440
Qy 4441 CTCTGTCTTAAATAAATAAATAAAGTGGCTGACATTAAGAGGTGTGCAATGCAATAG 4500
Dh 4441 CTCTGTCTTAAATAAATAAATAAAGTGGCTGACATTAAGAGGTGTGCAATGCAATAG 4500
Qy 4501 TTGCCAGCAACATGTTTAAGAAATGTGAGGCTCGCTTCATGCTCTGTAAAAAC 4560
Dh 4501 TTGCCAGCAACATGTTTAAGAAATGTGAGGCTCGCTTCATGCTCTGTAAAAAC 4560
Qy 4561 CACCTCTAAGGCGAGGTGCAAGTGTCTATGTCTTAATCCAGCACTTTGGAGGCGAG 4620
Dh 4561 CACCTCTAAGGCGAGGTGCAAGTGTCTATGTCTTAATCCAGCACTTTGGAGGCGAG 4620
Qy 4621 GCGGATGATCAGCTGAGAGTGTGAGAGCTCGAGACAGCTCAACCAATGTGAAT 4680
Dh 4621 GCGGATGATCAGCTGAGAGTGTGAGAGCTCGAGACAGCTCAACCAATGTGAAT 4680
Qy 4681 CCAACCTCTACTAAATAATACAAATTAAGATAGAGATGTGTGATGCTGTAAATCCAC 4740
Dh 4681 CCAACCTCTACTAAATAATACAAATTAAGATAGAGATGTGTGATGCTGTAAATCCAC 4740

OY	4741	TTTTACTGGGAGCGTGGAGGACAGAAAATCACTAGAAACCAAGGGAGGGAGGCTGTGAAGAG	4800
Db	4741	CTACTTGGGAGGCTGAAGGACGAAAATCACTAGAAACCAAGGGAGGGAGGCTGTGAAGAG	4800
OY	4801	CCGAGATCTGTCCATTTGGCATCCAGCCCTGACCAATGAGCGAAAGCTCATCTCTCAAAAAAAC	4860
Db	4801	CCGAGATCTGTCCATTTGGCATCCAGCCCTGACCAATGAGCGAAAGCTCATCTCTCAAAAAAAC	4860
OY	4861	AACAAACAAAAACCACTCTTCACTCCAGGAGCTGGGTACAGAGCTGGCCACATCAGT	4920
Db	4861	AACAAACAAAAACCACTCTTCACTCCAGGAGCTGGGTACAGAGCTGGCCACATCAGT	4920
OY	4921	GCAAGGTCTGAGCCACAGAGCTTAAGGGGGAGCTGACAGGACCGGGACACATTAACAGTG	4980
Db	4921	GCAAGGTCTGAGCCACAGAGCTTAAGGGGGAGCTGACAGGACCGGGACACATTAACAGTG	4980
OY	4981	TGTGAGATCAGTGTGTGAGATCAGACGTCCCTGCCATTGTGTGACACCAGGGGGCCCCCA	5040
Db	4981	TGTGAGATCAGTGTGTGAGATCAGACGTCCCTGCCATTGTGTGACACCAGGGGGCCCCCA	5040
OY	5041	AGCAACACAGATGGGGCCCATCCAGTCACACATCCACTCTTCATCCAGAGATGTCTGTTT	5100
Db	5041	AGCAACACAGATGGGGCCCATCCAGTCACACATCCACTCTTCATCCAGAGATGTCTGTTT	5100
OY	5101	CTTGGCACGCTGGGGTAAATTAGACAGAGGTGACAGCTTTGGGTGTGTCACTCAGAC	5160
Db	5101	CTTGGCACGCTGGGGTAAATTAGAGCACAAAGGTGACAGCTTTGGGTGTGTCACTCAGAC	5160
OY	5161	TGCCCCAGGACGGGCTTGTGGCTGTGAAAAAGCTGAGGCTGAGGGCCGGGACAGGTGGC	5220
Db	5161	TGCCCCAGGACAGGCTTGTGGCTGTGAAAAAGCTGAGGCTGAGGGCCGGGACAGGTGGC	5220
OY	5221	TCAGGCGCTGTAAATCCACAGCACTTTGGGAGGCCAGGCGGCTGATCAAGAGTCAAGAGA	5280
Db	5221	TCAGGCGCTGTAAATCCACAGCACTTTGGGAGGCCAGGCGGCTGATCAAGAGTCAAGAGA	5280
OY	5281	TCGTGACCATCTGTGGCTTAACACGGGTGAACCCCGTCTACTTAAAAATACAAAAATTGG	5340
Db	5281	TCGTGACCATCTGTGGCTTAACACGGGTGAACCCCGTCTACTTAAAAATACAAAAATTGG	5340
OY	5341	CCGGGCAATGTGGGGGGGACCTGTGATGTTCCAGCTACTCTGGGAGGCTGAGGACGAGAAATG	5400
Db	5341	CCGGGCAATGTGGGGGGGACCTGTGATGTTCCAGCTACTCTGGGAGGCTGAGGACGAGAAATG	5400
OY	5401	GCGGTGAACCCAGAGAGCGAGAGTTTGTCAATGACCGAGATCGCGCATCTGCACCTCCAGCT	5460
Db	5401	GCGGTGAACCCAGAGAGCGAGAGTTTGTCAATGACCGAGATCGCGCATCTGCACCTCCAGCT	5460
OY	5461	GGGGGACAGACCAAGACTCCTCATCTGTGAAAAAAGAAAAAGAAAGCTTCAGAGTCTGAAGCCGA	5520
Db	5461	GGGGGACAGACCAAGACTCCTCATCTGTGAAAAAAGAAAAAGAAAGCTTCAGAGTCTGAAGCCGA	5520
OY	5521	GGCCCAAGGCTTAATTCTGTGCACTTACCATGACCTTGGGCAAGGACACTTCTTCCCTGGC	5580
Db	5521	GGCCCAAGGCTTAATTCTGTGCACTTACCATGACCTTGGGCAAGGACACTTCTTCCCTGGC	5580
OY	5581	CCAGTTCCAGGGGTGTGAAATGAGCTCCAAAGGTCCTTCCAGCATTAACAGCTGAAGGTTTC	5640
Db	5581	CCAGTTCCAGGGGTGTGAAATGAGCTCCAAAGGTCCTTCCAGCATTAACAGCTGAAGGTTTC	5640
OY	5641	TAAAGATGAAGATGGGGCACTTCCCTCTCAACCCAGCCGCTGTCCACTTCAAGGT	5700
Db	5641	TAAAGATGAAGATGGGGCACTTCCCTCTCAACCCAGCCGCTGTCCACTTCAAGGT	5700
OY	5701	GAATGACCAAGGAAGTCACTGTGCCCAATCCCGCACTTCCAAAGCCTTGGGGACCTTAC	5760
Db	5701	GAATGACCAAGGAAGTCACTGTGCCCAATCCCGCACTTCCAAAGCCTTGGGGACCTTAC	5760
OY	5761	TGTAGAGGTCTGTGACAGAGAGGTGAAGGTCAAGGTGAACCGCTCGAAAGGCTCTTG	5820
Db	5761	TGTAGAGGTCTGTGACAGAGAGGTGAAGGTCAAGGTGAACCGCTCGAAAGGCTCTTG	5820
OY	5821	CCCTAATTCGGGACAGACATCCGGTTTCTCTGCGCTTACCGGGATTTCTAGGGGCTTTAGC	5880

Db	5821	CCTATTTCGGACAGACATCCGGTTTCTTGCGCTTACCGGATTTTACGGGCTTTAGC	5880
Qy	5881	CGAATGAGTCATGGGGGGGGGGGGTTCGGGGAGTTCCAGCTAATCACTTGGGA	5940
Db	5881	CGAATGAGTCATGGGGGGGGGGGGTTCGGGGAGTTCCAGCTAATCACTTGGGA	5940
Qy	5941	CAGACAGCCCTGGAACTTTGCATGTGCTTCCAACTGTCGGGTGGGCACAGAGCCAA	6000
Db	5941	CAGACAGCCCTGGAACTTTGCATGTGCTTCCAACTGTCGGGTGGGCACAGAGCCAA	6000
Qy	6001	GACCAATATGTCCTTATCTCAGTAGGGGCTCAGAGGTCCTCCAGACAGGACGCTCGG	6060
Db	6001	GACCAATATGTCCTTATCTCAGTAGGGGCTCAGAGGTCCTCCAGACAGGACGCTCGG	6060
Qy	6061	AGAGTTTGGGGGTAGGAATGGGAGCAACAGAGCTTCTTTTCTCTTGAATTTGGG	6120
Db	6061	AGAGTTTGGGGGTAGGAATGGGAGCAACAGAGCTTCTTTTCTCTTGAATTTGGG	6120
Qy	6121	GGCTTGGGGGACAGGCTTGAGATATCCCAAGAGAGGGGCAAGAGACCTCCCAACAG	6180
Db	6121	GGCTTGGGGGACAGGCTTGAGATATCCCAAGAGAGGGGCAAGAGACCTCCCAACAG	6180
Qy	6181	TTCTCCAGAGCGAGAGAGGAGAGCCCGACTCAGCTGCCTCTCCACAGGCTT	6235
Db	6181	TTCTCCAGAGCGAGAGAGGAGAGCCCGACTCAGCTGCCTCTCCACAGGCTT	6235
RESULT 2			
US-09-525-160B-6			
; Sequence 6, Application US/09525160B			
; Patent No. 6569681			
; GENERAL INFORMATION:			
; APPLICANT: Ivanov, Evgenii			
; TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION			
; FILE REFERENCE: 10278/016001			
; CURRENT APPLICATION NUMBER: US/09/525,160B			
; CURRENT FILING DATE: 2000-03-14			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 6			
; LENGTH: 6235			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-525-160B-6			
Query Match 100.0%; Score 6235; DB 4; Length 6235;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GATCACTTGAGGACAGTAGTTCAAGACACGCTTGGGAGCACTTAGGAGACTGTCTACG	60
Db	1	GATCACTTGAGGACAGTAGTTCAAGACACGCTTGGGAGCACTTAGGAGACTGTCTACG	60
Qy	61	AAAAATCAAAAAATATGCGCGGCGCATGCTGCTCAGCTCTGTAATCCCTGAATTTGGG	120
Db	61	AAAAATCAAAAAATATGCGCGGCGCATGCTGCTCAGCTCTGTAATCCCTGAATTTGGG	120
Qy	121	ACATCAAGGCAAGTGGATCACTTAGGTCAGGAGTTGCAGACTGAGCTGGCCAAATGCT	180
Db	121	ACATCAAGGCAAGTGGATCACTTAGGTCAGGAGTTGCAGACTGAGCTGGCCAAATGCT	180
Qy	181	GAAACCCATATCCACTTAAATAAATTAACAAATTTAGCCAGGATGTGGCAGGCACTGTA	240
Db	181	GAAACCCATATCCACTTAAATAAATTAACAAATTTAGCCAGGATGTGGCAGGCACTGTA	240
Qy	241	ATCCCGGCTACTCAGAGGCTGAGGCGAGGAGAAATCACTTGAACCCAGAGGCGAGGTTG	300
Db	241	ATCCCGGCTACTCAGAGGCTGAGGCGAGGAGAAATCACTTGAACCCAGAGGCGAGGTTG	300
Qy	301	CAGTAGCTGAGATCACACCACTGCACTCCAGCTGGGTGACAGACAGACTTATCTC	360
Db	301	CAGTAGCTGAGATCACACCACTGCACTCCAGCTGGGTGACAGACAGACTTATCTC	360

OY	361	AAAAAAAAAATTAATAAAATTTACCAGGCA	TGGTATGTGCACACTCTAGTCACG	420
Dd	361	AAAAAAAAAATTAATAAAATTTACCAGGCA	TGGTATGTGCACACTCTAGTCACG	420
OY	421	CTACTCAGAGCGCTGAGGTGGAGGATCAT	TTGAACCTGGGGCAGTCAGGCTACAGTGA	480
Dd	421	CTACTCAGAGCGCTGAGGTGGAGGATCAT	TTGAACCTGGGGCAGTCAGGCTACAGTGA	480
OY	481	GCCAAAGATCATGCCACTACACTCCAGCT	GGGCAACAGAGAGACCTGTCTTAAAA	540
Dd	481	GCCAAAGATCATGCCACTACACTCCAGCT	GGGCAACAGAGAGACCTGTCTTAAAA	540
OY	541	AATAATAATTAATAAAGAAAAAACAGCT	CTGTATTGTCTCTGCTCATACATCTACT	600
Dd	541	AATAATAATTAATAAAGAAAAAACAGCT	CTGTATTGTCTCTGCTCATACATCTACT	600
OY	601	ATGTATATAGTTTGCAAACCTAAGAATC	CAGATPACTCAATTTTTTAGGCTGTGGCCGT	660
Dd	601	ATGTATATAGTTTGCAAACCTAAGAATC	CAGATPACTCAATTTTTTAGGCTGTGGCCGT	660
OY	661	ATGGCTCTGTCAACAATCTGCCCCCTT	TTTACACAAAAGCCTTAACAT	720
Dd	661	ATGGCTCTGTCAACAATCTGCCCCCTT	TTTACACAAAAGCCTTAACAT	720
OY	721	ACATACATGAATTTTTTATAGACATCGA	ATTTGAATTTCAATGATTTTTTACATTTTAT	780
Dd	721	ACATACATGAATTTTTTATAGACATCGA	ATTTGAATTTCAATGATTTTTTACATTTTAT	780
OY	781	AAAAATATCTTTTAAAAATTTTCCCCT	TACCATTTTAAAAAGTGTAAAAACCGGCCAGCC	840
Dd	781	AAAAATATCTTTTAAAAATTTTCCCCT	TACCATTTTAAAAAGTGTAAAAACCGGCCAGCC	840
OY	841	GCCATCTGCACAGCCTGTAAATTCACAG	CACTTTTGGGAGGCTGAGGTGGAGAGATCACTTGAG	900
Dd	841	GCCATCTGCACAGCCTGTAAATTCACAG	CACTTTTGGGAGGCTGAGGTGGAGAGATCACTTGAG	900
OY	901	ATCAACAGTTTGGAGACAGCCTGGCCA	CATATAGCAAAAACCCATTCTACTAAAAATAAA	960
Dd	901	ATCAACAGTTTGGAGACAGCCTGGCCA	CATATAGCAAAAACCCATTCTACTAAAAATAAA	960
OY	961	AAAAATAGCTGGGCAATGTGGTGACAC	ACTGTGATCCAGTACTTGGGAGGCTTAGGCA	1020
Dd	961	AAAAATAGCTGGGCAATGTGGTGACAC	ACTGTGATCCAGTACTTGGGAGGCTTAGGCA	1020
OY	1021	GGAGAATCTGTTGAACCTGGGAAGCGA	GGATTTGTCAGTAGGCCAATATGCGACTGCAC	1080
Dd	1021	GGAGAATCTGTTGAACCTGGGAAGCGA	GGATTTGTCAGTAGGCCAATATGCGACTGCAC	1080
OY	1081	TTCACGCTGGGTGACAGAGTAGACTT	GTCTCAACGAAAAAAAAGTGTAAANAGCAT	1140
Dd	1081	TTCACGCTGGGTGACAGAGTAGACTT	GTCTCAACGAAAAAAAAGTGTAAANAGCAT	1140
OY	1141	TCCAAATTCAGTGTATACATCACTGTAT	CAAGCTGGCTGAGGAT	1200
Dd	1141	TCCAAATTCAGTGTATACATCACTGTAT	CAAGCTGGCTGAGGAT	1200
OY	1201	ACCTGAGAAGTAGAGTTGCTTGGTGCAC	AGGACATACATTTCCACATTAATCTAGACACT	1260
Dd	1201	ACCTGAGAAGTAGAGTTGCTTGGTGCAC	AGGACATACATTTCCACATTAATCTAGACACT	1260
OY	1261	ACCAAGTTTGCATCAAGAGAGGTTTT	TTTTTACAAATCTACACCTCCCCACAGCAACAAT	1320
Dd	1261	ACCAAGTTTGCATCAAGAGAGGTTTT	TTTTTACAAATCTACACCTCCCCACAGCAACAAT	1320
OY	1321	GAGAGTTACTTCAGATCTTTTACAAAG	ATGCTCTTAGGCCAGTACAGATTAATAACAGGA	1380
Dd	1321	GAGAGTTACTTCAGATCTTTTACAAAG	ATGCTCTTAGGCCAGTACAGATTAATAACAGGA	1380
OY	1381	AGTGGAGGGGAGAGCTGCAAGCCCTT	CTTAACATGAAGAAATACCTGTAGAGCCTTCT	1440
Dd	1381	AGTGGAGGGGAGAGCTGCAAGCCCTT	CTTAACATGAAGAAATACCTGTAGAGCCTTCT	1440

QY	1441	GGATGCTGGAGAGATGAAATTAACGGGGGGTCTCGAGAGCCTGGCCCTCTGCAATCACTGTG	1500
Db	1441	GGATGCTGGAGAGATGAAATTAACGGGGGGTCTCGAGAGCCTGGCCCTCTGCAATCACTGTG	1500
QY	1501	ACTTGTGAGCCCTCCAGTCCAGTCTCAGGCCCATGTGTATGGCCAGTATATAGAGCCCT	1560
Db	1501	ACTTGTGAGCCCTCCAGTCCAGTCTCAGGCCCATGTGTATGGCCAGTATATAGAGCCCT	1560
QY	1561	CACCTCTGTGTTGGTCTTATATCTCCCATGTGGGGCTGAAGTCTGATGAGCCGTAT	1620
Db	1561	CACCTCTGTGTTGGTCTTATATCTCCCATGTGGGGCTGAAGTCTGATGAGCCGTAT	1620
QY	1621	TCAAAATGTACAGCTTCTTGTGACAGAAAGTAGTGTACAGAAACAGAGAGGGCTTGGCA	1680
Db	1621	TCAAAATGTACAGCTTCTTGTGACAGAAAGTAGTGTACAGAAACAGAGAGGGCTTGGCA	1680
QY	1681	AGATGATCTAACTGGAAATCCATCCATGGCTCAGCCACGAGTATCTGTATCTTGAAC	1740
Db	1681	AGATGATCTAACTGGAAATCCATCCATGGCTCAGCCACGAGTATCTGTATCTTGAAC	1740
QY	1741	AAGTTTTTTCACCTTCTGTAGAGCCATCCCTTGGCTACAACAACACAGTTGGTTGACAGA	1800
Db	1741	AAGTTTTTTCACCTTCTGTAGAGCCATCCCTTGGCTACAACAACACAGTTGGTTGACAGA	1800
QY	1801	TGAATATGACAGAGTCCCTTACACCTGTATCCAGCACTTTGGAGGCGCAAGCGGGTGG	1860
Db	1801	TGAATATGACAGAGTCCCTTACACCTGTATCCAGCACTTTGGAGGCGCAAGCGGGTGG	1860
QY	1861	ATGGGTTGAGCCTTGAGAGGTGACACATAGCGGGCAGTCCCTACACACCCCTCGTTGCTCTC	1920
Db	1861	ATGGGTTGAGCCTTGAGAGGTGACACATAGCGGGCAGTCCCTACACACCCCTCGTTGCTCTC	1920
QY	1921	GGCGGCTCCTCTGCTGTGGGCTCCCACTTCGGTGGCACTTGAAGAGCCCTTGAAGCCACAG	1980
Db	1921	GGCGGCTCCTCTGCTGTGGGCTCCCACTTCGGTGGCACTTGAAGAGCCCTTGAAGCCACAG	1980
QY	1981	CTGCACTGTGGAGAGCCCTTCTTGTGGGCTGGCCAGGCCAGAGCCGGCTCCTCAGCTTGC	2040
Db	1981	CTGCACTGTGGAGAGCCCTTCTTGTGGGCTGGCCAGGCCAGAGCCGGCTCCTCAGCTTGC	2040
QY	2041	AGGAGGAGTGTGAAGGAGAGAGGCTCAAGAGAGAAACCGGGGGTGGCCAGCGGCTTGGGGC	2100
Db	2041	AGGAGGAGTGTGAAGGAGAGAGGCTCAAGAGAGAAACCGGGGGTGGCCAGCGGCTTGGGGC	2100
QY	2101	CAGCTGTGAGTTCCGGGGTGGGGCTGTGGCGGGGCCCGGCACTGTGAGACAGCGGGCCAG	2160
Db	2101	CAGCTGTGAGTTCCGGGGTGGGGCTGTGGCGGGGCCCGGCACTGTGAGACAGCGGGCCAG	2160
QY	2161	CCCTGCCAGGCCCCGGGGCAATGAGAGGCTTAGACACCGGGCCAGCGGCTCGGGAGGCT	2220
Db	2161	CCCTGCCAGGCCCCGGGGCAATGAGAGGCTTAGACACCGGGCCAGCGGCTCGGGAGGCT	2220
QY	2221	ACTGGGTGCCCCAGAGATGTGCCAGCCCGCGGCGCTGTCTGGCTGATTTCTCAGTGGGC	2280
Db	2221	ACTGGGTGCCCCAGAGATGTGCCAGCCCGCGGCGCTGTCTGGCTGATTTCTCAGTGGGC	2280
QY	2281	CTTACACAGCTTCCCGGGGGGAGGGGCTCGGGACCTTGAGGCCCGGCAATGCCCTGAGCCCTC	2340
Db	2281	CTTACACAGCTTCCCGGGGGGAGGGGCTCGGGACCTTGAGGCCCGGCAATGCCCTGAGCCCTC	2340
QY	2341	CCTCCATGGGCTCGTGTGCGGGCCGAGGCTCCCGAGAGAGACACACCCCTGTCTCACAG	2400
Db	2341	CCTCCATGGGCTCGTGTGCGGGCCGAGGCTCCCGAGAGAGACACACCCCTGTCTCACAG	2400
QY	2401	CGCCAGTCCATGACACACCAAGGGCTGAGAAAGTGGGGCGGACAGGCAACGGGAATGG	2460
Db	2401	CGCCAGTCCATGACACACCAAGGGCTGAGAAAGTGGGGCGGACAGGCAACGGGAATGG	2460
QY	2461	CAGGAGGTACCCCTGCAAGCCCTGGTGGGAATCCATCGGGGTGAAAGCCAGTGGGGCTCT	2520
Db	2461	CAGGAGGTACCCCTGCAAGCCCTGGTGGGAATCCATCGGGGTGAAAGCCAGTGGGGCTCT	2520
QY	2521	GAGTCTGTGTGAGACTTGGAGAACCTTATATCTAGCTCAGAGGATCTGTAATATACCAAT	2580

|||||
Db 2521 GAGTCTGTGAGACCTTGGAGAACCTTTATGTCTAGCTCAGGGATCGTAATATACCAAT 2580
QY 2581 CAGACCCCTGTGTCTAGCTCAGGGCTGTGTAAATGACCAATCCACACTCTGTATCTAGT 2640
Db 2581 CAGAGCCCTGTGTCTAGCTCAGGGCTGTGTAAATGACCAATCCACACTCTGTATCTAGT 2640
QY 2641 ACTGTGTGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATATACCAATC 2700
Db 2641 ACTGTGTGGGGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATATACCAATC 2700
QY 2701 GGCACCTGTATCTAGCTCAGGGCTTGTAAACACCAATCAGACCCCTGTGTACTCTC 2760
Db 2701 GGCACCTGTATCTAGCTCAGGGCTTGTAAACACCAATCAGACCCCTGTGTACTCTC 2760
QY 2761 AGGGTATGTAAATGACCAATCCAGACTGTGTATCTAGCTCAGGGATGTAAATATACCAATC 2820
Db 2761 AGGGTATGTAAATGACCAATCCAGACTGTGTATCTAGCTCAGGGATGTAAATATACCAATC 2820
QY 2821 GAAGAGACCAACCAAGCGCTTGTGTAGCAATAAAGCTTCTATCCTGGGTGAGGT 2880
Db 2821 GAAGAGACCAACCAAGCGCTTGTGTAGCAATAAAGCTTCTATCCTGGGTGAGGT 2880
QY 2881 GGGCTGATCCGAAAGAGATCGAGAGGAGATAAAGGTGGGGCTTTTATAGAT 2940
Db 2881 GGGCTGATCCGAAAGAGATCGAGAGGAGATAAAGGTGGGGCTTTTATAGAT 2940
QY 2941 TTGGGTAGGTAAAGGAAATTTACAGTCAAAAGGGGCTTGTCTGTGGCGGAGAGTGG 3000
Db 2941 TTGGGTAGGTAAAGGAAATTTACAGTCAAAAGGGGCTTGTCTGTGGCGGAGAGTGG 3000
QY 3001 GGGGTGCAAGGTCTAGTGGGGGCTTTTGTAGCCAGAGTGGCAAGGAAAGACT 3060
Db 3001 GGGGTGCAAGGTCTAGTGGGGGCTTTTGTAGCCAGAGTGGCAAGGAAAGACT 3060
QY 3061 TTCAAGAGTATGTCTATCAATTAAGGCAAGGAGCCGCAATTAACACTTGTGTGGTG 3120
Db 3061 TTCAAGAGTATGTCTATCAATTAAGGCAAGGAGCCGCAATTAACACTTGTGTGGTG 3120
QY 3121 GAATGTATCAATTAAGTGGGGGAGGCAATTAACACTTGTGTGTAGTCTTCAAGTTAC 3180
Db 3121 GAATGTATCAATTAAGTGGGGGAGGCAATTAACACTTGTGTGTAGTCTTCAAGTTAC 3180
QY 3181 TTGAGGCACTGTGGGCTATATGTGCAAGTTACAGGAGGATGCGATGGCTTGGCT 3240
Db 3181 TTGAGGCACTGTGGGCTATATGTGCAAGTTACAGGAGGATGCGATGGCTTGGCT 3240
QY 3241 CAGAGGCTTACAGACTCTGTGGGGGCTTGGAGAAATGTTGTGCGACACTCTGTAT 3300
Db 3241 CAGAGGCTTACAGACTCTGTGGGGGCTTGGAGAAATGTTGTGCGACACTCTGTAT 3300
QY 3301 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTAGCTCAGGGATGTAAAGCA 3360
Db 3301 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTAGCTCAGGGATGTAAAGCA 3360
QY 3361 CCATATCAGGCGCTGTCTAAACAGACACTCGGCTCTACCAATCAGAGATGTGGGTG 3420
Db 3361 CCATATCAGGCGCTGTCTAAACAGACACTCGGCTCTACCAATCAGAGATGTGGGTG 3420
QY 3421 GGGCAGATAGAGAAATAAAGCAGGCTGCCGAGCCAGAGTGGCAACGGCAGAGTCC 3480
Db 3421 GGGCAGATAGAGAAATAAAGCAGGCTGCCGAGCCAGAGTGGCAACGGCAGAGTCC 3480
QY 3481 CTATCCAAATATGAGAGCTTTGTCTTTGTGTGTGCGATAAATCTTACTGCTG 3540
Db 3481 CTATCCAAATATGAGAGCTTTGTCTTTGTGTGTGCGATAAATCTTACTGCTG 3540
QY 3541 CTTTGGGTGTCACACGCTTTTATAGCTGTAAACACTCAGCAAGAGGCTGTGAGCTTC 3600
Db 3541 CTTTGGGTGTCACACGCTTTTATAGCTGTAAACACTCAGCAAGAGGCTGTGAGCTTC 3600
QY 3601 ACTCTGAAAGCACTAAGACAGAGCCAGCGGAGAGATGAACAACTCGGGCGGCGT 3660
|||||

Db 3601 ACTCTGAAAGCACTAAGACAGACCCAGCGGAGAGATGAACAACTCCGGCGGCT 3660
QY 3661 GCTTTAAGAGCTATTAAGACTCACCGCAAGGCTGTGAGCTTCACTCCAGCCAGCAGA 3720
Db 3661 GCTTTAAGAGCTATTAAGACTCACCGCAAGGCTGTGAGCTTCACTCCAGCCAGCAGA 3720
QY 3721 CCAGGAAACCCAGGAAAGAAATGCGAATCATCTGAACATCAGAAAGAAACT 3780
Db 3721 CCAGGAAACCCAGGAAAGAAATGCGAATCATCTGAACATCAGAAAGAAACT 3780
QY 3781 CCAGATCACACCTTAAAGAGCTGTAAACACTCAGTGGAGGCTCGGGCTCTCTTG 3840
Db 3781 CCAGATCACACCTTAAAGAGCTGTAAACACTCAGTGGAGGCTCGGGCTCTCTTG 3840
QY 3841 AAGTCACTGAGACCAACACTCAGCAATTTGAGACAGCCAGAGATTGAGATCAGC 3900
Db 3841 AAGTCACTGAGACCAACACTCAGCAATTTGAGACAGCCAGAGATTGAGATCAGC 3900
QY 3901 CTGGGCAACATGATGAATGCGCTCTGTGCAAAAAAATTTACAAAAATTTGGCGG 3960
Db 3901 CTGGGCAACATGATGAATGCGCTCTGTGCAAAAAAATTTACAAAAATTTGGCGG 3960
QY 3961 AGCATGGGTGCGTGGCTGTGGTCCAGCTACCGCGGAGGCTAAAGTGGAGATCGCT 4020
Db 3961 AGCATGGGTGCGTGGCTGTGGTCCAGCTACCGCGGAGGCTAAAGTGGAGATCGCT 4020
QY 4021 TGAGCCTGGGAGGTGAAGACTGCAAGTGTGTATTTGACCAAGCCCTCTAGCTGGG 4080
Db 4021 TGAGCCTGGGAGGTGAAGACTGCAAGTGTGTATTTGACCAAGCCCTCTAGCTGGG 4080
QY 4081 GGCAGACTGAGACCTGTGTTCCCTCCGCAAAAAATTTGCAAAAGTGTAAAGGT 4140
Db 4081 GGCAGACTGAGACCTGTGTTCCCTCCGCAAAAAATTTGCAAAAGTGTAAAGGT 4140
QY 4141 GCTGTATATGGCTAGGGGAGGCTGATGCTGTATCCAGACTTTGGGAAAGCGAG 4200
Db 4141 GCTGTATATGGCTAGGGGAGGCTGATGCTGTATCCAGACTTTGGGAAAGCGAG 4200
QY 4201 GCGGGCGGGTCACTAAGGTGAGAGGTGTAGACACCTGCGCAACATGAGAAAGCCC 4260
Db 4201 GCGGGCGGGTCACTAAGGTGAGAGGTGTAGACACCTGCGCAACATGAGAAAGCCC 4260
QY 4261 ATCTCTTCTAAAAATTAACAAATTTAGCGGCTGTGGGGAGTGTGAGACATGCTTAA 4320
Db 4261 ATCTCTTCTAAAAATTAACAAATTTAGCGGCTGTGGGGAGTGTGAGACATGCTTAA 4320
QY 4321 TCCAGCTACTCAGAGGCTGAGGAGAGATCACTTGAACCCAGAGGGGGGCTTGC 4380
Db 4321 TCCAGCTACTCAGAGGCTGAGGAGAGATCACTTGAACCCAGAGGGGGGCTTGC 4380
QY 4381 AGTGAGCCGAGATCGTCATTTGCACTCAACCCACTCCAGCTGGGCAAGAGCCAAA 4440
Db 4381 AGTGAGCCGAGATCGTCATTTGCACTCAACCCACTCCAGCTGGGCAAGAGCCAAA 4440
QY 4441 CTCTGTCTTAAAAAATTTAAAAAATTTGCTGTGCAATTAAGAGGTGTGCAATAG 4500
Db 4441 CTCTGTCTTAAAAAATTTAAAAAATTTGCTGTGCAATTAAGAGGTGTGCAATAG 4500
QY 4501 TTGCGAGGCAACATGTTTAAAGATGTGAGACTCTGCTTCCATGTGCTGTAAACC 4560
Db 4501 TTGCGAGGCAACATGTTTAAAGATGTGAGACTCTGCTTCCATGTGCTGTAAACC 4560
QY 4561 CACCTTCAGAGCCAGGTGAGTGGCTCATGTATTAATCCAGCACTTTTGGAGGCGAG 4620
Db 4561 CACCTTCAGAGCCAGGTGAGTGGCTCATGTATTAATCCAGCACTTTTGGAGGCGAG 4620
QY 4621 GCGGGTGTGATCAGCTGTGAGGAGTTCAGAGACCACTGAGCACCACATGTGAAAT 4680
Db 4621 GCGGGTGTGATCAGCTGTGAGGAGTTCAGAGACCACTGAGCACCACATGTGAAAT 4680
QY 4681 CCCAGCTCTACTAAAAATTAACAAATTTAGATGAGAGATGTTGATGCTTAAATCCAC 4740
Db 4681 CCCAGCTCTACTAAAAATTAACAAATTTAGATGAGAGATGTTGATGCTTAAATCCAC 4740

4741 CTACTTGGAGGCTGAGGAGGAAATCATCTAGAACAGGGAGGCGGAGGTTGTGTGAG 4800
4741 CTACTTGGAGGCTGAGGAGGAAATCATCTAGAACAGGGAGGCGGAGGTTGTGTGAG 4800
4801 CCGAGATGATGTCATCTGACCTCAGCCTGAGCAATGAGCGAAATCTCATCTCAAAAAAAC 4860
4801 CCGAGATGATGTCATCTGACCTCAGCCTGAGCAATGAGCGAAATCTCATCTCAAAAAAAC 4860
4861 AACAAACAAAAACCCACTCTCTACTCCAGGAGGAGCTGGGTACAGAGCTGGCCACATCACT 4920
4861 AACAAACAAAAACCCACTCTCTACTCCAGGAGGAGCTGGGTACAGAGCTGGCCACATCACT 4920
4921 GCAAGGTCTGAGGACACAGAGCTAAGGGGAGAGCTCAGAGACCGGGAGCAGATAACAGAG 4980
4921 GCAAGGTCTGAGGACACAGAGCTAAGGGGAGAGCTCAGAGACCGGGAGCAGATAACAGAG 4980
4981 TGTGAGATCACTGTGTGAGATCAGACGTCCTGCCATTGTTGTTGACCAAGGAGGCGCCCA 5040
4981 TGTGAGATCACTGTGTGAGATCAGACGTCCTGCCATTGTTGTTGACCAAGGAGGCGCCCA 5040
5041 AGCAGCAGAGATGGCCCATCAGTACACATCCATCTTCATCCAGAGATGTCTGTTT 5100
5041 AGCAGCAGAGATGGCCCATCAGTACACATCCATCTTCATCCAGAGATGTCTGTTT 5100
5101 CTGGCAGCTGGGGTAAATTAGACAGAGAGTGAAGTCTGTTGGTGTGTCAGTCAAGAC 5160
5101 CTGGCAGCTGGGGTAAATTAGACAGAGAGTGAAGTCTGTTGGTGTGTCAGTCAAGAC 5160
5161 TGCCCCAGGAGGCTTGTGGCTGTGTAGAAAAAGTTACAGGCTTAGCGGGGACGGTGGC 5220
5161 TGCCCCAGGAGGCTTGTGGCTGTGTAGAAAAAGTTACAGGCTTAGCGGGGACGGTGGC 5220
5221 TCAGGCGGTATATCCAGACCTTGGGAGGCGGAGGGGTGATCAGAGGTTCAGAGA 5280
5221 TCAGGCGGTATATCCAGACCTTGGGAGGCGGAGGGGTGATCAGAGGTTCAGAGA 5280
5281 TCAGGCGGTATATCCAGACCTTGGGAGGCGGAGGGGTGATCAGAGGTTCAGAGA 5280
5281 TCAGGCGGTATATCCAGACCTTGGGAGGCGGAGGGGTGATCAGAGGTTCAGAGA 5280
5341 CCGGCGAGTGTGGGGGACCTGTAGTTCCAGCTCTGGGAGGCTGAGAGGAGAAATG 5400
5341 CCGGCGAGTGTGGGGGACCTGTAGTTCCAGCTCTGGGAGGCTGAGAGGAGAAATG 5400
5401 GCGTGAACCGAGAGGCGAGATTTGACAGTCCAGATTCGGCCACAGCTCCAGCCT 5460
5401 GCGTGAACCGAGAGGCGAGATTTGACAGTCCAGATTCGGCCACAGCTCCAGCCT 5460
5461 GGGGAGCAGAGCAAGACTCCATCTGGAAGAAAAAGAAAGTTCAAGTCTGAGCCAGA 5520
5461 GGGGAGCAGAGCAAGACTCCATCTGGAAGAAAAAGAAAGTTCAAGTCTGAGCCAGA 5520
5521 GGGCCAGGCTTAATTTCTGTACATTACCATGACCTTGGGCAAGGACCTTCCTCCCTGGC 5580
5521 GGGCCAGGCTTAATTTCTGTACATTACCATGACCTTGGGCAAGGACCTTCCTCCCTGGC 5580
5581 CCAATTCAGGGGTTGGAAATGCACTCCAAAGTCCCTTCCAGCATTAACGCTGATGTTTC 5640
5581 CCAATTCAGGGGTTGGAAATGCACTCCAAAGTCCCTTCCAGCATTAACGCTGATGTTTC 5640
5641 CCAATTCAGGGGTTGGAAATGCACTCCAAAGTCCCTTCCAGCATTAACGCTGATGTTTC 5640
5641 CCAATTCAGGGGTTGGAAATGCACTCCAAAGTCCCTTCCAGCATTAACGCTGATGTTTC 5640
5641 TAAATGAGAGATGGGGAGTTCCTCCCTCCTCAGCCAGCCGCTGTCACCTTAAGT 5700
5641 TAAATGAGAGATGGGGAGTTCCTCCCTCCTCAGCCAGCCGCTGTCACCTTAAGT 5700
5701 GAATGAGAGAGTCACTGTCTCCATCCCGAGTTCCTCAAGGCTTGGGAGACCTTAC 5760
5701 GAATGAGAGAGTCACTGTCTCCATCCCGAGTTCCTCAAGGCTTGGGAGACCTTAC 5760
5761 TGTGAGGCTGTGACAGAGAGTGAAGTCAAGTGAAGCCCAATGCTCGAAGGGTCTTG 5820
5761 TGTGAGGCTGTGACAGAGAGTGAAGTCAAGTGAAGCCCAATGCTCGAAGGGTCTTG 5820

5821 CCTCATTCGGGACAGACATCCGGTTTCTCTGCTCTACCGGAGATTAGGGGCTTAC 5880
5821 CCTCATTCGGGACAGACATCCGGTTTCTCTGCTCTACCGGAGATTAGGGGCTTAC 5880
5881 CGAATGATCATGGGGGGGGGGGGTCTGGGGGAGTTCCAGCTAATCAATTTGGGA 5940
5881 CGAATGATCATGGGGGGGGGGGGTCTGGGGGAGTTCCAGCTAATCAATTTGGGA 5940
5941 CAGGACAGCTTGAATCTTCAATGTTGCTATCCAAAGTGTGGGTGGGACAGACCAA 6000
5941 CAGGACAGCTTGAATCTTCAATGTTGCTATCCAAAGTGTGGGTGGGACAGACCAA 6000
6001 GACCAATGCTTATCTCAGTGAAGGCTCAGAGAGTCTCCAGACAGGAGCTCCGG 6060
6001 GACCAATGCTTATCTCAGTGAAGGCTCAGAGAGTCTCCAGACAGGAGCTCCGG 6060
6061 AGAGTTTGGGGTAGAATGGAGAACCCAGCTTCTTTTCTCTCTTGAATTTGGG 6120
6061 AGAGTTTGGGGTAGAATGGAGAACCCAGCTTCTTTTCTCTCTTGAATTTGGG 6120
6121 GGGTTGGGGAGAGGCTTGAAGATCCCAAGAGAGGGGCAAGACATCCCAAG 6180
6121 GGGTTGGGGAGAGGCTTGAAGATCCCAAGAGAGGGGCAAGACATCCCAAG 6180
6181 TCTGCAGAGCAG 6235
6181 TCTGCAGAGCAG 6235

RESULT 3
US-09-305-384-1
; Sequence 1, Application US/09305384
; Patent No. 6242218
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/017001
; CURRENT APPLICATION NUMBER: US/09/305,384
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,649
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-305-384-1

Query Match 100.0%; Score 6235; DB 3; Length 6679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GATCACTGAGGACAGTAGTTCAGAACCAAGCCTGGGAGCATAGGAGACGTCTCTACG 60
20 GATCACTGAGGACAGTAGTTCAGAACCAAGCCTGGGAGCATAGGAGACGTCTCTACG 79
61 AAAAATCAAAAAATATATGCGCGGATGGTGTGCTACAGTCTTAATCCCTGAACCTTGGG 120
80 AAAAATCAAAAAATATATGCGCGGATGGTGTGCTACAGTCTTAATCCCTGAACCTTGGG 139
121 ACATCAAGGCAAGTGGATCACTTGAAGTTCAGAGTTCGAGACTAGCTGGCCACATGCT 180
140 ACATCAAGGCAAGTGGATCACTTGAAGTTCAGAGTTCGAGACTAGCTGGCCACATGCT 199
181 GAAACCTTATCTCAGTCAAAAAATATACCAAGGATGTGTGACAGGACACTGTA 240
200 GAAACCTTATCTCAGTCAAAAAATATACCAAGGATGTGTGACAGGACACTGTA 259
241 ATCCGGGTACTCAGAGAGGCTGAGGACAGAGATGCACTGAAACCAAGAGGGGAGGTTG 300

Dh 260 ATCCCGGCTACTAGGAGGCTGAGGCGAGGAACTCACTTAACCCAGAGCGGAGGTTG 319
Qy 301 CAGTAGCTGAGATCACACCACCTGCTCCAGCCTGGGTGACAGAGCAACTCTATCTC 360
Dh 320 CAGTAGCTGAGATCACACCACCTGCTCCAGCCTGGGTGACAGAGCAACTCTATCTC 379
Qy 361 AAAAAAAAAAAAAAAAAAATTAGCCAGGCATGTAGTGCACACCTCTAGTCTCAG 420
Dh 380 AAAAAAAAAAAAAAAAAAATTAGCCAGGCATGTAGTGCACACCTCTAGTCTCAG 439
Qy 421 CTACTCGAGGCTGAGTGGGAGGATCACTTGAACCTGGGGGCGTAAGGCTTCACTGA 480
Dh 440 CTACTCGAGGCTGAGTGGGAGGATCACTTGAACCTGGGGGCGTAAGGCTTCACTGA 499
Qy 481 GCCAAGATCATGCCACTACATCCAGCCTGGGCAACAGAGAGAGACCCTCTCTAATAAA 540
Dh 500 GCCAAGATCATGCCACTACATCCAGCCTGGGCAACAGAGAGAGACCCTCTCTAATAAA 559
Qy 541 AATTAATTAATTAAGAAAAAACAGCTGTGTTATGTCTCTGCTGCTCAATCACTACT 600
Dh 560 AATTAATTAATTAAGAAAAAACAGCTGTGTTATGTCTCTGCTGCTCAATCACTACT 619
Qy 601 ATGATATAGTTGGCAAACTCAAGATCCAGATGTAATTTTATAGGCTTGGGGCGT 660
Dh 620 ATGATATAGTTGGCAAACTCAAGATCCAGATGTAATTTTATAGGCTTGGGGCGT 679
Qy 661 ATGCTCTGTCACAATCACTGCTGCTCTCTTCTAGCACAAAGCAGCTATTAACAAT 720
Dh 680 ATGCTCTGTCACAATCACTGCTGCTCTCTTCTAGCACAAAGCAGCTATTAACAAT 739
Qy 721 ACATACATGAATTTTATAGACATCGAGATTTGAATTCATATGATTTTACATTTTAT 780
Dh 740 ACATACATGAATTTTATAGACATCGAGATTTGAATTCATATGATTTTACATTTTAT 799
Qy 781 AAAAAAAAAAAAAAAAAATTTCCCTAACACATTTAAAGTGAAGGCGGCGCACGCG 840
Dh 800 AAAAAAAAAATTTTAAATTTTCCCTAACACATTTAAAGTGAAGGCGGCGCACGCG 859
Qy 841 GCCATGTCACGCGCTGTAATTCAGCACTTTGGAGGCTGAGTGGGCGAGATCACTTGAG 900
Dh 860 GCCATGTCACGCGCTGTAATTCAGCACTTTGGAGGCTGAGTGGGCGAGATCACTTGAG 919
Qy 901 ATCAACAGTTTCGAGACCAAGCCTGGCCAACTAGCAAAACCCCATTTTACTAAAAATAA 960
Dh 920 ATCAACAGTTTCGAGACCAAGCCTGGCCAACTAGCAAAACCCCATTTTACTAAAAATAA 979
Qy 961 AAAAAAAAAAGCTGAGTGCACACCTGTGATCCAGCTACTTGGAGGCTGAGGCA 1020
Dh 980 AAAAAAAAAAGCTGAGTGCACACCTGTGATCCAGCTACTTGGAGGCTGAGGCA 1039
Qy 1021 GGAAGATCGCTGTAACCTGGGAAAGCGGAGGTTGCAGTGAAGCCAACTATGCACTGCAC 1080
Dh 1040 GGAAGATCGCTGTAACCTGGGAAAGCGGAGGTTGCAGTGAAGCCAACTATGCACTGCAC 1099
Qy 1081 TCCAGCCTGGGTGACAGAGTGAAGTCTCTCAACGAAAAAAAAAAAGTGTAAAGGCAT 1140
Dh 1100 TCCAGCCTGGGTGACAGAGTGAAGTCTCTCAACGAAAAAAAAAAAGTGTAAAGGCAT 1159
Qy 1141 TCCTAATTCAGTACATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1200
Dh 1160 TCCTAATTCAGTACATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1219
Qy 1201 ACCGTGAAGTAGAGTTGCTGTGCACAGAGATACACATTTCCATTAATAGACACT 1260
Dh 1220 ACCGTGAAGTAGAGTTGCTGTGCACAGAGATACACATTTCCATTAATAGACACT 1279
Qy 1261 ACCAAGTTGCCATCCAGAGAGGTTTTTTTTTACAACTTACACTCCCCCAGCAACAAT 1320
Dh 1280 ACCAAGTTGCCATCCAGAGAGGTTTTTTTTTACAACTTACACTCCCCCAGCAACAAT 1339
Qy 1321 GAGAGTTACTCAGATCTTTTACAAAGATGCTTAAAGCCAGTACAGATGAAGAAAGGA 1380
Dh 1340 GAGAGTTACTCAGATCTTTTACAAAGATGCTTAAAGCCAGTACAGATGAAGAAAGGA 1399

Qy 1381 AGTGGAGGGGAAAGCTCCAGCCCTTTCTAACTGAAGAAATACCTGTAGAGCCTTCT 1440
Dh 1400 AGTGGAGGGGAAAGCTCCAGCCCTTTCTAACTGAAGAAATACCTGTAGAGCCTTCT 1459
Qy 1441 GGATGCTGGAAGATGAATTAACGGGGGCTCTGTGAGGCTCCGCCCTGTCAATCACTGTG 1500
Dh 1460 GGATGCTGGAAGATGAATTAACGGGGGCTCTGTGAGGCTCCGCCCTGTCAATCACTGTG 1519
Qy 1501 ACTTCTGAGCCTCCAGTCCAGTCTCAGCCCCCATGTGTCATGGCCAGTGAATAGGCCCT 1560
Dh 1520 ACTTCTGAGCCTCCAGTCCAGTCTCAGCCCCCATGTGTCATGGCCAGTGAATAGGCCCT 1579
Qy 1561 CACTCTGTGTTGGTCTTATTTCTCCCATGTGGGGCTGAAGTCTGTGATTAAGCCGTTAT 1620
Dh 1580 CACTCTGTGTTGGTCTTATTTCTCCCATGTGGGGCTGAAGTCTGTGATTAAGCCGTTAT 1639
Qy 1621 TCAAGATGTACAGCTTTCTTGACAGGAAGTGTGTACAGAAACAGCAGGGGCTTGGA 1680
Dh 1640 TCAAGATGTACAGCTTTCTTGACAGGAAGTGTGTGTACAGAAACAGCAGGGGCTTGGA 1699
Qy 1681 AGATGATCTAATCCGCAAAATCCTACCTGGTCCAGCCACAGCTAGTTGTGATCTTGAC 1740
Dh 1700 AGATGATCTAATCCGCAAAATCCTACCTGGTCCAGCCACAGCTAGTTGTGATCTTGAC 1759
Qy 1741 AAGTTTTTCACTTCTGTGAGGCCATCCCTTGGCTACACACACACATTTGTTGACAGGA 1800
Dh 1760 AAGTTTTTCACTTCTGTGAGGCCATCCCTTGGCTACACACACACATTTGTTGACAGGA 1819
Qy 1801 TGAAGATGACGAATCCCTTACACCTGTATATCCAGCACTTTGGAGGCCCAAGGGGCTGG 1860
Dh 1820 TGAAGATGACGAATCCCTTACACCTGTATATCCAGCACTTTGGAGGCCCAAGGGGCTGG 1879
Qy 1861 ATGGGCTGAGCCTGAGAGGTGACAGCATGGCGGAGTCCACAGCCCTGTGGCGCTC 1920
Dh 1880 ATGGGCTGAGCCTGAGAGGTGACAGCATGGCGGAGTCCACAGCCCTGTGGCGCTC 1939
Qy 1921 GGGCGCTCTCTGCTGGGCTGCCACTTGGGTGACACTTTGAGAGAGCCCTTCAAGCCACG 1980
Dh 1940 GGGCGCTCTCTGCTGGGCTGCCACTTGGGTGACACTTTGAGAGAGCCCTTCAAGCCACG 1999
Qy 1981 CTGCACGTGTGGAGAGCCCTTTTGTGGGTGGGCAAGGCAAGCGGCTCCCTCACTTGC 2040
Dh 2000 CTGCACGTGTGGAGAGCCCTTTTGTGGGTGGGCAAGGCAAGCGGCTCCCTCACTTGC 2059
Qy 2041 AGGAGGTGTGAGAGGAGGAGGCTCAACAGAGAACGGGGCTGGCGACAGGCGCTTGGGGG 2100
Dh 2060 AGGAGGTGTGAGAGGAGGAGGCTCAACAGAGAACGGGGCTGGCGACAGGCGCTTGGGGG 2119
Qy 2101 CAGCTGAGTTCCGGGTGGGCTGTGGGCTTGGCGGGCCCGCACTGGAGACGCGGGCAG 2160
Dh 2120 CAGCTGAGTTCCGGGTGGGCTGTGGGCTTGGCGGGCCCGCACTGGAGACGCGGGCAG 2179
Qy 2161 CCCTGCCAGGCCCCCGGCAATGAGAGGCTTGAACCCCGGGGCGAGGCGCTCGAGAGGTGT 2220
Dh 2180 CCCTGCCAGGCCCCCGGCAATGAGAGGCTTGAACCCCGGGGCGAGGCGCTCGAGAGGTGT 2239
Qy 2221 ACTGGGTGCCCAAGCAAGTGCACGCGCGGCGCTGTGCTCGCTGATTTCTCACTGGGC 2280
Dh 2240 ACTGGGTGCCCAAGCAAGTGCACGCGCGGCGCTGTGCTCGCTGATTTCTCACTGGGC 2299
Qy 2281 CTTAGCAGCTTCCCGGGGGCAAGGCTCGGGAACCTGACGCGCGCATGAGCTTCC 2340
Dh 2300 CTTAGCAGCTTCCCGGGGGCAAGGCTCGGGAACCTGACGCGCGCATGAGCTTCC 2359
Qy 2341 CTTTCATGGGCTCTGTGTGGGCGCGGAGGCTCCCGGAGACACACACCCCTGCTCCACAG 2400
Dh 2360 CTTTCATGGGCTCTGTGTGGGCGCGGAGGCTCCCGGAGACACACACCCCTGCTCCACAG 2419
Qy 2401 CGCCCAAGTCCCATGACACAGCAAGGCTGAGAAGTGTGGGGCCAGCGGCAAGCGGACTGG 2460
Dh 2420 CGCCCAAGTCCCATGACACAGCAAGGCTGAGAAGTGTGGGGCCAGCGGCAAGCGGACTGG 2479

QY 2461 CAGCAGCTACCCCTGAGCCCTGTGGGGAATCCACTGGGTGAAGCCAGCTGGGCTCT 2520
|||||
Db 2480 CAGCAGCTACCCCTGAGCCCTGTGGGGAATCCACTGGGTGAAGCCAGCTGGGCTCT 2539
|||||
QY 2521 GAGTCTGTGTGAGACTTGTGAGAACCTTATGTCTAGCTCAAGGATCGTAATATACCAAT 2580
|||||
Db 2540 GAGTCTGTGTGAGACTTGTGAGAACCTTATGTCTAGCTCAAGGATCGTAATATACCAAT 2599
|||||
QY 2581 CAGCAGCCCTGTGTCTAGCTCAAGGCTGTGTGATGATCACCACATCCACACTCTGTATAGCT 2640
|||||
Db 2600 CAGCAGCCCTGTGTCTAGCTCAAGGCTGTGTGATGATCACCACATCCACACTCTGTATAGCT 2659
|||||
QY 2641 ACTGTATGGGGCTGTGAGAACCTTATGTCTAGCTCAAGGATCGTAATATACCAATC 2700
|||||
Db 2660 ACTGTATGGGGCTGTGAGAACCTTATGTCTAGCTCAAGGATCGTAATATACCAATC 2719
|||||
QY 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCCTGTGTAGCTC 2760
|||||
Db 2720 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCCTGTGTAGCTC 2779
|||||
QY 2761 AGGCTATGTATGATCACCACATCCAGACTCTGTATCTGGCTACTTTCATGGGCATCCGTCT 2820
|||||
Db 2780 AGGCTATGTATGATCACCACATCCAGACTCTGTATCTGGCTACTTTCATGGGCATCCGTCT 2839
|||||
QY 2821 GAAGAGACCAACCAAGAGCTTGTGTGAGCAATAAAGCTCTATCACCCTGGGTGACAGT 2880
|||||
Db 2840 GAAGAGACCAACCAAGAGCTTGTGTGAGCAATAAAGCTCTCTATCACCCTGGGTGACAGT 2899
|||||
QY 2881 GGGCTGAGTCCGAAAAGAGAGTCAAGCAAGGAGATAAAGGTGGGGCCGTTTATAGAT 2940
|||||
Db 2900 GGGCTGAGTCCGAAAAGAGAGTCAAGCAAGGAGATAAAGGTGGGGCCGTTTATAGAT 2959
|||||
QY 2941 TTGGGTAGTAAAGAAAATTTACAGTCAAAAGGGGTTTGTCTCTGGGGGACAGAGTGG 3000
|||||
Db 2960 TTGGGTAGTAAAGAAAATTTACAGTCAAAAGGGGTTTGTCTCTGGGGGACAGAGTGG 3019
|||||
QY 3001 GGGGTCCCAAGGCTCTAGTGGGGGCTTTTGTAGCCAGAGATGAGCCAGGAAAAGACT 3060
|||||
Db 3020 GGGGTCCCAAGGCTCTAGTGGGGGCTTTTGTAGCCAGAGATGAGCCAGGAAAAGACT 3079
|||||
QY 3061 TTCAAGATATATTCATCAATTAAGGCAAGACCCTGATTAACACCTCTTTTGTGTG 3120
|||||
Db 3080 TTCAAGATATATTCATCAATTAAGGCAAGACCCTGATTAACACCTCTTTTGTGTG 3139
|||||
QY 3121 GAATGTATCATGTTAAGTGGGGGAGGCAATATTCATCTTTTGTGTATTTCTTAGTATAC 3180
|||||
Db 3140 GAATGTATCATGTTAAGTGGGGGAGGCAATATTCATCTTTTGTGTATTTCTTAGTATAC 3199
|||||
QY 3181 TTCAAGCCATCTGGGCGTATATGTGCAAGTTACAGGGGATCGATGGCTTGGCTTGGGCT 3240
|||||
Db 3200 TTCAAGCCATCTGGGCGTATATGTGCAAGTTACAGGGGATCGATGGCTTGGCTTGGGCT 3259
|||||
QY 3241 CAGAGGCTTGACACCTACTGTGTGGGGCTTGGAGAAATGTTTGTGTGACACTCTGTAT 3300
|||||
Db 3260 CAGAGGCTTGACACCTACTGTGTGGGGCTTGGAGAAATGTTTGTGTGACACTCTGTAT 3319
|||||
QY 3301 CTACTTATCTAGTGGGAGCTGAGAACTTGTGTCTAGCTCAAGGATGTTTAACCA 3360
|||||
Db 3320 CTACTTATCTAGTGGGAGCTGAGAACTTGTGTCTAGCTCAAGGATGTTTAACCA 3379
|||||
QY 3361 CCAATCAGCGCCCTGTCAAAAAGACCACTGGGCTCTACCAATCAGAGATGTGGGTGG 3420
|||||
Db 3380 CCAATCAGCGCCCTGTCAAAAAGACCACTGGGCTCTACCAATCAGAGATGTGGGTGG 3439
|||||
QY 3421 GGGCAGATTAAGATATAAAGCAGAGCTGCCGAGCCAGCAGTGGCAAGCCAGAGCTCC 3480
|||||
Db 3440 GGGCAGATTAAGATATAAAGCAGAGCTGCCGAGCCAGCAGTGGCAAGCCAGAGCTCC 3499
|||||
QY 3481 CTATCCACAATATGGAGCTTGTCTTTTCTGTCTGGTAAATCTTCTAGTCTGCTG 3540
|||||
Db 3500 CTATCCACAATATGGAGCTTGTCTTTTCTGTCTGGTAAATCTTCTAGTCTGCTG 3559
|||||
QY 3541 CTTTGTGGTCCACAGCTTTTATGAGCTGTAACACTCACAGGAAGGTCTGACGCTTC 3600
|||||

Db 3560 CTTTGTGGTCCACAGCTCTTTATGAGCTTTAACACTCACAGGAAGGTCTGACGCTTC 3619
|||||
QY 3601 ACTCCTGAAGCCACTTAAGACCAGACGCCACCGGAGAGATGAACAACCTCCGGCCGCT 3660
|||||
Db 3620 ACTCCTGAAGCCACTTAAGACCAGACGCCACCGGAGAGATGAACAACCTCCGGCCGCT 3679
|||||
QY 3661 GCTTTAAGAGCTATTAACCTCACCAGGAGTCTGAGCTTCTACTCTCCACCGAGCGAGA 3720
|||||
Db 3680 GCTTTAAGAGCTATTAACCTCACCAGGAGTCTGAGCTTCTACTCTCCACCGAGCGAGA 3739
|||||
QY 3721 CCAGAACCCCAAGAGAAAGAAATCCGAACATCTGAATCAGAGAAAGAACT 3780
|||||
Db 3740 CCAGAACCCCAAGAGAAAGAAATCCGAACATCTGAATCAGAGAAAGAACT 3799
|||||
QY 3781 CCAGATGACACCACTTAAGAGCTGTAACTCTGAGAGGCTCCGGGCTTCTCTTGG 3840
|||||
Db 3800 CCAGATGACACCACTTAAGAGCTGTAACTCTGAGAGGCTCCGGGCTTCTCTTGG 3859
|||||
QY 3841 AAGTCAAGTGAACCAAGCACTCACAGTTTGGACACAGCCAGAGATTGAGATCAGC 3900
|||||
Db 3860 AAGTCAAGTGAACCAAGCACTCACAGTTTGGACACAGCCAGAGATTGAGATCAGC 3919
|||||
QY 3901 CTGGCAACATGATGAATGACCTCTCTGCAAAAAAATTTACAAAAATTTGGCGG 3960
|||||
Db 3920 CTGGCAACATGATGAATGACCTCTCTGCAAAAAAATTTACAAAAATTTGGCGG 3979
|||||
QY 3961 AGCATGTGTGTCGCTGCTGTGTGCTCCAGCTACCGGGAGCTAAAGTGGAGATCGCT 4020
|||||
Db 3980 AGCATGTGTGTCGCTGCTGTGTGCTCCAGCTACCGGGAGCTAAAGTGGAGATCGCT 4039
|||||
QY 4021 TGAGCTGGGAGTGAACAGTGAAGTGAAGTGTATGACACAGCCCTTAGGCTGG 4080
|||||
Db 4040 TGAGCTGGGAGTGAACAGTGAAGTGAAGTGTATGACACAGCCCTTAGGCTGG 4099
|||||
QY 4081 GGACAGACTGAGACCTCTTCCCTCCGCAAAAAAATTTGCAAAAAATGTAATAGAGT 4140
|||||
Db 4100 GGACAGACTGAGACCTCTTCCCTCCGCAAAAAAATTTGCAAAAAATGTAATAGAGT 4159
|||||
QY 4141 GCTGTATATGGCTAGCGCCAGTGGCTATGCCCTGTATCCAGCACTTTGGAGAGCCAG 4200
|||||
Db 4160 GCTGTATATGGCTAGCGCCAGTGGCTATGCCCTGTATCCAGCACTTTGGAGAGCCAG 4219
|||||
QY 4201 GGGGGGGGTACCTAAGGTGAGAGTGAAGACAGCTGGCCAAATGGAAGAGCC 4260
|||||
Db 4220 GGGGGGGGTACCTAAGGTGAGAGTGAAGACAGCTGGCCAAATGGAAGAGCC 4279
|||||
QY 4261 ATCTCTTAAATAATACAAATTAACCGGCTGTGGGGCAGTGTGTGAGCATGTGCTTAA 4320
|||||
Db 4280 ATCTCTTAAATAATACAAATTAACCGGCTGTGGGGCAGTGTGTGAGCATGTGCTTAA 4339
|||||
QY 4321 TCCAGACTACTGAGAGCTGAGGAGAGATCACTTGAACCCAGAGAGGGCGGTGGC 4380
|||||
Db 4340 TCCAGACTACTGAGAGCTGAGGAGAGATCACTTGAACCCAGAGAGGGCGGTGGC 4399
|||||
QY 4381 AGTGAAGAGATGCTGCATTTGCACTCACCACTCCAGCTGGGCAACAAGAGCCAAA 4440
|||||
Db 4400 AGTGAAGAGATGCTGCATTTGCACTCACCACTCCAGCTGGGCAACAAGAGCCAAA 4459
|||||
QY 4441 CTCTGTCTTAAAAAATTAAGAGTGTGCAATGCAATAG 4500
|||||
Db 4460 CTCTGTCTTAAAAAATTAAGAGTGTGCAATGCAATAG 4519
|||||
QY 4501 TTGCCAGCAACATGTTTAAAGATGTGAAGTCTCGCTTCCATGCTCTGTAAAAAAC 4560
|||||
Db 4520 TTGCCAGCAACATGTTTAAAGATGTGAAGTCTCGCTTCCATGCTCTGTAAAAAAC 4579
|||||
QY 4561 CACCTCAAGGCGAGGTGCAAGTGTCAATGCTTAATCCAGCACTTTGGAGGCGAG 4620
|||||
Db 4580 CACCTCAAGGCGAGGTGCAAGTGTCAATGCTTAATCCAGCACTTTGGAGGCGAG 4639
|||||
QY 4621 GCGGGTGAATCAGCTGAGAGTTCGAGAGCTGACCAACCAATGTGGAAT 4680
|||||

D 4640 GCGGGTGGATCACCCTGAGGTTCAGAGACTTCGAGACCAAGCTTGACCAACAATGGTGAAT 4639
Q 4681 CCCACCTCTACTAAAAATACAAAAATTAGATGAGCATGGTGTGCATCCTGTAAATCCAC 4740
D 4700 CCCACCTCTACTAAAAATACAAAAATTAGATGAGCATGGTGTGCATCCTGTAAATCCAC 4759
Q 4741 CTACTTGGAGGGCTGAGGAGGAAATCATTAGAACCAAGGAGGCGGAGGTTGTAGAG 4800
D 4760 CTACTTGGAGGGCTGAGGAGGAAATCATTAGAACCAAGGAGGCGGAGGTTGTAGAG 4819
Q 4801 CCGAGATCGTGCCATTGCACTCCAGCTGAGCATGAGCAAAATCCATCTCAAAAAAAC 4860
D 4820 CCGAGATCGTGCCATTGCACTCCAGCTGAGCATGAGCAAAATCCATCTCAAAAAAAC 4879
Q 4861 AACAAACAAAAACCACTCTCTACTCCAGGAGCTGGGTACAGAGCTGGGCCACATAGT 4920
D 4880 AACAAACAAAAACCACTCTCTACTCCAGGAGCTGGGTACAGAGCTGGGCCACATAGT 4939
Q 4921 GCAAGGTGCTGAGGACACAGAGCTTAAGGCGGAGCTGCAAGACCGGCGCAAGATTAACATG 4980
D 4940 GCAAGGTGCTGAGGACACAGAGCTTAAGGCGGAGCTGCAAGACCGGCGCAAGATTAACATG 4999
Q 4981 TGTGAGATCAGTGTGTAGATCAGACGTCCCTGCCATTGGTGAACACAGGCGGCCCA 5040
D 5000 TGTGAGATCAGTGTGTAGATCAGACGTCCCTGCCATTGGTGAACACAGGCGGCCCA 5059
Q 5041 AGCAACCAAGATGCCCCATCCAGTCAACATCCACTTCTCATCCAGAGATGTCTGTT 5100
D 5060 AGCAACCAAGATGCCCCATCCAGTCAACATCCACTTCTCATCCAGAGATGTCTGTT 5119
Q 5101 CTGGGACGCTGGGGTTAAATTAGGACAGAGGTGACAGCTGTGGGTGGTCACTGAC 5160
D 5120 CTGGGACGCTGGGGTTAAATTAGGACAGAGGTGACAGCTGTGGGTGGTCACTGAC 5179
Q 5161 TGGCCCAAGGAGGCTTGTGGCTGTGAAAAACCTTCAGGCTTAGCGCGGACAGTGGC 5220
D 5180 TGGCCCAAGGAGGCTTGTGGCTGTGAAAAACCTTCAGGCTTAGCGCGGACAGTGGC 5239
Q 5221 TCACGCTGTAAATCCAGCACTTTGGAGGCGGAGGCGGTGATCAGAGTCAAGAGA 5280
D 5240 TCACGCTGTAAATCCAGCACTTTGGAGGCGGAGGCGGTGATCAGAGTCAAGAGA 5299
Q 5281 TCGTGAACCATCTGGGCTTAACAGGTTGAACCCGCTCTCTAAATACAAAAAATTGG 5340
D 5300 TCGTGAACCATCTGGGCTTAACAGGTTGAACCCGCTCTCTAAATACAAAAAATTGG 5359
Q 5341 CCGGGCATGGTGGCGGACCTGTAGTTCAGCTACTCGGAGGCTGAGGACAGAGAAATG 5400
D 5360 CCGGGCATGGTGGCGGACCTGTAGTTCAGCTACTCGGAGGCTGAGGACAGAGAAATG 5419
Q 5401 GCGTGAACCCGAGAGGACAGATTGACAGTACCGGAGATGCGGCACCTGCACCTCAGCT 5460
D 5420 GCGTGAACCCGAGAGGACAGATTGACAGTACCGGAGATGCGGCACCTGCACCTCAGCT 5479
Q 5461 GGGCGACAGAGCAAGACTCCATCTGGAAGAAAAAGAAAAACGTTCAGGCTGAGCCAGA 5539
D 5480 GGGCGACAGAGCAAGACTCCATCTGGAAGAAAAAGAAAAACGTTCAGGCTGAGCCAGA 5539
Q 5521 GGGCCAGGCTGTAAATCTGTCACTTACATGACCTTGGCAAGGACATTCCTCCCTGGC 5580
D 5540 GGGCCAGGCTGTAAATCTGTCACTTACATGACCTTGGCAAGGACATTCCTCCCTGGC 5599
Q 5581 CCAATTACAGGGGTTGGATCGACTCCAGAGTCCCTTCAGCATTAACGCTGATGGTTG 5640
D 5600 CCAATTACAGGGGTTGGATCGACTCCAGAGTCCCTTCAGCATTAACGCTGATGGTTG 5659
Q 5641 TAAGATGAGAGATGGGGAGTTCCCTCTCTACCCCAAGCCCGCTGTCACTTCAAGGT 5700
D 5660 TAAGATGAGAGATGGGGAGTTCCCTCTCTACCCCAAGCCCGCTGTCACTTCAAGGT 5719
Q 5701 GAATGACAGAGGAAATGACGTGTCCCAATCCGCAAGTTCGAAGACCTTGGAGACCTTAC 5760
D 5720 GAATGACAGAGGAAATGACGTGTCCCAATCCGCAAGTTCGAAGACCTTGGAGACCTTAC 5779

Q 5761 TGTGAGGCTGTGACAGAGAGGTGAAGGTTCAGGTGAGCCAAATCCCTCGAAGGCTTGG 5820
D 5780 TGTGAGGCTGTGACAGAGAGGTGAAGGTTCAGGTGAGCCAAATCCCTCGAAGGCTTGG 5839
Q 5821 CCGTATTCGGGACAGACATCCGGTTTCCCTGTGGCTTACCGGGATTTAGGGCTTACG 5880
D 5840 CCGTATTCGGGACAGACATCCGGTTTCCCTGTGGCTTACCGGGATTTAGGGCTTACG 5899
Q 5881 CGAATGAGTATGGGGGCGGGGGGTTTCTGGGGAGATTCCAGTAAATCAATTGGGA 5940
D 5900 CGAATGAGTATGGGGGCGGGGGGTTTCTGGGGAGATTCCAGTAAATCAATTGGGA 5959
Q 5941 CAGGACAGCTCGAATTTTGATGTGCTTATCCAAATGTGGGTGGGACAGAGCCAA 6000
D 5960 CAGGACAGCTCGAATTTTGATGTGCTTATCCAAATGTGGGTGGGACAGAGCCAA 6019
Q 6001 GAACCAATGTCTTATCTACAGGTGGGGGCTCAGAGGTCTCCAGACAGGACGCTCCG 6060
D 6020 GAACCAATGTCTTATCTACAGGTGGGGGCTCAGAGGTCTCCAGACAGGACGCTCCG 6079
Q 6061 AGAATTTGGGGGTAGGAATGGAGCAACAGGCTTCTTTTCTCTTAAATTTGGG 6120
D 6080 AGAATTTGGGGGTAGGAATGGAGCAACAGGCTTCTTTTCTCTTAAATTTGGG 6139
Q 6121 GCGTTGGGGGACAGCTTGAAGATCCCAAGAGAGGGGCAAGAGACTCCCCACAG 6180
D 6140 GCGTTGGGGGACAGCTTGAAGATCCCAAGAGAGGGGCAAGAGACTCCCCACAG 6199
Q 6181 TCGGCCAGAGGAGAGAGGAGACCCGCACTCAGCTCCACTTCCCAAGGCT 6235
D 6200 TCGGCCAGAGGAGAGAGGAGACCCGCACTCAGCTCCACTTCCCAAGGCT 6254

RESULT 4
US-09-525-160B-5
; Sequence 5, Application us/09525160B
; Patent No. 6569681
; GENERAL INFORMATION:
; APPLICANT: Ivanov, Evgenii
; TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 10278/016001
; CURRENT APPLICATION NUMBER: US/09/525.160B
; CURRENT FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-160B-5

Query Match 100.0%; Score 6235; DB 4; Length 6679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 1 GATCACTTGGAGCAGAGTTCAAAGACCAAGCTTGGGACAGATAGGAGATGCTCTACG 60
D 20 GATCACTTGGAGCAGAGTTCAAAGACCAAGCTTGGGACAGATAGGAGATGCTCTACG 79
Q 61 AAAAATCAAAAAATTATGCGCGGACATGTGCTCACTCTGTAAATCTTGGG 120
D 80 AAAAATCAAAAAATTATGCGCGGACATGTGCTCACTCTGTAAATCTTGGG 139
Q 121 ACATCAAGGCAAGTGAATCACTGAGGTGAGGATTCGAGATACCTTGGCCAAATGGT 180
D 140 ACATCAAGGCAAGTGAATCACTGAGGTGAGGATTCGAGATACCTTGGCCAAATGGT 199
Q 181 GAAACCTTATCTCCACTAAAAATACAAAAATTAGCCAGGACGATGGGACGACCTGA 240
D 200 GAAACCTTATCTCCACTAAAAATACAAAAATTAGCCAGGACGATGGGACGACCTGA 259
Q 241 ATCCGCGCTACTCAGAGAGCTGAGGACAGAGAAATCACTTGAACCCAGAGAGGAGTTG 300

QY	2461	CAGCAGCTACCCCTGCAGCCCTGTGCGGAATCACTGGTGAAGCCAGCTGGCTCT	2520
Db	2480	CAGCAGCTACCCCTGCAGCCCTGTGCGGAATCACTGGTGAAGCCAGCTGGCTCT	2539
QY	2521	GAGCTGGTGGAGACTGGAGAACCTTTATGTCAGCTCAGGGATCGTAATACCAAT	2580
Db	2540	GAGCTGGTGGAGACTGGAGAACCTTTATGTCAGCTCAGGGATCGTAATACCAAT	2599
QY	2581	CAGCACCCTGTGTAGCTCAGGGTCTGTGAATGCACCAATCCACACTCTATCTAGCT	2640
Db	2600	CAGCACCCTGTGTAGCTCAGGGTCTGTGAATGCACCAATCCACACTCTATCTAGCT	2659
QY	2641	ACTGTGATGGGGCCTTGGAGAACCTTTATGTCTAGCTCAGGATTTGTAAATACACAATC	2700
Db	2660	ACTGTGATGGGGCCTTGGAGAACCTTTATGTCTAGCTCAGGATTTGTAAATACACAATC	2719
QY	2701	GGCACTCTGTATCTAGCTCAAGGTTTGTAAACACACCAATATAGCACCCTGTGTAGCTC	2760
Db	2720	GGCACTCTGTATCTAGCTCAAGGTTTGTAAACACCAATATAGCACCCTGTGTAGCTC	2779
QY	2761	AGGCTATGTGAATGACCAATCGACAGTCTGTATCTGTACTTTCATGGGCATCTCGT	2820
Db	2780	AGGCTATGTGAATGACCAATCGACAGTCTGTATCTGTACTTTCATGGGCATCTCGT	2839
QY	2821	GAAAGAGACACCAAAACAGGCTTTTGTGTAGGAATTAACCTTATACCTGGGTGACAGT	2880
Db	2840	GAAAGAGACACCAAAACAGGCTTTTGTGTAGGAATTAACCTTATACCTGGGTGACAGT	2899
QY	2881	GGGCTGAGTCCGAAAAAGAGTCAAGCGAAGGAGATTAAGGTGGGGCCGTTTATAGAT	2940
Db	2900	GGGCTGAGTCCGAAAAAGAGTCAAGCGAAGGAGATTAAGGTGGGGCCGTTTATAGAT	2959
QY	2941	TTGGTGGTAAAGGAAATTAACGTCAAGGGGTTTGTCTCTGGGGGCAGAGTGG	3000
Db	2960	TTGGTGGTAAAGGAAATTAACGTCAAGGGGTTTGTCTCTGGGGGCAGAGTGG	3019
QY	3001	GGGGTCGCAAGGTGCTAGTGGGGTGTCTTTTGTAGCCAGATGAGCCAGAAAAAGCAT	3060
Db	3020	GGGGTCGCAAGGTGCTAGTGGGGTGTCTTTTGTAGCCAGATGAGCCAGAAAAAGCAT	3079
QY	3061	TTTCACAAGGTATGTCAATTAAGGCAAGACCCGCCATTATACACCTCTTGTGTGTG	3120
Db	3080	TTTCACAAGGTATGTCAATTAAGGCAAGACCCGCCATTATACACCTCTTGTGTGTG	3139
QY	3121	GAATGTCAATGTTAAGTTGGGGCAGGCAATTCATCTCTTGTGTATTTCTACATTAC	3180
Db	3140	GAATGTCAATGTTAAGTTGGGGCAGGCAATTCATCTCTTGTGTATTTCTACATTAC	3199
QY	3181	TTTCAGGCCATTTGGGCGTATATGTGTGCAAGTTACAGGGATCGATGGTTGGCTGGGCT	3240
Db	3200	TTTCAGGCCATTTGGGCGTATATGTGTGCAAGTTACAGGGATCGATGGCTTGGCTGGGCT	3259
QY	3241	CAGAGGCTTGAAGCTACTCTGTGTGGGCGCTTGGAGAAATGTTTGTGTGCACACTCTGAT	3300
Db	3260	CAGAGGCTTGAAGCTACTCTGTGTGGGCGCTTGGAGAAATGTTTGTGTGCACACTCTGAT	3319
QY	3301	CTAGTTAATCTAGTGGGAGCGTGGAGAACCTTGTGTACTCTCAGGATTTGTAAACCA	3360
Db	3320	CTAGTTAATCTAGTGGGAGCGTGGAGAACCTTGTGTACTCTCAGGATTTGTAAACCA	3379
QY	3361	CCAATCTAGCGCCCTGTCAAAAACAGACCACTGGGCTCTACATCAGCAGATGTGGGTGG	3420
Db	3380	CCAATCTAGCGCCCTGTCAAAAACAGACCACTGGGCTCTACATCAGCAGATGTGGGTGG	3439
QY	3421	GGCCAGATTAAGAGATTAAGACAGGCTGCCGAGCCAGCAGTGGCCAAACGCGCACAGTCC	3480
Db	3440	GGCCAGATTAAGAGATTAAGACAGGCTGCCGAGCCAGCAGTGGCCAAACGCGCACAGTCC	3499
QY	3481	CTATTCACAATATGGCAGCTTGTCTTCTTGTCTGTTGCGATTAATCTTGCTACTGCTCG	3540
Db	3500	CTATTCACAATATGGCAGCTTGTCTTCTTGTCTGTTGCGATTAATCTTGCTACTGCTCG	3559

QY	3541	CTTTTGGGTCACACTGCTTTTATATAGCTGTATACACTACACAGAAAGTCTGCAGTTC	3600
Db	3560	CTTTTGGGTCACACTGCTTTTATATAGCTGTATACACTACACAGAAAGTCTGCAGTTC	3619
QY	3601	ACTCCGAAGCCACTTAAGACACAGAGCCACCGGGGGAATGAACAACCTCCGGCCGGCT	3660
Db	3620	ACTCCTGAAGCCACTTAAGACACAGAGCCACCGGGGGAATGAACAACCTCCGGCCGGCT	3679
QY	3661	GCCTTAAGACTATTAACACTCAACCGGAAGGTCTGCAGTTCACCTCCACGACGAGAGA	3720
Db	3680	GCCTTAAGAGCTATTAACACTCAACCGGAAGGTCTGCAGTTCACCTCCACGACGAGAGA	3739
QY	3721	CCAGCAACCCACCAGAGAGAAGAACTGGCAACACTCTGACATCATGAAGAACAACACT	3780
Db	3740	CCAGCAACCCACCAGAGAGAAGAACTGGCAACACTCTGACATCATGAAGAACAACACT	3799
QY	3781	CCAGATGCACCACTTAAGAGCTTAACACTCACTCCGAGGGGTCCGGGCTTCCTTCTTG	3840
Db	3800	CCAGATGCACCACTTAAGAGCTTAACACTCACTCCGAGGGGTCCGGGCTTCCTTCTTG	3859
QY	3841	AAGTCAGTAGAGCAACAGCACTCACCAAGTTTCGACACAAAGCCACAGAGATTGAGATAGC	3900
Db	3860	AAGTCAGTAGAGCAACAGCACTCACCAAGTTTCGACACAAAGCCACAGAGATTGAGATAGC	3919
QY	3901	CTGGGCACATGATGATAATGCCCTCTCTCGAAAAAAAATTTACAAAAATTGGCCG	3960
Db	3920	CTGGGCACATGATGATAATGCCCTCTCTCGAAAAAAAATTTACAAAAATTGGCCG	3979
QY	3961	AGCATGTGTGTCCTGCTGCTGTGGTCCAGCTACGCGGAGGCTAAAGTGGAGAGATGCT	4020
Db	3980	AGCATGTGTGTCCTGCTGCTGTGGTCCAGCTACGCGGAGGCTAAAGTGGAGAGATGCT	4039
QY	4021	TGAGCCTGGAGGTGAAGACTGCAGTGAAGCTGATTTTACCAAGCCCTTAGGCTGGG	4080
Db	4040	TGAGCCTGGAGGTGAAGACTGCAGTGAAGCTGATTTTACCAAGCCCTTAGGCTGGG	4099
QY	4081	GGACAGACTGAGAACCTGTTTCCCTCCGCAAAAAAATTACAAAAAGTGTATTAAGAGT	4140
Db	4100	GGACAGACTGAGAACCTGTTTCCCTCCGCAAAAAAATTACAAAAAGTGTATTAAGAGT	4159
QY	4141	GGCTGATATGGGTAGAGGCGAGTGGCTCATGCCCTGTATCCACACTTTGGGAAGCGAG	4200
Db	4160	GGCTGATATGGGTAGAGGCGAGTGGCTCATGCCCTGTATCCACACTTTGGGAAGCGAG	4219
QY	4201	GGGGGGGGGTCACTTAAGGTCAAGAGTGTGAGACCAAGCCCTGGCCAAACATGGAGAAACCC	4260
Db	4220	GGGGGGGGGTCACTTAAGGTCAAGAGTGTGAGACCAAGCCCTGGCCAAACATGGAGAAACCC	4279
QY	4261	ATCTCTTCTTAATAAATTAAGCCGCGTGTGGGGGCGAGTGGTGGAGCATGCTGTAA	4320
Db	4280	ATCTCTTCTTAATAAATTAAGCCGCGTGTGGGGGCGAGTGGTGGAGCATGCTGTAA	4339
QY	4321	TCCCAAGCTACTAGAGAGGCTGAGGCGAGAGAACTCACTTGAACCCAGAGAGCGCGGTTC	4380
Db	4340	TCCCAAGCTACTAGAGAGGCTGAGGCGAGAGAACTCACTTGAACCCAGAGAGCGCGGTTC	4399
QY	4381	AGTGAGCCAGATTCGTCATTCGACTCCACACCACTTCAGACTGGGCAACAAGAGCCAAA	4440
Db	4400	AGTGAGCCAGATTCGTCATTCGACTCCACACCACTTCAGACTGGGCAACAAGAGCCAAA	4459
QY	4441	CTCTGCTTTAAAAAAAATTAAGTGCCTGACATATTAAGAGTGTGCAATGCAATAG	4500
Db	4460	CTCTGCTTTAAAAAAAATTAAGTGCCTGACATATTAAGAGTGTGCAATGCAATAG	4519
QY	4501	TTGCCAAGGCAACATGTTTAAGAAATGTGAGACTCTGCTTCCATGGTCTGTTAAAAAC	4560
Db	4520	TTGCCAAGGCAACATGTTTAAGAAATGTGAGACTCTGCTTCCATGGTCTGTTAAAAAC	4579
QY	4561	CACCCCTAAGGGCAGGTGCAGTGGCTCAATGCCATATATCCACACTTTGGGAGGCGAG	4620
Db	4580	CACCCCTAAGGGCAGGTGCAGTGGCTCAATGCCATATATCCACACTTTGGGAGGCGAG	4639
QY	4621	GGGGGTGATTCACCTAGGTCAAGATTTGAGACCAAGCCCTGAGCACCACATGTTGTAAT	4680

Db 4640 GCGGGTGGATCAGCTGAGGTGAGAGTCCAGACACCTGACCAACCATGGTGAAT 4639
OY 4681 CCCACCTCTACTAAAAATACAAAAATTAGATGAGCATGGTGGTCATCCCTGAATCCAC 4740
Db 4700 CCCACCTCTACTAAAAATACAAAAATTAGATGAGCATGGTGGTCATCCCTGAATCCAC 4739
OY 4741 CTACTTGGAGGCTGAGGAGGAGAAATCATTAGAACAGGAGGCGGAGGTTGATGAG 4800
Db 4760 CTACTTGGAGGCTGAGGAGGAGAAATCATTAGAACAGGAGGCGGAGGTTGATGAG 4819
OY 4801 CCAGATCGTGCCTTCTGCTCCAGCTGAGCATGAGCGAACTCATGCAAAAAAC 4860
Db 4820 CCAGATCGTGCCTTCTGCTCCAGCTGAGCATGAGCGAACTCATGCAAAAAAC 4879
OY 4861 AACAAACAAAAACCCACTCTCTACTCCAGGAGCTGGGTACAGAGTGGGCCACATAGT 4920
Db 4880 AACAAACAAAAACCCACTCTCTACTCCAGGAGCTGGGTACAGAGTGGGCCACATAGT 4939
OY 4921 GCAAGGTGCTGAGCCACAGAGCTAAGGCGGAGCTGCGAGACCGCGGACAGATTAACAGT 4980
Db 4940 GCAAGGTGCTGAGCCACAGAGCTAAGGCGGAGCTGCGAGACCGCGGACAGATTAACAGT 4999
OY 4981 TGTGAGATCAGTGTGAGATCAGAGCTCCCTGCTGCTGAGACACAGGCGGCCCA 5040
Db 5000 TGTGAGATCAGTGTGAGATCAGAGCTCCCTGCTGCTGAGACACAGGCGGCCCA 5059
OY 5041 AGACACAGAGATGGCCCCATCCAGTACACACATCCACTTCTCATCCAGAGATGTCTTT 5100
Db 5060 AGACACAGAGATGGCCCCATCCAGTACACACATCCACTTCTCATCCAGAGATGTCTTT 5119
OY 5101 CTGGCAGCTGGGGTAAATTAAGACAGAGAGTGAAGCTCTGGGCTGGTCACTGAC 5160
Db 5120 CTGGCAGCTGGGGTAAATTAAGACAGAGAGTGAAGCTCTGGGCTGGTCACTGAC 5179
OY 5161 TGCCCCAGGAGGAGCTTGTGGCTGTAGAAAAAGTTAGAGCTTAGGCGGAGACGTGGC 5220
Db 5180 TGCCCCAGGAGGAGCTTGTGGCTGTAGAAAAAGTTAGAGCTTAGGCGGAGACGTGGC 5239
OY 5221 TCACGCTGTAAATCCAGACATTTGGAGGCGGAGGCGGTGATCAGAGGTGACGAGA 5280
Db 5240 TCACGCTGTAAATCCAGACATTTGGAGGCGGAGGCGGTGATCAGAGGTGACGAGA 5299
OY 5281 TCCTGACATCTGGCTAATACAGGTGAACCCGCTCTCTAATAAATAAAAAATTGG 5340
Db 5300 TCCTGACATCTGGCTAATACAGGTGAACCCGCTCTCTAATAAATAAAAAATTGG 5339
OY 5341 CCGGGCATGTGGCGGGACCTGTAGTTCCAGTACTCGGAGGCTGAGCAGAGATG 5400
Db 5360 CCGGGCATGTGGCGGGACCTGTAGTTCCAGTACTCGGAGGCTGAGCAGAGATG 5419
OY 5401 GCCTGAACCCGAGAGGAGGATTTGCAGTGAAGCCGAGATGCGCCACTGCACTCAGCT 5460
Db 5420 GCCTGAACCCGAGAGGAGGATTTGCAGTGAAGCCGAGATGCGCCACTGCACTCAGCT 5479
OY 5461 GGGCGACAGAGCAAGACTCCATCTGAAAAAGAAAAAGTTCAGTCTGAGCCAGA 5520
Db 5480 GGGCGACAGAGCAAGACTCCATCTGAAAAAGAAAAAGTTCAGTCTGAGCCAGA 5539
OY 5521 GGGCGACAGGCTGTAATCTGTCACTTACATGACCTTGGGAGGAGCACTTCTCCCTGGC 5580
Db 5540 GGGCGACAGGCTGTAATCTGTCACTTACATGACCTTGGGAGGAGCACTTCTCCCTGGC 5599
OY 5581 CCAATTCAGGAGGTTGGAATCGACTCAGAGGCTCTTCCAGCATTAACGTGATGGTTG 5640
Db 5600 CCAATTCAGGAGGTTGGAATCGACTCAGAGGCTCTTCCAGCATTAACGTGATGGTTG 5659
OY 5641 TAAGATGAGAGATGGGAGGTTTCCCTCTCACCCAGCCGCTGCACTCAAGGT 5700
Db 5660 TAAGATGAGAGATGGGAGGTTTCCCTCTCACCCAGCCGCTGCACTCAAGGT 5719
OY 5701 GAATGACAGAGGATGACGTGTCCCATCCGAGTTCCAAAGCCCTTGGGAGCCCTAC 5760

Db 5720 GAATGACAGAGGAGTACAGTGTCCCATCCGAGTTCCTCAAAAGCCCTTGGGAGCCCTAC 5779
OY 5761 TGTGAGGCTGTGACAGAGAGGTGAAGGTTCAGGTGAGCCAAATCCCTGAAAGGCTTTG 5820
Db 5780 TGTGAGGCTGTGACAGAGAGGTGAAGGTTCAGGTGAGCCAAATCCCTGAAAGGCTTTG 5839
OY 5821 CCTCATTCGGAGACAGATCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5880
Db 5840 CCTCATTCGGAGACAGATCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5899
OY 5881 CGAATGAGTATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5940
Db 5900 CGAATGAGTATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5959
OY 5941 CAGGACAGCTGGAATCTTGAGTGTGCTATCCAAAGTGTGGGTGGGACAGAGCCAA 6000
Db 5960 CAGGACAGCTGGAATCTTGAGTGTGCTATCCAAAGTGTGGGTGGGACAGAGCCAA 6019
OY 6001 GACCAATGCTTATCTCAGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6060
Db 6020 GACCAATGCTTATCTCAGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6079
OY 6061 AGACTTGGGAGTGAATGGAGCAACAGAGCTTCTTTTCTCTTGAATTTGGG 6120
Db 6080 AGACTTGGGAGTGAATGGAGCAACAGAGCTTCTTTTCTCTTGAATTTGGG 6139
OY 6121 GCTTGGGAGGAGGCTTGAATCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6180
Db 6140 GCTTGGGAGGAGGCTTGAATCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6199
OY 6181 TCTGCCAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6235
Db 6200 TCTGCCAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6254

RESULT 5
US-09-305-384-6
: Sequence 6, Application US/09305384
: Patent No. 6242218
: GENERAL INFORMATION:
: APPLICANT: Treco, Douglas A.
: APPLICANT: Heartlein, Michael W.
: APPLICANT: Selden, Richard F.
: TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
: FILE REFERENCE: 07236/017001
: CURRENT APPLICATION NUMBER: US/09/305,384
: EARLIER FILING DATE: 1999-05-05
: EARLIER FILING DATE: 1998-05-07
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 2834
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-305-384-6

Query Match 45.5%; Score 2834; DB 3; Length 2834;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2834; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1890 CCGGCAATCCTCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1949
OY 1950 GGTGGCACTTGAAGAGCCCTTCAAGCCAGCTGAGTGTGGAGCCCTTCTGGGCTG 2009
Db 61 GGTGGCACTTGAAGAGCCCTTCAAGCCAGCTGAGTGTGGAGCCCTTCTGGGCTG 120
OY 2010 GCCAAGGCCAGAGCCGCTTCTGAGCTTCAAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAG 2069
Db 121 GCCAAGGCCAGAGCCGCTTCTGAGCTTCAAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAG 180

QY	2070	GGAA	CCGGGGCTGCGCAGGCGCGCTTGGGGCCAGCTGGATGTCGGGGTGGCGCTT	2129
Db	181	GGAA	CCGGGGCTGGCGCAGGCGCGCTTGGCGGGCCAGCTGGATGTCGGGGTGGCGCTT	240
QY	2130	GGCGGG	CCCCCAGCTCGGAGGAGGGGGCCAGCCCTGCCAGGGCCCCGGGCATGAGAGCT	2189
Db	241	GGCGGG	CCCCCAGCTCGGAGGAGGGGGCCAGCCCTGCCAGGGCCCCGGGCATGAGAGCT	300
QY	2190	TAGC	ACCCGGGCGCAGCGGCTCGGAGGGGTGTACTGGGTGCCAGAGTAATGCCAGCCGC	2249
Db	301	TAGC	ACCCGGGCGCAGCGGCTCGGAGGGGTGTACTGGGTGCCAGAGTAATGCCAGCCGC	360
QY	2250	GGCGGT	GTGCTCGCTCGATTTTCTCACTGGGCTTACAGACCTTCCCGCGGGGACGGCTC	2309
Db	361	GGCGGT	GTGCTCGCTCGATTTTCTCACTGGGCTTACAGACCTTCCCGCGGGGACGGCTC	420
QY	2310	GGGACCT	CAGCGCCGCATAGCCTGAGGCTGCCCTCCATGAGGGCTCCTGTGGGGCCGAGCC	2369
Db	421	GGGACCT	CAGCGCCGCATAGCCTGAGGCTGCCCTCCATGAGGGCTCCTGTGGGGCCGAGCC	480
QY	2370	TCCCGAG	CAGCACACCCTGCTCACAGAGGCCAGTCCCATCGACGACGCAAGGAGCT	2429
Db	481	TCCCGAG	CAGCACACCCTGCTCACAGAGGCCAGTCCCATCGACGACGCAAGGAGCT	540
QY	2430	GAGAA	GTCCGGGGCGCAGCGGACCGGGAATGGCAGGCACTACCCCTGACGCCCTGTGGCG	2489
Db	541	GAGAA	GTCCGGGGCGCAGCGGACCGGGAATGGCAGGCACTACCCCTGACGCCCTGTGGCG	600
QY	2490	GAAT	CCACTGGGTGAAAGCAGCTGGGGCTCTGAGTCTGGTGGAGACTTGGAAACCTTTA	2549
Db	601	GAAT	CCACTGGGTGAAAGCAGCTGGGGCTCTGAGTCTGGTGGAGACTTGGAAACCTTTA	660
QY	2550	TGTCTAG	CTCAGGGATCGTAAATACCAACATCAGACACCCTGTCTAGCTCAGGGTCTGT	2609
Db	661	TGTCTAG	CTCAGGGATCGTAAATACCAACATCAGACACCCTGTCTAGCTCAGGGTCTGT	720
QY	2610	GAAT	GCACCAATCCCACTCTGTATCTAGTACTGTATGGGGCTTGGAAACCTTTAT	2669
Db	721	GAAT	GCACCAATCCCACTCTGTATCTAGTACTGTATGGGGCTTGGAAACCTTTAT	780
QY	2670	GTCTAG	CTCAGGGATGTAAATACACCAATGGGCACTGTATCTAGCTCAAGGTTTGT	2729
Db	781	GTCTAG	CTCAGGGATGTAAATACACCAATGGGCACTGTATCTAGCTCAAGGTTTGT	840
QY	2730	AAACAC	CAATCAGCACCCCTGTCTAGCTCAGGGTATGTAAATGCACCAATCGACACTC	2789
Db	841	AAACAC	CAATCAGCACCCCTGTCTAGCTCAGGGTATGTAAATGCACCAATCGACACTC	900
QY	2790	TGTATCT	GGCTACTTTCATGGGCATCCGTGTGAAGAGCCACCAACAGGCTTGTGTGA	2849
Db	901	TGTATCT	GGCTACTTTCATGGGCATCCGTGTGAAGAGCCACCAACAGGCTTGTGTGA	960
QY	2850	GCAAT	AAAGCTTATCACTGGGGTGGAGGGGTGATCCGAAAGAGAGTCAAGCA	2909
Db	961	GCAAT	AAAGCTTATCACTGGGGTGGAGGGGTGATCCGAAAGAGAGTCAAGCA	1020
QY	2910	GGGAG	ATAAAGGTGGGGCGCTTTTATAGAGATTGGGTAGTAAAGAAATTAACATCAA	2969
Db	1021	GGGAG	ATAAAGGTGGGGCGCTTTTATAGAGATTGGGTAGTAAAGAAATTAACATCAA	1080
QY	2970	AGGGGG	TTTGTCTCTGGCGGGCAGAGATGGGGGTGCGAAGGTCTCAGTGGGGTGTCT	3029
Db	1081	AGGGGG	TTTGTCTCTGGCGGGCAGAGATGGGGGTGCGAAGGTCTCAGTGGGGTGTCT	1140
QY	3030	TTTTG	GAGCGAAGATGAGCAAGAAAGACTTTACAAAGGTAAATGTCAATTAAGGCA	3089
Db	1141	TTTTG	GAGCGAAGATGAGCAAGAAAGACTTTACAAAGGTAAATGTCAATTAAGGCA	1200
QY	3090	AGGAC	CCCGCCATTAACACTCTTTTGTGGTGAATGATCAATAGTTAAGTTGGGCAAGGC	3149
Db	1201	AGGAC	CCCGCCATTAACACTCTTTTGTGGTGAATGATCAATAGTTAAGTTGGGCAAGGC	1260
QY	3150	ATAT	TCACTTCTTTGTGATCTTCAAGTACTCAGGCCATCTGGGGGTATATCTGCAAG	3209

Db	1261	ATATTACCTTCTTTTGTAATTCCTCACTACTTCAGGCCAATCGGGCCTATATGTGCAAG	1320
Oy	3210	TTTACAGGGGAATGCATATGGCTTGGGCTTGGGCTCAGAGGCTTTACAAGCTACTCTGGGGGGC	3269
Db	1321	TTTACAGGGGAATGCATATGGCTTGGGCTTGGGCTCAGAGGCTTTACAAGCTACTCTGGGGGGC	1380
Oy	3270	CTTGGAGAATGTTTGTGTGCACACTCTGTATCTTAGTTAAATCATGTAGTGGGAGCTGGAGAAC	3329
Db	1381	CTTGGAGAATGTTTGTGTGCACACTCTGTATCTTAGTTAAATCATGTAGTGGGAGCTGGAGAAC	1440
Oy	3330	CTTTGTGTCTAGCTAGGGATTTGTAAAGCACCAATCAGCCGCTCTGTAAAAACAGACCAC	3389
Db	1441	CTTTGTGTCTAGCTAGGGATTTGTAAAGCACCAATCAGCCGCTCTGTAAAAACAGACCAC	1500
Oy	3390	TGCGGCTTACCAATCAGCAGAGATGTGGGTGGGGCCAGATTAAGAGAAATAAAGACAGCTGC	3449
Db	1501	TGCGGCTTACCAATCAGCAGAGATGTGGGTGGGGCCAGATTAAGAGAAATAAAGACAGCTGC	1560
Oy	3450	CCGAGCCAGCAGCTGGCCAACGGCGACAGGTCCCTATCCAAATATNGCAGCTTGTCTTCT	3509
Db	1561	CCGAGCCAGCAGCTGGCCAACGGCGACAGGTCCCTATCCAAATATNGCAGCTTGTCTTCT	1620
Oy	3510	TGCTGTTTGCCATTAATCTTGCTACTGCTCGTTTTTGGGTCCACACTGCTTTTATGAGC	3569
Db	1621	TGCTGTTTGCCATTAATCTTGCTACTGCTCGTTTTTGGGTCCACACTGCTTTTATGAGC	1680
Oy	3570	TGTAACACTCACACGAGAGGTCTGCAGCTTCACTCCTAAGCGACTAAGACACAGCAGAGCCC	3629
Db	1681	TGTAACACTCACACGAGAGGTCTGCAGCTTCACTCCTAAGCGACTAAGACACAGCAGAGCCC	1740
Oy	3630	ACCGGGAGGAATGAACCAATCCGGCGCGCTTCCCTTAAAGACTATATMACACTACCGCGAA	3689
Db	1741	ACCGGGAGGAATGAACCAATCCGGCGCGCTTCCCTTAAAGACTATATMACACTACCGCGAA	1800
Oy	3690	GGTCTGGCAGCTTCACTCCTCAGCGCCAGAGACCAAGAACCCACAGAGAAAGAAACATGCG	3749
Db	1801	GGTCTGGCAGCTTCACTCCTCAGCGCCAGAGACCAAGAACCCACAGAGAAAGAAACATGCG	1860
Oy	3750	GAACACATCTGAACATCAGAAAGGAACAAATCTCAGATCCACACCTTAAAGACTGTATACA	3809
Db	1861	GAACACATCTGAACATCAGAAAGGAACAAATCTCAGATCCACACCTTAAAGACTGTATACA	1920
Oy	3810	CTCAGTCGGAGGGTCCGGCGCTTCTTGTGAAGTCAGTGAGACCAAGCACTCAGCAGTT	3869
Db	1921	CTCAGTCGGAGGGTCCGGCGCTTCTTGTGAAGTCAGTGAGACCAAGCACTCAGCAGTT	1980
Oy	3870	TGCGACACAGCCCGAGGATTTGAGATCAGCCTGGGCAACATGATGAATGCCCCCTCTG	3929
Db	1981	TGCGACACAGCCCGAGGATTTGAGATCAGCCTGGGCAACATGATGAATGCCCCCTCTG	2040
Oy	3930	CAAAAAAAAAAAAAATTAACAAAATTTGGCGGAGCATGGTGGGCGCTGCTGGGCGCCAG	3989
Db	2041	CAAAAAAAAAAAAAATTAACAAAATTTGGCGGAGCATGGTGGGCGCTGCTGGGCGCCAG	2100
Oy	3990	CTACCGCGGAGGCTTAAAGTGGGAGGATGCTTGAAGCTCTGGGAGGGAAGACTGCAGTAG	4049
Db	2101	CTACCGCGGAGGCTTAAAGTGGGAGGATGCTTGAAGCTCTGGGAGGGAAGACTGCAGTAG	2160
Oy	4050	CTGTGATTTGTACACAGCCCTCTAGAGCTGGGGGAGACAGTGAAGCCCTGTTCCCTCCG	4109
Db	2161	CTGTGATTTGTACACAGCCCTCTAGAGCTGGGGGAGACAGTGAAGCCCTGTTCCCTCCG	2220
Oy	4110	CAAAAAAAAAATTTGACAAAAGTGTATTAAGAGGTGCCGATATGCGTATAGGGCGCAGTGGCTAT	4169
Db	2221	CAAAAAAAAAATTTGACAAAAGTGTATTAAGAGGTGCCGATATGCGTATAGGGCGCAGTGGCTAT	2280
Oy	4170	GCGCTTAATCCAGCAGCTTTGGGAAAGCCGAGAGCGGGCGGCTACCTTAAGTCAAGAGAGT	4229
Db	2281	GCGCTTAATCCAGCAGCTTTGGGAAAGCCGAGAGCGGGCGGCTACCTTAAGTCAAGAGAGT	2340
Oy	4230	GAGACAGCCTGGGCCAATGAGAAAGCCCATCTCTTAAAAATACAAAATTAAGCGG	4289

Db 2341 GAGACAGCCTGGCAACATGAGAAAGCCACTCTCTTCTAATAAATACAAATATTAGCCG 2400
QY 4290 CTGTGGGGGACGTGTGGAGCATGCTGTATATCCAGCTACTAGAGAGCTGAGGACGA 4349
Db 2401 CTGTGGGGGACGTGTGGAGCATGCTGTATATCCAGCTACTAGAGAGCTGAGGACGA 2460
QY 4350 GAATCACTTGAACCCAGAGAGCGGCTTGCAGTGAAGAGATCGTGCATTGCACTCC 4409
Db 2461 GAATCACTTGAACCCAGAGAGCGGCTTGCAGTGAAGAGATCGTGCATTGCACTCC 2520
QY 4410 ACCCACTCAGCCTGGGCAACAAGACCAACTCTGTCTTAAATAAAAAAAAAAAAAAGTG 4469
Db 2521 ACCCACTCAGCCTGGGCAACAAGACCAACTCTGTCTTAAATAAAAAAAAAAAAAAGTG 2580
QY 4470 CCTGACATATTAAGAGTGTGCAATGCAATGTTGCCAGGACACATGTTTAAAGATGGA 4529
Db 2581 CCTGACATATTAAGAGTGTGCAATGCAATGTTGCCAGGACACATGTTTAAAGATGGA 2640
QY 4530 GCTCTGCTTCATGCTGTCTGTAAATAAACCCACCTCAAGGCGCAGTGGCTCAT 4589
Db 2641 GCTCTGCTTCATGCTGTCTGTAAATAAACCCACCTCAAGGCGCAGTGGCTCAT 2700
QY 4590 GCTATTAATCCAGCACTTTGGAGGCGAGGCGGTGTGATCACTGAGGTCAAGAGTTTC 4649
Db 2701 GCTATTAATCCAGCACTTTGGAGGCGAGGCGGTGTGATCACTGAGGTCAAGAGTTTC 2760
QY 4650 GAGACAGCCTGACCAACCATGTTGAATCCCACTTACTTAAATAATCAAAATTAGA 4709
Db 2761 GAGACAGCCTGACCAACCATGTTGAATCCCACTTACTTAAATAATCAAAATTAGA 2820
QY 4710 TGAGCATGCTGTG 4723
Db 2821 TGAGCATGCTGTG 2834

RESULT 6
US-09-305-384-7
; Sequence 7, Application US/09305384
; Patent No. 6242218
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/017001
; CURRENT APPLICATION NUMBER: US/09/305,384
; FILING DATE: 1999-05-05
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-305-384-7

Query Match 20.1%; Score 1252; DB 3; Length 1252;
Best Local Similarity 100.0%; Pred. No. 9.2e-292;
Matches 1252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4728 CCTGTATCCCACTACTTGGAGGCTGAGGAGGAAATCACTAGACAGGAGAGCGG 4787
Db 1 CCTGTATCCCACTACTTGGAGGCTGAGGAGGAAATCACTAGACAGGAGAGCGG 60
QY 4788 AGTGTAGTGAAGCCAGATCGTGCATTGCACTCCAGCTGAGCATGAGCAAACTCC 4847
Db 61 AGTGTAGTGAAGCCAGATCGTGCATTGCACTCCAGCTGAGCATGAGCAAACTCC 120
QY 4848 ATCTCAAAAACACAAACAAACCACTCTTACTCCAGGAGCTGGGTACAGAGCT 4907
Db 121 ATCTCAAAAACACAAACAAACCACTCTTACTCCAGGAGCTGGGTACAGAGCT 180

QY 4908 GGGCAATCATGATGCAAGGTCGTGACCAAGAGCTAAGGCGGAGCTGCAGAGACCGCGA 4967
Db 181 GGGCAATCATGATGCAAGGTCGTGACCAAGAGCTAAGGCGGAGCTGCAGAGACCGCGA 240
QY 4968 CCAGATTAACAGTGTGTAGATCAGTGTGTAGATCAGAGTCCCTCCATTGGTGAACAC 5027
Db 241 CCAGATTAACAGTGTGTAGATCAGTGTGTAGATCAGAGTCCCTCCATTGGTGAACAC 300
QY 5028 CAGGGGCCCCCAGACACAGATGAGGCCCATCCAGTCAACCAATCCACTTCTATCCA 5087
Db 301 CAGGGGCCCCCAGACACAGATGAGGCCCATCCAGTCAACCAATCCACTTCTATCCA 360
QY 5088 GAGATGCTGTTCTTGGGCGCTGGGGTAAATTAGACAGAGTGAAGTCTTGGG 5147
Db 361 GAGATGCTGTTCTTGGGCGCTGGGGTAAATTAGACAGAGTGAAGTCTTGGG 420
QY 5148 TGGTCACTGACACTGCCCCAGGAGCCTTGGGCTGTAGAAACGTTAGAGCTTAGG 5207
Db 421 TGGTCACTGACACTGCCCCAGGAGCCTTGGGCTGTAGAAACGTTAGAGCTTAGG 480
QY 5208 CCGGACAGGTGCTCAGCGCTGTATCCAGCACTTTGGAGGCGAGGCGGTGATCA 5267
Db 481 CCGGACAGGTGCTCAGCGCTGTATCCAGCACTTTGGAGGCGAGGCGGTGATCA 540
QY 5268 CGAGGTCAAGAGATCGTGAACCATCGGGTAAACAGGTGAACCCGCTCTACTATAAA 5327
Db 541 CGAGGTCAAGAGATCGTGAACCATCGGGTAAACAGGTGAACCCGCTCTACTATAAA 600
QY 5328 TACAAAAAATTTGGCCGGGATGTTGGCGGACCTGTAGTCCAGTACTCGGAGGCTG 5387
Db 601 TACAAAAAATTTGGCCGGGATGTTGGCGGACCTGTAGTCCAGTACTCGGAGGCTG 660
QY 5388 AGCAGAGAGATGCGTGAACCCGAGAGCAGATTTGCACTGAGCCGAGATCGCCAC 5447
Db 661 AGCAGAGAGATGCGTGAACCCGAGAGCAGATTTGCACTGAGCCGAGATCGCCAC 720
QY 5448 TGCAGTCCAGCCGCGGCGAGAGCAAGACTCCATCGGAAAGAAAGAAACGTTCA 5507
Db 721 TGCAGTCCAGCCGCGGCGAGAGCAAGACTCCATCGGAAAGAAAGAAACGTTCA 780
QY 5508 GGTCTGAGCCAGAGGCGCAGGCTGTATTTCTGTCACTTACATGACCTTGGGCAAGCAC 5567
Db 781 GGTCTGAGCCAGAGGCGCAGGCTGTATTTCTGTCACTTACATGACCTTGGGCAAGCAC 840
QY 5568 TTCTCTCCCTGGGCGCAGTTACAGGGGTGGAATCAGACTCCAGAGTCCCTTCAGCATTA 5627
Db 841 TTCTCTCCCTGGGCGCAGTTACAGGGGTGGAATCAGACTCCAGAGTCCCTTCAGCATTA 900
QY 5628 CGCTGATGTTCTTAAGATGAGAATGGGAGTTTCCCTCTCACCCAGCCGCTG 5687
Db 901 CGCTGATGTTCTTAAGATGAGAATGGGAGTTTCCCTCTCACCCAGCCGCTG 960
QY 5688 TCCACTTCAAGGTGAATGACACAGGAGTCACTGTCCCAATCCGCACTTCCAAAGCC 5747
Db 961 TCCACTTCAAGGTGAATGACACAGGAGTCACTGTCCCAATCCGCACTTCCAAAGCC 1020
QY 5748 TTGGGACCCCTACTGTACAGGTGTGCAGAGAGTGAAGTCAAGTGAAGCCATCGC 5807
Db 1021 TTGGGACCCCTACTGTACAGGTGTGCAGAGAGTGAAGTCAAGTGAAGCCATCGC 1080
QY 5808 TCGAAGGTCCTTCCCTCATTCGGGACAGACATCGGTTTCCCTCTGCTACCGGGATTTC 5867
Db 1081 TCGAAGGTCCTTCCCTCATTCGGGACAGACATCGGTTTCCCTCTGCTACCGGGATTTC 1140
QY 5868 TAGGGCTTTAGCCGATGATGATGAGGGGCGGGGGGTTTCTGGGGGATTCACAGCT 5927
Db 1141 TAGGGCTTTAGCCGATGATGATGAGGGGCGGGGGGTTTCTGGGGGATTCACAGCT 1200
QY 5928 AATCAACTTGGGACAGACAGCTGCAACTTTTGAATGTGTCTATCCAACTG 5979
Db 1201 AATCAACTTGGGACAGACAGCTGCAACTTTTGAATGTGTCTATCCAACTG 1252


```

QY 3627 CCCACGGAGATGAACAACCTCCGCGCGCTGCTTAAAGCTATTAACACTACCGC 3686
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1447 CCCACC -GAGAGAAAGAACTCCAGAGCGCGC- CTTAAGAGCTGGAACCTTACTT 1504
QY 3687 GAAGGTTCAGACTTCTACTCTCAGCAGCAGACGAGAACCCACGAAGAGAAAC 3746
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1505 GAAGGTTCAGACTTCTACTCTCAGCAGCAGACGAGAACCCACGAAGAGAA-- 1562
QY 3747 TCGCAACACTTGAATCAGAGAGAAACAACTCCAGATGACCACTTAAAGCTGTA 3806
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1563 CTCGAACACTTCAACATCAGAAACGAACTCCACACAGCAGCTTTAAGAACTGTA 1622
QY 3807 ACACACTGCGAGGCTCCGCGCTTCTTGAAGTCAAGAGACCAAGACACTACCA 3866
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1623 ACACACTGCGAGGCTCCGCGCTTCTTGAAGTCAAGAGAAACCAAGAACCA 1682
QY 3867 GTTTCGAGACA 3878
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1683 ATTCCGAGACACA 1694

```

RESULT 8

```

US-09-814-951A-3
; Sequence 3, Application US/09814951A
; Patent No. 6387661
; GENERAL INFORMATION:
; APPLICANT: SHAO, Wei et al
; TITLE OF INVENTION: ISOLATED HUMAN AMINOACYLASE, NUCLEIC
; FILE REFERENCE: C1001179
; CURRENT APPLICATION NUMBER: US/09/814,951A
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9704
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-951A-3

```

```

Query Match          9.0%; Score 563.8; DB 4; Length 9704;
Best Local Similarity 86.9%; Pred. No. 1.1e-125;
Matches 686; Conservative 0; Mismatches 77; Indels 26; Gaps 5;

```

```

QY 1873 TGAGAGGTGACAGATGCCGCGACTCTCACAAGCCCTGTTGGCTGCGCCCTCTCT 1932
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8883 TGAGAGGTGACAGCTGTGCGAGTCTCACAGCCCTGCTCTCCCGCTCTCTCT 8942
QY 1933 GCTGAGGCTCCCACTTGGTGGCACTTGAAGAGAGCCCTTCAAGCCAGCGCTGACTGTGG 1992
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8943 GCTGAGGCTCCCACTTGGTGGCACTTGAAGAGAGCCCTTCAAGCCAGCGCTGACTGTAG 9002
QY 1993 AGCCCTTTTGGGCTGGCCAAAGGCGAGAGCGGCTCCCTCAGCTTGAAGAGAGTGTGG 2052
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9003 AACCCCTTTGGGCTGGCCAAAGGCGAGAGCGGCTCCCTCAGCTTGAAGAGAGTGTGG 9062
QY 2053 AGGAGAGGCTCAAGCAGGAACCGGGGCTGGCAGCGGCTTGGGGGCCAGCTGAGTTTC 2112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9063 AGGAGAGGCTCAAGCAGGAACCGGGGCTGGCAGCGGCTTGGGGGCCAGCTGAGTTTC 9122
QY 2113 CGGAGGCGCTGGGCTTGGCGGGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGG 2166
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9123 CGGAGGCGCTGGGCTTGGCGGGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGG 9182
QY 2167 -----CAGGCCCGGGCAATGAGAGCTTGAAGACCGGGCCAGCGGCTGGAGAGGT 2218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9183 GGTCCCGCGCTCCCGGGCAATGAGAGGCTTGAAGACCGGGCCAGTGGCTGGAGAGGT 9242
QY 2219 GTACTGGGTGCCCGCAGAGTGCAGCGCGGCGGCTGTGCTGCTGCTTCTCACTGG 2278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9243 GTACTGGGTGCCCGCAGAGTGCAGCGCGGCTGCTGCTGCTTCTCACTGG 9298

```

```

QY 2279 GCCTTAGCAGCTTCCCGGGGAGAGGCTCGGAGACTGACCGCCGCAATGCT----- 2332
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9299 GTCTTAGCTGCTTCCCGGGGCTCAAGGTTTGGAGCTGACCCAGCACTGCTTAGAGCC 9358
QY 2333 -GAGCTCCCTTCATGAGGCTCTGTGGGCGCCGAGCTCCCGAGACACACCCCT 2391
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9359 CTCGCCACCCCTTCAGCTGCTCCGTTGGGCGCCAGCTCCCGCAATGAGCGCGCCGCC 9418
QY 2392 GCTCCAGAGCGCCGAGCTCCATGACACAGCAGAGGCTGAGAAATGCGGGGCCAGAGCAC 2451
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9419 GCTCCAGCGCACAGCTCCATGACACAGCAGAGGCTGAGAAATGCGGGGCCAGAG -AG 9477
QY 2452 CGGAGCTGGCAGAGCTACCTGCGTCCGAGCGGTCGAGCAATCCATGGGTGAAGCAGC 2511
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9478 CAGAGCTGGCAGAGCTACCTGAGCGCCGCTGCGGATTCAGCTGGGTGAAGCAGC 9537
QY 2512 TGGGCTCCGAGTCTGTGGAGACTTGAAGAACTTTATGTAGCTCAGGAGATGTAA 2571
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9538 TGGGCTCCGAGTCTGTGGAGACTTGAAGAACTTTATGTAGCTCAGGAGATGTAA 9597
QY 2572 TACACCAATCAGACCTGTGTAGCTCAGGCTGTGATGACCAATCCACTCTG 2631
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9598 TACACCAATCAGACCTGTGTAGCTCAGGCTGTGATGACCAATCCACTCTG 9657
QY 2632 TATCTAGCT 2640
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9658 TGTCTAGCT 9666

```

RESULT 9

```

US-09-422-576D-5
; Sequence 5, Application US/09422576D
; Patent No. 639549
; GENERAL INFORMATION:
; APPLICANT: Tuan, Dorothy
; APPLICANT: Long, Qiaoming
; APPLICANT: Bengra, Chikh
; TITLE OF INVENTION: Long Terminal Repeat, Enhancer, and Insulator Sequences for US
; FILE REFERENCE: M0351-205010
; CURRENT APPLICATION NUMBER: US/09/422,576D
; CURRENT FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/105,256
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Sequence
; NAME/KEY: misc_feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n = any nucleotide
US-09-422-576D-5

```

```

Query Match          7.4%; Score 462.2; DB 4; Length 1091;
Best Local Similarity 88.8%; Pred. No. 1.2e-101;
Matches 522; Conservative 0; Mismatches 64; Indels 2; Gaps 2;

```

```

QY 3293 CTCGTATCTATTAATCTAGTGGGAGCTGAGAAACCTTGTGCTAGCTAGGAGATTG 3352
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 410 CTCGTATCTATTAATCTAGTGGGAGCTGAGAAACCTTGTGCTAGCTAGGAGATTG 469
QY 3353 TAAAGCAACCAATCAGCGCTGTCAAAAACAGACCACTGAGCTC-TAACCAATCAGAGGA 3411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 470 TAAATGCAACCAATCAGTGGCTGTCAAAAACAGACCACTGAGCTC-TAACCAATCAGAGGA 529
QY 3412 TGTGGGTGGGGCAGATTAAGATAAAGCAGGCTGCCGAGCAGCAGTGGCAACGG 3471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 530 TGTGGGTGGGGCAGATTAAGATAAAGCAGGCTGCCGAGCAGCAGTGGCAACCG 589

```


327 CTTTGTCTTTCCTCTTCTTTCGAATAATCTTGTCTGTCTGTCTCACTGTTTGGTCTACACTG 386
3559 CTTTATGAGCTGTATACACTCCAGCAAGGTCTGCAGTCTGACCTCCGTAACCCACTAG 3618
387 CTTTACGAGCTATACGCTACAC-CGAAAGTCTGAGTCTTCTTGAACCCAGCGAG 445
3619 ACCAGAGCCACCGGAGGAATGAACAACCTCCGGCGCTGCTTTAAGACTATAC 3678
446 ACCAGAACCCACTGGAGGAGAACAACTCCAAACGACCGCTTAAGACTGSAAG 505
3679 CTCACCGGAGAGTGTGACGCTTCACTCTCTCAACGAGCAACCAACCAAG 3738
506 TTTCACTGTGAAGGTGTGAGCTTCTCACTCTGAGCGAGAGACCAAGCCATCAGAG 565
3739 GAAGAACTCGCAACATCTGAACATGAGAGAAACCACTCCAGATCCACACC-TTA 3797
566 GAAGAACTCGCAACATCTGAACATGAGAGAAACCACTCCAGATCCACACC-TTA 625
3798 AGAGCTGTACACTCTGCGAGGGT-CGCGGCTTCTCTTGTG-AAGTCACTGAGACCA 3855
626 AGAACTGTACACTCTGCGAGGGTCCCGGCTTCTTGTGAAGTCACTGAGAACCA 685
3856 AGCACTCACAGTT 3869
686 AGAACTCACAAAT 699

RESULT 12

US-09-422-576D-6

Sequence 6, Application US/09422576D

Patent No. 6395549

GENERAL INFORMATION:

APPLICANT: Tuan, Dorothy

APPLICANT: Long, Qiaoming

APPLICANT: Bengra, Chikh

TITLE OF INVENTION: Long Terminal Repeat, Enhancer, and Insulator Sequences for Use

FILE REFERENCE: M0351-205010

CURRENT APPLICATION NUMBER: US/09/422,576D

CURRENT FILING DATE: 1999-10-21

PRIOR APPLICATION NUMBER: US 60/105,256

PRIOR FILING DATE: 1998-10-22

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 1043

TYPE: DNA

ORGANISM: Homo sapiens

US-09-422-576D-6

Query Match 6.8%; Score 426.4; DB 4; Length 1043;
Best Local Similarity 88.5%; Pred. No. 4,9e-93;

Matches 483; Conservative 0; Mismatches 61; Indels 2; Gaps 2;

3333 TGTGTCTAGCTCAGGATTTTAAACGCAATCAGCGCCCTGTCAAAAACAGACACTG 3392
402 TGTGTCTAGCTCAGGATTTTAAACGCAATCAGCGCCCTGTCAAAAACAGACACTG 461
3333 GCTTCAATCAGCAGATGTGGTGGGCCAGATTAAGAAATAAAGCAGGCTGCCG 3452
462 GCTTCAATCAGCAGATGTGGTGGGCCAGATTAAGAAATAAAGCAGGCTGCCG 521
3453 AGCAGCAGTGGCAACGCGCAAGTCCCTATCCCAATATGAGAGCTTTGTTCTTTGG 3512
522 AGCAGCAGTGGCAACGCGCTGGGCTCCCTTCCACACTGTGGAAGCTTTGTTCTTTGG 581
3513 TGTGTCTAGCTCAGGATTTTAAACGCAATCAGCGCCCTGTCAAAAACAGACACTG 3572
582 TGTGTCTAGCTCAGGATTTTAAACGCAATCAGCGCCCTGTCAAAAACAGACACTG 641
3573 AACACTCACAGAGAGTGTGACGCTTCACTCTGAAGCCACTAAGACGACGAGCCAC 3632
642 AACGCTCACAGAGAGTGTGACGCTTCACTCTGAAGCCACTAAGACGAGACGAGCCAC 701

3633 GGGAGGATGAAACAACTCCGCGCGCTGCTTAAAGAGCTATTAACACTCAC-CGGAAG 3691
702 GGGAGGATGAAACAACTCCGCGCGCTGCTTAAAGAGCTATTAACACTCAC-CGGAAG 761
3692 TCTGAGCTTCACTCTCTGAGCAGGAGACCAAGCAACCCAGCAAGAGAAAGTGTGCA 3751
762 TCTGAGCTTCACTCTCTGAGCAGGAGACCAAGCAACCCAGCAAGAGAAAGTGTGCA 821
3752 ACACATCTGAACATGAGAGAGAAACAACTCTGAGATGACACACC-TTAAAGTGTGAC 3810
822 ACACATCTGAACATGAGAGAGAAACAACTCTGAGATGACACACC-TTAAAGTGTGAC 881
3811 TCACATGAG 3870
882 TCACATGAG 941
3871 CGGACACA 3878
942 CGGACACA 949

RESULT 13

US-09-078-294-4

Sequence 4, Application US/09078294

Patent No. 6265211

GENERAL INFORMATION:

APPLICANT: Choo, Kong-Hong Andy

APPLICANT: Du Sart, Desirée

APPLICANT: Cancilla, Michael R.

TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE

CURRENT APPLICATION NUMBER: US/09/078,294

CURRENT FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.0.

SEQ ID NO 4

LENGTH: 80246

TYPE: DNA

ORGANISM: Nucleotide sequence of NC-contig

US-09-078-294-4

Query Match 6.6%; Score 413.8; DB 3; Length 80246;
Best Local Similarity 66.0%; Pred. No. 3,7e-89;

Matches 806; Conservative 0; Mismatches 357; Indels 56; Gaps 12;

3259 TCTGTGGGGCTTGGAGATGTGTGTGACACTGTATCTAATTAATCTAGTGGGG 3318
59197 TCAGGTGGGGCTTGGAGATGTGTGTGACACTGTATCTAATTAATCTAGTGGGG 59247
3319 ACCTGAGAACCTTTGT 3378
59248 ACCAATCAGACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 59307
3379 AAACAGACACCTCGGTCTACCAATCAGAGATGTGTGTGTGTGTGTGTGTGTGTGT 3438
59308 AA-----TGAAACCAATCAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 59353
3439 AAGCAGCTCCCGAGCCAGACAGTGGCAACGCGCAGTCCCTATCCCAATATGCGAG 3498
59354 AAACCTGCGACCGGAGCGAGTGGCAACCGCAGTCCCTATCCCAATATGCGAG 59413
3499 CTTTGTCTTGT 3558
59414 CTTTGTCTTGT 59473
3559 CTTTATGAGCTGTATACACTCTGAGAGAGTGTGAGCTTCACTCTGAGAGAGAGAG 3618
59474 CTTTATGAGCTGTATACACTCTGAGAGAGTGTGAGCTTCACTCTGAGAGAGAGAG 59532
3619 ACCAGAGCCACCGGAGAGATGAACAATCTCCGCGGCTGCC-TTAAAGCTATTAAC 3677
59533 ACCAGAGCCACCGGAGAGATGAACAATCTCCGCGGCTGCC-TTAAAGCTATTAAC 59592

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2003, 16:05:11 ; Search time 955 Seconds
(without alignments)
14611.055 Million cell updates/sec

Title: US-09-845-020A-5

Perfect score: 6235

Sequence: 1 gatcacttgagacagtagt.....tgcacattcccaagcgt 6235

Scoring table:

IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1504479 seqs, 1118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCr_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCrUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6235	100.0	6235	11	US-09-845-020A-5
2	6235	100.0	6679	11	US-09-845-020A-1
3	2834	45.5	2834	11	US-09-845-020A-6
4	1252	20.1	1252	11	US-09-845-020A-7
5	1002.2	16.1	36221	11	US-09-954-556-29
6	744.8	11.9	260209	12	US-10-025-966A-23
7	744.8	11.9	260209	12	US-10-265-071-23
8	683.2	11.0	91000	14	US-10-002-491-10
9	670	10.7	104000	14	US-10-012-984-14
10	652.8	10.5	10351	9	US-09-874-470-5
11	647.2	10.4	161552	15	US-10-081-327-40
12	645.4	10.4	7126	12	US-10-017-161-1529
13	588.6	9.4	128779	15	US-10-081-327-38
14	583.8	9.4	6766	10	US-09-764-847-1878
15	583.8	9.4	6766	14	US-10-092-154-1878
16	564.4	9.1	28818	10	US-09-764-877-2266

17	563.8	9.0	9704	13	US-10-109-860-3	Sequence 3, Appl1
18	563.8	9.0	175590	11	US-09-911-077A-13	Sequence 13, Appl
19	562.4	9.0	54945	11	US-09-967-669-10	Sequence 10, Appl
20	562	9.0	2845	13	US-10-027-632-112134	Sequence 112134,
21	560	9.0	1503841	9	US-09-795-668-1	Sequence 1, Appl1
22	560	9.0	1503841	9	US-09-795-668-1	Sequence 1, Appl1
23	560	9.0	1503841	10	US-09-946-807-1	Sequence 1, Appl1
24	533.6	8.6	19172	10	US-09-764-877-3474	Sequence 3474, Ap
25	533	8.5	1192	13	US-10-027-632-118931	Sequence 118931,
26	522.2	8.4	5281	11	US-09-764-881-6949	Sequence 6949, Ap
27	509	8.2	2324	13	US-10-027-632-102474	Sequence 102474,
28	506.4	8.1	378361	11	US-09-901-136-3	Sequence 3, Appl1
29	500.2	8.0	776	10	US-09-764-847-1256	Sequence 1256, Ap
30	500.2	8.0	776	14	US-10-092-154-1256	Sequence 1256, Ap
31	500.2	8.0	900	10	US-09-764-847-1257	Sequence 1257, Ap
32	500.2	8.0	900	14	US-10-092-154-1257	Sequence 1257, Ap
33	499.6	8.0	142299	11	US-09-911-077A-14	Sequence 14, Appl
34	497.8	8.0	300000	14	US-10-262-552-33	Sequence 33, Appl
35	490.4	7.9	78025	14	US-10-020-141-9	Sequence 9, Appl1
36	486.4	7.8	27148	9	US-09-764-860-1046	Sequence 1046, Ap
37	486.4	7.8	27148	14	US-10-074-095-1046	Sequence 1046, Ap
38	468.6	7.5	3824	11	US-09-931-836-22	Sequence 22, Appl
39	468.6	7.5	3824	12	US-10-035-977-22	Sequence 22, Appl
40	468.6	7.5	3824	12	US-10-137-870-541	Sequence 541, App
41	468.6	7.5	3824	12	US-10-140-018-541	Sequence 541, App
42	468.6	7.5	3824	12	US-10-140-021-541	Sequence 541, App
43	468.6	7.5	3824	12	US-10-140-274-541	Sequence 541, App
44	468.6	7.5	3824	12	US-10-140-471-541	Sequence 541, App
45	468.6	7.5	3824	12	US-10-140-807-541	Sequence 541, App

ALIGNMENTS

RESULT 1
US-09-845-020A-5
Sequence 5, Application US/09845020A
Publication No. US20030022850A1
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michel W.
TITLE OF INVENTION: Selden, Richard F.
TITLE OF INVENTION: Genomic Sequences for Protein Production
FILE REFERENCE: 50010/017003
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 09/845,020A
CURRENT FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: US 60/084,649
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 6235
TYPE: DNA
ORGANISM: Homo sapiens
US-09-845-020A-5
Query Match
Best Local Similarity 100.0%: Score 6235; DB 11; Length 6235;
Matches 6235: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATCACTTGAGACAGTAGTTCACAGCAGCTGGGACATAGGAGAGACTGTCTACG 60
DB 1 GATCACTTGAGACAGTAGTTCACAGCAGCTGGGACATAGGAGAGACTGTCTACG 60
QY 61 AAAATTCAAAAATATGCGCGGCGATGCTGCTTAAATCCCTGAACCTTTGGG 120
DB 61 AAAATTCAAAAATATGCGCGGCGATGCTGCTTAAATCCCTGAACCTTTGGG 120
QY 121 ACATAGAGCAAGTCAGTACCTGAGTTCAGAGTTCGAGTACCTGAGTTCGAGTTCG 180

Db 121 ACATCAAGGCAAGTGGATCTAGCTGAGGAGTTGGAGACTAGCTGGCCCAACATGCT 180
Qy 181 GAAACCCATCTCCACTAAAAAATATACAAAGCATGGTGGCAGGACCTGTA 240
Db 181 GAAACCCATCTCCACTAAAAAATATACAAAGCATGGTGGCAGGACCTGTA 240
Qy 241 ATCCCGGCTACTCAGGAGGCTGAGGCGAGGAATCACTTGAAACCAGAGAGCGGAGGTG 300
Db 241 ATCCCGGCTACTCAGGAGGCTGAGGCGAGGAATCACTTGAAACCAGAGAGCGGAGGTG 300
Qy 301 CAGTAGCTGAGATCACACCACCTGCACAGCCTGGGTGACAGAGAGACCTGATCTC 360
Db 301 CAGTAGCTGAGATCACACCACCTGCACAGCCTGGGTGACAGAGAGACCTGATCTC 360
Qy 361 AAAAAAATAAAAAATAAAAAATATAGCCAGGATGTAAGTGCACACCTCTACTCTAG 420
Db 361 AAAAAAATAAAAAATAAAAAATATAGCCAGGATGTAAGTGCACACCTCTACTCTAG 420
Qy 421 CTACTCAGAGGCTGAGGTGGAGGATCACTTGAACTGGGGCAGTCAGGCTACAGTGA 480
Db 421 CTACTCAGAGGCTGAGGTGGAGGATCACTTGAACTGGGGCAGTCAGGCTACAGTGA 480
Qy 481 GCCAAGATCAGGACCTACACTCCAGCCTGGGCAACAGAGAGAGACCTGCTCTAAAA 540
Db 481 GCCAAGATCAGGACCTACACTCCAGCCTGGGCAACAGAGAGAGACCTGCTCTAAAA 540
Qy 541 AATATATATATATAAAGAAAAAACAAGCTGTATTGTCTCTGTCATACATACAT 600
Db 541 AATATATATATATAAAGAAAAAACAAGCTGTATTGTCTCTGTCATACATACAT 600
Qy 601 ATGATATATATTTGCAAACTCAAGATCCAGATAGTCAATTTTTTAGGCTTGTGGCGT 660
Db 601 ATGATATATATTTGCAAACTCAAGATCCAGATAGTCAATTTTTTAGGCTTGTGGCGT 660
Qy 661 ATGGTCTCTGACAAATCACTCTGCCCTGCTTCTCTGACAAAGAGAGCTATAAACAT 720
Db 661 ATGGTCTCTGACAAATCACTCTGCCCTGCTTCTCTGACAAAGAGAGCTATAAACAT 720
Qy 721 ACATACATGAATTTTTATAGACATCGAGATTTGAATTTTCATATGATTTTACATTTAT 780
Db 721 ACATACATGAATTTTTATAGACATCGAGATTTGAATTTTCATATGATTTTACATTTAT 780
Qy 781 AAAAAATCTTTTTAAAAATTTTCCCTAACCATTTAAAGTGTAAAAACCGGCACACGC 840
Db 781 AAAAAATCTTTTTAAAAATTTTCCCTAACCATTTAAAGTGTAAAAACCGGCACACGC 840
Qy 841 GCCATCGTCAAGCCTGTAAATTCAGACACTTTGGAGGCTGAGGTGGCAGATCACTTGAG 900
Db 841 GCCATCGTCAAGCCTGTAAATTCAGACACTTTGGAGGCTGAGGTGGCAGATCACTTGAG 900
Qy 901 ATCAACAGTTGAGAGACCAAGCCTGGCAACATAGCAAAACCCCATTTCTACTAAAAATAAA 960
Db 901 ATCAACAGTTGAGAGACCAAGCCTGGCAACATAGCAAAACCCCATTTCTACTAAAAATAAA 960
Qy 961 AAAAAATGCTGGGATAGTGTGACACACCTGTATCCACGCTACTTTGGAGGCTGAGGCA 1020
Db 961 AAAAAATGCTGGGATAGTGTGACACACCTGTATCCACGCTACTTTGGAGGCTGAGGCA 1020
Qy 1021 GGAGAAATCGTTGAACTGGGAAAGCGAGGATTCAGAGTGCAGCAATCATCTCCACTGCAC 1080
Db 1021 GGAGAAATCGTTGAACTGGGAAAGCGAGGATTCAGAGTGCAGCAATCATCTCCACTGCAC 1080
Qy 1081 TCCAGCCTGGGTGACAGAGTGCAGCTGCTCAACGAAAAAAGTGTAAAAAGCCAT 1140
Db 1081 TCCAGCCTGGGTGACAGAGTGCAGCTGCTCAACGAAAAAAGTGTAAAAAGCCAT 1140
Qy 1141 TCCGAATTCAGTGTACATCACTGTACATCACTGAGTCTGCTGCTGAGGAT 1200
Db 1141 TCCGAATTCAGTGTACATCACTGTACATCACTGAGTCTGCTGCTGAGGAT 1200
Qy 1201 ACCGTAGAGTAGAGTGTGCTGCTCAGAGACATACATTTCCACATTAAGTACAGACT 1260
Db 1201 ACCGTAGAGTAGAGTGTGCTGCTCAGAGACATACATTTCCACATTAAGTACAGACT 1260

Qy 1261 ACCAAGTTGCCATCCAAGAGGTTTTTTTTTACAAATCTACACTCCCCCAACAACAT 1320
Db 1261 ACCAAGTTGCCATCCAAGAGGTTTTTTTTTACAAATCTACACTCCCCCAACAACAT 1320
Qy 1321 GAGAGTACTCCAAATCCTTTACAAAGATGCTTACAGCCGACTCCGATGAAAAAGGA 1380
Db 1321 GAGAGTACTCCAAATCCTTTACAAAGATGCTTACAGCCGACTCCGATGAAAAAGGA 1380
Qy 1381 AGTGGAGGGGAACTCCAGACCCCTTCTAACCATGAAAGAAATACCTGTAGAGCTTCT 1440
Db 1381 AGTGGAGGGGAACTCCAGACCCCTTCTAACCATGAAAGAAATACCTGTAGAGCTTCT 1440
Qy 1441 GGATGCTGGAAGATGATAAAGGGGGTCTCTGAGGCTGCCCCCTGTCAAGATCACTGTG 1500
Db 1441 GGATGCTGGAAGATGATAAAGGGGGTCTCTGAGGCTGCCCCCTGTCAAGATCACTGTG 1500
Qy 1501 ACTTCTAGACCTCCAGTCCAGTCTCAGACCCCATGTGTATGATGGCAGTGAATGACCCCT 1560
Db 1501 ACTTCTAGACCTCCAGTCCAGTCTCAGACCCCATGTGTATGATGGCAGTGAATGACCCCT 1560
Qy 1561 CACTCTGCTTGTGCTTTATTTCTCCCATGTGGGGTGAAGTCTGGATTGAGCGTTAT 1620
Db 1561 CACTCTGCTTGTGCTTTATTTCTCCCATGTGGGGTGAAGTCTGGATTGAGCGTTAT 1620
Qy 1621 TCAAGATGTACAGCTTTCTTGACAGAAAGTGTACAGAAACAGAGGGGCTTGGA 1680
Db 1621 TCAAGATGTACAGCTTTCTTGACAGAAAGTGTACAGAAACAGAGGGGCTTGGA 1680
Qy 1681 AGATGATCTAACCTCAAAATCTACCTGCTGACACACAGTAACTTGTGATCTTGAAAC 1740
Db 1681 AGATGATCTAACCTCAAAATCTACCTGCTGACACACAGTAACTTGTGATCTTGAAAC 1740
Qy 1741 AAGTTTTTCACTTCTCTGAGGCAATCCCTTGGCTTACAAACACACAGTTGGTTGACAGGA 1800
Db 1741 AAGTTTTTCACTTCTCTGAGGCAATCCCTTGGCTTACAAACACACAGTTGGTTGACAGGA 1800
Qy 1801 TGAATATGCAAGATCCCTTACACTGTATATCCAGACACTTTGGAGGCAAGCGGGGTGG 1860
Db 1801 TGAATATGCAAGATCCCTTACACTGTATATCCAGACACTTTGGAGGCAAGCGGGGTGG 1860
Qy 1861 ATGGCTTGAGGCTGAGAGGTGACAGACATGGCGGAGTCTACAGACCTGCTGGCTCTC 1920
Db 1861 ATGGCTTGAGGCTGAGAGGTGACAGACATGGCGGAGTCTACAGACCTGCTGGCTCTC 1920
Qy 1921 GGGCCTCTCTCTGCTGGGCTCCCACTTGGGTGCTGACTTGAAGAGCCCTTCAGGCCACCG 1980
Db 1921 GGGCCTCTCTCTGCTGGGCTCCCACTTGGGTGCTGACTTGAAGAGCCCTTCAGGCCACCG 1980
Qy 1981 CTGCACTGTGGAGCCCTTTCTGGGCTGGCCAAAGCCAGAGCCGCTCCCTCAAGCTTGC 2040
Db 1981 CTGCACTGTGGAGCCCTTTCTGGGCTGGCCAAAGCCAGAGCCGCTCCCTCAAGCTTGC 2040
Qy 2041 AGGAGAGTGTGAGAGGAGGAGGCTCAAGAGGAACCGGGGCTGGCCAGAGGCGCTGGCGGGC 2100
Db 2041 AGGAGAGTGTGAGAGGAGGAGGCTCAAGAGGAACCGGGGCTGGCCAGAGGCGCTGGCGGGC 2100
Qy 2101 CAGCTGAGATTCCCGGCTGGGCTTGGCGGGGCCCGCACTCGGAGAGAGCGGGGCGAG 2160
Db 2101 CAGCTGAGATTCCCGGCTGGGCTTGGCGGGGCCCGCACTCGGAGAGAGCGGGGCGAG 2160
Qy 2161 CCTGTCAGAGGCCCGGGCAATGAGAGGCTTACACCCGGGCGAGCGGCTGCGGAGGGGTGT 2220
Db 2161 CCTGTCAGAGGCCCGGGCAATGAGAGGCTTACACCCGGGCGAGCGGCTGCGGAGGGGTGT 2220
Qy 2221 ACTGGGTGCCCAAGACATGCGAGCGCCCGCGGCTGTGCTGCTGCAATTTCTACATGGGC 2280
Db 2221 ACTGGGTGCCCAAGACATGCGAGCGCCCGCGGCTGTGCTGCTGCAATTTCTACATGGGC 2280
Qy 2281 CTTAGCAGAGCTTCCCGGGGGGCAAGGCTCGGGACCTCAGGCCGCACTGCTGAGCCTCC 2340
Db 2281 CTTAGCAGAGCTTCCCGGGGGGCAAGGCTCGGGACCTCAGGCCGCACTGCTGAGCCTCC 2340

OY	2341	UCTCCATGAGGCTCTGTGCGGGCCCGAGAGCTCCCGAGAGACCAACCCCTGCTCCACAG	2400
Db	2341	CCTCCATGAGGCTCTGTGCGGGCCCGAGAGCTCCCGAGAGACCAACCCCTGCTCCACAG	2400
OY	2401	CGCCCAAGCCCATGAGACAGCAAGGGGTGGAAGTGGGGCGAGGGCACCGGAGACTGG	2460
Db	2401	CGCCCAAGTCCCATGAGACCAAGGGGTGGAAGTGGGGCGAGGGCACCGGAGACTGG	2460
OY	2461	CAGGACAGCTACCCCTGCAAGCCCTGGTGGGAAATCCACTGGGTGGAAGCCAGCTGGGCTCT	2520
Db	2461	CAGGACAGCTACCCCTGCAAGCCCTGGTGGGAAATCCACTGGGTGGAAGCCAGCTGGGCTCT	2520
OY	2521	GAGTCTGGTGGAGACTTGGAGAACCTTTATCTAGCTCAGGGATCGTAAATACACCAAT	2580
Db	2521	GAGTCTGGTGGAGACTTGGAGAACCTTTATCTAGCTCAGGGATCGTAAATACACCAAT	2580
OY	2581	CAGACACCTGTGTAGCTCAGGGTCTGTGAATGCACCAATCCACACTCTGTATCTAGCT	2640
Db	2581	CAGACACCTGTGTAGCTCAGGGTCTGTGAATGCACCAATCCACACTCTGTATCTAGCT	2640
OY	2641	ACTGTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGATTTGTAATACACCAATC	2700
Db	2641	ACTGTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGATTTGTAATACACCAATC	2700
OY	2701	GGCACTCTGTATCTAGCTCAGAGTTTGTAAACACACCAATACAGACCTGTGTCTAGCTC	2760
Db	2701	GGCACTCTGTATCTAGCTCAGAGTTTGTAAACACACCAATACAGACCTGTGTCTAGCTC	2760
OY	2761	AGGGATGTGAATGCACCAATCGACAGCTGTATCTGGCTACTTCAATGGGCAATCCGGT	2820
Db	2761	AGGGATGTGAATGCACCAATCGACAGCTGTATCTGGCTACTTCAATGGGCAATCCGGT	2820
OY	2821	GAAAGAGACACCAAAACAGGCTTTGTGTAGCAATAAAGCTTCTATCAACCTGGGTGCAAGT	2880
Db	2821	GAAAGAGACACCAAAACAGGCTTTGTGTAGCAATAAAGCTTCTATCAACCTGGGTGCAAGT	2880
OY	2881	GGCGTGAATCCGAAAAGAGAGTCAAGCAAGGAGGATAAAGGTGGGCGCTTTATAGAT	2940
Db	2881	GGCGTGAATCCGAAAAGAGAGTCAAGCAAGGAGGATAAAGGTGGGCGCTTTATAGAT	2940
OY	2941	TTGGGTAGGTAAAGAAAATTATACAGTCAAGGGGTTTGTCTGTGGCGGGCAGAGAGCG	3000
Db	2941	TTGGGTAGGTAAAGAAAATTATACAGTCAAGGGGTTTGTCTGTGGCGGGCAGAGAGTGG	3000
OY	3001	GGGGTCGCAAGGTCTCAGTGGGGGTGCTTTTGAAGCCAGGATAGCCAGAGAAAAGACT	3060
Db	3001	GGGGTCGCAAGGTCTCAGTGGGGGTGCTTTTGAAGCCAGGATAGCCAGAGAAAAGACT	3060
OY	3061	TTCCACAAGGTATGTCTATCAATTAAGGCAAGGACCCGCAATTTACACTCTTTTGTGGTG	3120
Db	3061	TTCCACAAGGTATGTCTATCAATTAAGGCAAGGACCCGCAATTTACACTCTTTTGTGGTG	3120
OY	3121	GAATGTATCATGTTAAGTTGGGGGAGGCAATTCACCTCTTTGTGATCTCTTCAATTAC	3180
Db	3121	GAATGTATCATGTTAAGTTGGGGGAGGCAATTCACCTCTTTGTGATCTCTTCAATTAC	3180
OY	3181	TTTCAGGCGCATTTGGGCGTATGTGTGCAAGTATACAGGGATCCGATGGCTTGGGCT	3240
Db	3181	TTTCAGGCGCATTTGGGCGTATGTGTGCAAGTATACAGGGATCCGATGGCTTGGGCT	3240
OY	3241	CAGAGCGCTTGACAGCTACTCTGTGTGGGCGCTTGGAGAAATGTTTGTGTGCACACTGTAT	3300
Db	3241	CAGAGCGCTTGACAGCTACTCTGTGTGGGCGCTTGGAGAAATGTTTGTGTGCACACTGTAT	3300
OY	3301	CTACTTATATCTAAGTGGGAGCTGGAGAACTTTGTGTCTAGCTCAGGATTTGTAAAGCA	3360
Db	3301	CTACTTATATCTAAGTGGGAGCTGGAGAACTTTGTGTCTAGCTCAGGATTTGTAAAGCA	3360
OY	3361	CCAATCAAGCGCCCTGTCAAAACACCACTGGCTCTTACCAATBAGCAGGAGTGTGGGGG	3420
Db	3361	CCAATCAAGCGCCCTGTCAAAACACCACTGGCTCTTACCAATBAGCAGGAGTGTGGGGG	3420
OY	3421	GGCCAGATTAAGATAAAGCAGGCTGGCCCGAGCCACAGCATGTGCCACAGCCACAGGCTC	3480

Db	3421	GGCCAGATTAAGATTAAGCAAGGCGTCCCGAGCCAGAGTGGCAACCGCAAGCTCC		3480
Oy	3481	CTATCCACAATATGCGAGCTTTGTCTTTGCTTTGCTTTGGATTAATCTTGCTACAGCTCG		3540
Db	3481	CTATCCACAATATGCGAGCTTTGTCTTTGCTTTGCTTTGGATTAATCTTGCTACAGCTCG		3540
Oy	3541	CTTTTGGGTCACACATGCTTTTATGAGCTGTAACTACACGACGAGGCTGTGAGCTTC		3600
Db	3541	CTTTTGGGTCACACATGCTTTTATGAGCTGTAACTACACGACGAGGCTGTGAGCTTC		3600
Oy	3601	ACTCTGAAGCACTTAAGACCCAGAGCGCCACCGGGAGGAATGAAACACTCCGGCCGCGT		3660
Db	3601	ACTCTGAAGCACTTAAGACCCAGAGCGCCACCGGGAGGAATGAAACACTCCGGCCGCGT		3660
Oy	3661	GCCTTAAAGAGCTATTAACACTCACCGCGAAGTGTGAGCTTCACTCTCAGCAGCAGAGA		3720
Db	3661	GCCTTAAAGAGCTATTAACACTCACCGCGAAGTGTGAGCTTCACTCTCAGCAGCAGAGA		3720
Oy	3721	CCACGAACCCACCGAAGGAAGAACTCGAACAACATCTGAACATCAGAAGAACAACT		3780
Db	3721	CCACGAACCCACCGAAGGAAGAACTCGAACAACATCTGAACATCAGAAGAACAACT		3780
Oy	3781	CCAATATGACCACTTAAAGAGCTGTAACTATCATCTCGAGAGGTCCCGGCTTCCTTTG		3840
Db	3781	CCAATATGACCACTTAAAGAGCTGTAACTATCATCTCGAGAGGTCCCGGCTTCCTTTG		3840
Oy	3841	AAGTCAGAGAACCAACACTCACAGATTCGAGACACAAGCCAGAGATTGATCAGC		3900
Db	3841	AAGTCAGAGAACCAACACTCACAGATTCGAGACACAAGCCAGAGATTGATCAGC		3900
Oy	3901	CTGGGCAACATGATGAATAATGCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCGG		3960
Db	3901	CTGGGCAACATGATGAATAATGCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCGG		3960
Oy	3961	AGCATGTGTGCTCGCTGCTGTGTGCCAGTACCGGGAGGCTTAAAGTGGAGATCGT		4020
Db	3961	AGCATGTGTGCTCGCTGCTGTGTGCCAGTACCGGGAGGCTTAAAGTGGAGATCGT		4020
Oy	4021	TGAGCTGTGGAGGTGAAGACTGCGAGTAGTGTGATTTGACACAGCCCTTAAAGCTGGG		4080
Db	4021	TGAGCTGTGGAGGTGAAGACTGCGAGTAGTGTGATTTGACACAGCCCTTAAAGCTGGG		4080
Oy	4081	GGACAGACTGAGACCCGTCTTCCCTCCGCAAAAAAATTTGACAAAAAGTAAATAGAGGT		4140
Db	4081	GGACAGACTGAGACCCGTCTTCCCTCCGCAAAAAAATTTGACAAAAAGTAAATAGAGGT		4140
Oy	4141	GCCTGTATATGGCTTAGCGGCACTGCTATGCTGTATATCCAGCACTTTGGAGCCGAG		4200
Db	4141	GCCTGTATATGGCTTAGCGGCACTGCTATGCTGTATATCCAGCACTTTGGAGCCGAG		4200
Oy	4201	GGGGGGGGGTACCTAAGGTGAGAGTGTAGAGCCAGCGGGCCCAATGAGAAAAAGCC		4260
Db	4201	GGGGGGGGGTACCTAAGGTGAGAGTGTAGAGCCAGCGGGCCCAATGAGAAAAAGCC		4260
Oy	4261	ATCTCTCTTAAAAATTAACAAATTAGCCGCGTGTGGGGGAGTGTGGAGCATGCTGTAA		4320
Db	4261	ATCTCTCTTAAAAATTAACAAATTAGCCGCGTGTGGGGGAGTGTGGAGCATGCTGTAA		4320
Oy	4321	TCCAGAGCTACTCAGAGAGGTGAGGCGAGAGAACTCACTGAACCCAGAGAGGGCGGTTGC		4380
Db	4321	TCCAGAGCTACTCAGAGAGGTGAGGCGAGAGAACTCACTGAACCCAGAGAGGGCGGTTGC		4380
Oy	4381	AGTAAAGCCGAGATGTGTCCATTGCGATCCACCACTCCAGCCCTGGGCAACAAGAGCAAA		4440
Db	4381	AGTAAAGCCGAGATGTGTCCATTGCGATCCACCACTCCAGCCCTGGGCAACAAGAGCAAA		4440
Oy	4441	CTGCTGTCTTAAAAAATTTAAAAAAGTGGCTGACATATTAAGAGGTGTCAATGCAATAG		4500
Db	4441	CTGCTGTCTTAAAAAATTTAAAAAAGTGGCTGACATATTAAGAGGTGTCAATGCAATAG		4500
Oy	4501	TTGCGAGCAACATGTTAAGAAATGTGAGACTCTCTGCTTCAATGCTCTGTTAAAAAGC		4560
Db	4501	TTGCGAGCAACATGTTAAGAAATGTGAGACTCTCTGCTTCAATGCTCTGTTAAAAAGC		4560

D	b	4501	TTGCAGGCAACATGTTTAAGAAATGTGGAGCTCGTGGCTTCCATGTCGTGTTAAAAAC	4500
O	y	4501	CACCCCTAAGGCCAAGGTGACAGTGGCTCATGCTTATATCCAGCACTTTGGGAGGCCGAG	4620
D	b	4501		
D	b	4501	CACCCCTCAAGGCCAAGGTGACAGTGGCTCATGCTTATATCCAGCACTTTGGGAGGCCGAG	4620
O	y	4621	GGGGGTGGATACCGTAGGAGTCCAGAGTTTCGAGACCAGCTTACACCAACTGGTGAAT	4680
D	b	4621		
O	y	4681	CCCACTCTTACTAAAAATACAAAAATATAGATGAGCATGGTGTGCATGGCTCTATATCCAC	4740
D	b	4681	CCCACTCTTACTAAAAATACAAAAATATAGATGAGCATGGTGTGCATGGCTCTATATCCAC	4740
O	y	4741	CTACTTGGGAGCGCTGAGGCAAGAAAAATCCTAGAACCAAGGAGGCGGAGGTTGTAGTGAG	4800
D	b	4741	CTACTTGGGAGCGCTGAGGCAAGAAAAATCCTAGAACCAAGGAGGCGGAGGTTGTAGTGAG	4800
O	y	4801	CCGAGATGCTGCCATTGTGCATCTCCAGAGCTGAGCAATGAGCCAACTCCATTCTCAAAAAAC	4860
D	b	4801	CCGAGATGCTGCCATTGTGCATCTCCAGAGCTGAGCAATGAGCCAACTCCATTCTCAAAAAAC	4860
O	y	4861	AACAAACAAAAACCACTCTCTACGCCCGAGGAGCTGGGTATAGAGCTGGGCGACATGCT	4920
D	b	4861	AACAAACAAAAACCACTCTCTACGCCCGAGGAGCTGGGTATAGAGCTGGGCGACATGCT	4920
O	y	4921	GCAAGGTGCTGAGCCACAGAGCTTAAGGCGAGCTGCAGAGCACCGCGGACCAAGTAAACGTG	4980
D	b	4921	GCAAGGTGCTGAGCCACAGAGCTTAAGGCGAGCTGCAGAGCACCGCGGACCAAGTAAACGTG	4980
O	y	4981	TGTAGATCACTGTGTGAGATCAAGCTGCTGCCATTGGTGACCACCAGGGGCCCCA	5040
D	b	4981	TGTAGATCACTGTGTGAGATCAAGCTGCTGCCATTGGTGACCACCAGGGGCCCCA	5040
O	y	5041	AGCACAGAGATGGGCCCCATCCAGACACATCCACTCTTCATCCAGAGATGTGCTGTT	5100
D	b	5041	AGCACAGAGATGGGCCCCATCCAGACACATCCACTCTTCATCCAGAGATGTGCTGTT	5100
O	y	5101	CTTGGCAGCGTGGGGTAAATTAGACAGAAAGTGCAGTCTTGGGTGTGTCACTCAGAC	5160
D	b	5101	CTTGGCAGCGTGGGGTAAATTAGACAGAAAGTGCAGTCTTGGGTGTGTCACTCAGAC	5160
O	y	5161	TGCCCCAAGGCAAGGCTTGTGGCTGTAGAAAACTTCAGGCTTAGGCCGGGCAACGCTGGC	5220
D	b	5161	TGCCCCAAGGCAAGGCTTGTGGCTGTAGAAAACTTCAGGCTTAGGCCGGGCAACGCTGGC	5220
O	y	5221	TCAGGCTCTATCCACAGCACTTTGGGAGGCGGAGGGGGTGAATCAGAGCTCAGAGGA	5280
D	b	5221	TCAGGCTCTATCCACAGCACTTTGGGAGGCGGAGGGGGTGAATCAGAGAGTCAAGAGGA	5280
O	y	5281	TCGTGACCATCTGGCTTAACAGGGTGAACCCTGCTCTACTAAAAATACAAAAAATTGG	5340
D	b	5281	TCGTGACCATCTGGCTTAACAGGGTGAACCCTGCTCTACTAAAAATACAAAAAATTGG	5340
O	y	5341	CCGGGCAATGCTGGGGGACCTGTATGTTCCAGCTACTCTGGGAGGCTGAGGCAAGATG	5400
D	b	5341	CCGGGCAATGCTGGGGGACCTGTATGTTCCAGCTACTCTGGGAGGCTGAGGCAAGATG	5400
O	y	5401	GCGTGAACCCAGAGAGGCAAGATTTGGAGTGAAGCCAGATCGCGCACTGCACCTCAGGCT	5460
D	b	5401	GCGTGAACCCAGAGAGGCAAGATTTGGAGTGAAGCCAGATCGCGCACTGCACCTCAGGCT	5460
O	y	5461	GGGGGACAGAGCAAGACTCCTCTCGGAAAAAGAAAAAGTTCAGAGTGTGAGCCAGA	5520
D	b	5461	GGGGGACAGAGCAAGACTCCTCTCGGAAAAAGAAAAAGTTCAGAGTGTGAGCCAGA	5520
O	y	5521	GGCCCAAGGCTTAATTCTGTCACTTTACCATGACCTTGGGCAAGGCACTCTCTCCCTGGC	5580
D	b	5521	GGCCCAAGGCTTAATTCTGTCACTTTACCATGACCTTGGGCAAGGCACTCTCTCCCTGGC	5580
O	y	5581	CCAGTTCAACGGGGTGGGAATGCAATCCCAAGGTCCTCTCCAGCACTTAACGCTGCATGGTTC	5640
D	b	5581	CCAGTTCAACGGGGTGGGAATGCAATCCCAAGGTCCTCTCCAGCACTTAACGCTGCATGGTTC	5640

QY	564.1	TAAGATGAGAGATGGGGACATTTTCCCCTCTCAACCCACCCGTGTCACCTTCAAGST	5700
Db	564.1	TAAGATGAGAAATGGGGACATTTTCCCCTCTCTCAACCCACCCGTGTCACCTTCAAGST	5700
QY	570.1	GAATGACCAGGAAGTCACTGTGTCCCAATCCCGCAGTTCCAAAGCCCTTGGGGACCCAC	5760
Db	570.1	GAATGACCAGGAAGTCACTGTGTCCCAATCCCGCAGTTCCAAAGCCCTTGGGGACCCAC	5760
QY	576.1	TGTCAAGGTCGTGCACGAGAGGTGAAGTCAAGTCAAGCCAAATGCGCTCGAAGGGCTTTG	5820
Db	576.1	TGTCAAGGTCGTGCACGAGAGGTGAAGTCAAGTCAAGCCAAATGCGCTCGAAGGGCTTTG	5820
QY	582.1	CCTCATTTGGGACACAGACATTCGCGTTTCTCTGCGCTCTACCGGGANTTTAGGGGCTTTAGC	5880
Db	582.1	CCTCATTTGGGACACACATTCGCGTTTCTCTGCGCTCTACCGGGANTTTAGGGGCTTTAGC	5880
QY	588.1	CGAATGAGTCAATGGGGGGCGGGGGGGGTTTCTGGGGGAGTTTCCAGCTAATCAACTTGGGA	5940
Db	588.1	CGAATGAGTCAATGGGGGGCGGGGGGGGTTTCTGGGGGAGTTTCCAGCTAATCAACTTGGGA	5940
QY	594.1	CAGACACCCCTTGGAATCTTTCATGTTGCTTATCCAAATGTGGGGTGGGACAGACCCAA	6000
Db	594.1	CAGACACCCCTTGGAATCTTTCATGTTGCTTATCCAAATGTGGGGTGGGACAGACCCAA	6000
QY	600.1	GACCCAAATGTCCTTATCTCAGGTAGGGGCTCAGGAGGTCCTCCAGACAGGACGCTCCGG	6060
Db	600.1	GACCCAAATGTCCTTATCTCAGGTAGGGGCTCAGGAGGTCCTCCAGACAGGACGCTCCGG	6060
QY	606.1	AGAGTTTGGGGGTAGGAATGGGAGCAACAGGCTCTTTTCTTCTTATGAAATTTGGG	6120
Db	606.1	AGAGTTTGGGGGTAGGAATGGGAGCAACAGGCTCTTTTCTTCTTATGAAATTTGGG	6120
QY	612.1	GCGTTGGGGGACAGGCTTGAGATCCCAAGAGAGAGGGGCAAAAGACACTCCCCACAAAG	6180
Db	612.1	GCGTTGGGGGACAGGCTTGAGATCCCAAGAGAGAGGGGCAAAAGACACTCCCCACAAAG	6180
QY	618.1	TCTGCGAAGAGGAGAGAGGAGGAGACCCCGACATCAGCTGCACTTCCCAAGAGGCGT	6235
Db	618.1	TCTGCGAAGAGGAGAGGAGGAGAGACCCCGACATCAGCTGCACTTCCCAAGAGGCGT	6235
RESULT 2			
US-09-845-020A-1			
; Sequence 1, Application US/09845020A			
; Publication No. US20030022850A1			
; GENERAL INFORMATION:			
; APPLICANT: Treco, Douglas A.			
; APPLICANT: Healtlein, Michel F.			
; TITLE OF INVENTION: Genomic Sequences for Protein Production			
; TITLE OF INVENTION: and Delivery			
; FILE REFERENCE: 50010/017003			
; CURRENT APPLICATION NUMBER: US/09/845,020A			
; CURRENT FILING DATE: 2001-04-27			
; PRIOR APPLICATION NUMBER: US 09/305,384			
; PRIOR FILING DATE: 1999-05-05			
; PRIOR APPLICATION NUMBER: US 60/084,649			
; PRIOR FILING DATE: 1998-05-07			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 6679			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-845-020A-1			
Query Match			
Best Local Similarity 100.0%; Score 6235; DB 11; Length 6679;			
Matches 6235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GATCAGCTTGAGACAGTAGTTCAAGACACGCTTGGGACAGATAGGAGACTGTCTTACG	60

Db 20 GATCATTGAGGACAGTAGTTCAGAACCGCTGGGACATAGGAGACTGTCTACG 79
OY 61 AAAATCAAAAAATTATGGCCGGGATGTGGCTACCTCTGTATCCCTGAACCTTGGG 120
Db 80 AAAATTCAAAAATTATGGCCGGGATGTGGCTACCTCTGTATCCCTGAACCTTGGG 139
OY 121 ACATCAAGGCAAGTGTGATCTGTAGGTCTAGAGTTCAGACTAGCTGTGGCCAAACATGTT 180
Db 140 ACATCAAGGCAAGTGTGATCTGTAGGTCTAGAGTTCAGACTAGCTGTGGCCAAACATGTT 199
OY 181 GAAACCTTATCTCCACTTAAAAAATTCAAAAATTAGCCAGCATGGTGGCAGGCACTGTGA 240
Db 200 GAAACCTTATCTCCACTTAAAAAATTCAAAAATTAGCCAGCATGGTGGCAGGCACTGTGA 259
OY 241 ATCCGGCTACTCGAGGAGCTGAGGCGAGGAATACCTTGAATCCAGAGGCGGAGGTTG 300
Db 260 ATCCGGCTACTCGAGGAGCTGAGGCGAGGAATACCTTGAATCCAGAGGCGGAGGTTG 319
OY 301 CAGTGAAGCTGATGCACACCACTGCATCCAGCCCTGGGTGACAGAGCAAGACTCTATCTC 360
Db 320 CAGTGAAGCTGATGCACACCACTGCATCCAGCCCTGGGTGACAGAGCAAGACTCTATCTC 379
OY 361 AAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420
Db 380 AAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 439
OY 421 CTACTCAGAGGCTGAGGTGGGAGATACCTTGAACCTGGGCGACTCAAGGCTACAGTGA 480
Db 440 CTACTCAGAGGCTGAGGTGGGAGATACCTTGAACCTGGGCGACTCAAGGCTACAGTGA 499
OY 481 GCCAAGATCATGCCACTACCTCCAGCCCTGGGCAACAGAGAGAGACCTGTCTTAAAAA 540
Db 500 GCCAAGATCATGCCACTACCTCCAGCCCTGGGCAACAGAGAGAGACCTGTCTTAAAAA 559
OY 541 AATAATATATATAAAGAAAAAACAAGCTGTATTATGTCTCTGTGCTCATATATCTACT 600
Db 560 AATAATATATATAAAGAAAAAACAAGCTGTATTATGTCTCTGTGCTCATATATCTACT 619
OY 601 ATGTATATAGTTTGGCAAACTCAAGATCCAGATAGTCAATTTTAAAGCTTGTGGCCGT 660
Db 620 ATGTATATAGTTTGGCAAACTCAAGATCCAGATAGTCAATTTTAAAGCTTGTGGCCGT 679
OY 661 ATGCTCTGTGCACATCATCTGTGCCCTGTCTTCTAGCACAAAAAGCAGCTATAAACAT 720
Db 680 ATGCTCTGTGCACATCATCTGTGCCCTGTCTTCTAGCACAAAAAGCAGCTATAAACAT 739
OY 721 ACATACATGAATTTTATAGACATCGAGATTTGAATTCATATGATTTTACATTTTAT 780
Db 740 ACATACATGAATTTTATAGACATCGAGATTTGAATTCATATGATTTTACATTTTAT 799
OY 781 AAAATATCTTTTAAAAAATTTCCCTAACCATTTTAAAGGTAAAAAGCCGGCCAGGCG 840
Db 800 AAAATATATCTTTTAAAAAATTTCCCTAACCATTTTAAAGGTAAAAAGCCGGCCAGGCG 859
OY 841 GCCATCGTCAGCCCTGTAAATTCAGCACTTTGGAGGCTGAGTGGGCGAGATCATCTGAG 900
Db 860 GCCATCGTCAGCCCTGTAAATTCAGCACTTTGGAGGCTGAGTGGGCGAGATCATCTGAG 919
OY 901 ATCAACAGTTCGAACACCAAGCTGGCAACATAGCAAAACCCCATTTCTACTAAAAATAA 960
Db 920 ATCAACAGTTCGAACACCAAGCTGGCAACATAGCAAAACCCCATTTCTACTAAAAATAA 979
OY 961 AAAATTTAGCTGGGATAGTGGTGACACCTGTGATCCAGTACTTGGGAGGCTGAGGCA 1020
Db 980 AAAATTTAGCTGGGATAGTGGTGACACCTGTGATCCAGTACTTGGGAGGCTGAGGCA 1039
OY 1021 GGAGAAATCGCTTGAACCTGGGAGCGAGGTTGGAGTGGAGCAACATATCCCACTGAC 1080
Db 1040 GGAGAAATCGCTTGAACCTGGGAGCGAGGTTGGAGTGGAGCAACATATATCCCACTGAC 1099
OY 1081 TCCAGCCCTGGGTGACAGAGTGAACCTGTCTCAACGAAAAAAGTGTAAAAAGCAT 1140
Db 1100 TCCAGCCCTGGGTGACAGAGTGAACCTGTCTCAACGAAAAAAGTGTAAAAAGCAT 1159

OY 1141 TCCTATTCAGTGTACATCAGTGTACATCTCAGGCTGCCGTACCTGCTGAGCAT 1200
Db 1160 TCCTATTCAGTGTACATCAGTGTACATCTCAGGCTGCCGTGCTGAGCAT 1219
OY 1201 ACCTAGAAATGTAGATTTGCTTGTGACAGGACATACATTTTCCATTTAATACACT 1260
Db 1220 ACCTAGAAATGTAGATTTGCTTGTGACAGGACATACATTTTCCATTTAATACACT 1279
OY 1261 ACCAAGTTCATCCAGAGAGGTTTTTTTTTACAACTACACTCCCCAGCAACAAAT 1320
Db 1280 ACCAAGTTCATCCAGAGAGGTTTTTTTTTACAACTACACTCCCCAGCAACAAAT 1339
OY 1321 GAGATTTACTCCAGATCCCTTTCAAAAGATGCTTAAGCCAGTACAGATGAAGAAAGGA 1380
Db 1340 GAGATTTACTCCAGATCCCTTTCAAAAGATGCTTAAGCCAGTACAGATGAAGAAAGGA 1399
OY 1381 AGTGGAGGAGGAAGTGCAGCCCTTCTAACCATGAAGAAATACCTGGTAGGCTTCT 1440
Db 1400 AGTGGAGGAGGAAGTGCAGCCCTTCTAACCATGAAGAAATACCTGGTAGGCTTCT 1459
OY 1441 GGATCTGGAGAGATGAATACGGGGGTCTGTGAGCCTGCCCCCTGTACATCACTGTG 1500
Db 1460 GGATCTGGAGAGATGAATACGGGGGTCTGTGAGCCTGCCCCCTGTACATCACTGTG 1519
OY 1501 ACTTGAGCCCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 1560
Db 1520 ACTTGAGCCCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 1579
OY 1561 CACTCTGCTTGTGCTTATATCTCCCATAGTGGGGCTGAAGTGTGATAGGCGCTTAT 1620
Db 1580 CACTCTGCTTGTGCTTATATCTCCCATAGTGGGGCTGAAGTGTGATAGGCGCTTAT 1639
OY 1621 TCAAGATGTACAGCTTTCTTGTACAGAAAGTGTGTACAGAAACAGCAGGCGCTTGGCA 1680
Db 1640 TCAAGATGTACAGCTTTCTTGTACAGAAAGTGTGTACAGAAACAGCAGGCGCTTGGCA 1699
OY 1681 AGATGATCTAACCTGAAATCCATACCTGGCTCAGCAGCAGTGTGTGTATCTTGAAC 1740
Db 1700 AGATGATCTAACCTGAAATCCATACCTGGCTCAGCAGCAGTGTGTGTATCTTGAAC 1759
OY 1741 AAGTTTTTCACTTCTGAGGCAATCCCTTGGCTACAAACACACAGTGTGTGACAGA 1800
Db 1760 AAGTTTTTCACTTCTGAGGCAATCCCTTGGCTACAAACACACAGTGTGTGACAGA 1819
OY 1801 TGAATGTACAGAGTCCCTTACACCTGTATCCACACACTTGGGAGGCCAAGCGCGGTG 1860
Db 1820 TGAATGTACAGAGTCCCTTACACCTGTATCCACACACTTGGGAGGCCAAGCGCGGTG 1879
OY 1861 ATGGCTTGAAGCTGAGAGGTGACAGATCGCGGCGAGTCCCTACAGCCCTCGTGTCTC 1920
Db 1880 ATGGCTTGAAGCTGAGAGGTGACAGATCGCGGCGAGTCCCTACAGCCCTCGTGTCTC 1939
OY 1921 GCGCCCTCTGCTGCTGGGCTCCCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Db 1940 GCGCCCTCTGCTGCTGGGCTCCCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1999
OY 1981 CTGCACTGTGGAGCCCTTTCTGTGGCTGGCCAAAGCCAGAGCCGGCTCCCTCAGCTTGC 2040
Db 2000 CTGCACTGTGGAGCCCTTTCTGTGGCTGGCCAAAGCCAGAGCCGGCTCCCTCAGCTTGC 2059
OY 2041 AGGGAAGTGTGAGAGGAGAGGCTCAAGAGAGAACCGGGGCTGCCAGCGCGCTTGGGGC 2100
Db 2060 AGGGAAGTGTGAGAGGAGAGGCTCAAGAGAGAACCGGGGCTGCCAGCGCGCTTGGGGC 2119
OY 2101 CAGCTGAGATTCGCGGCTGGGCTGTGGCGGGCCCGCACTGCGAGACAGCGGCGAG 2160
Db 2120 CAGCTGAGATTCGCGGCTGGGCTGTGGCGGGCCCGCACTGCGAGACAGCGGCGAG 2179
OY 2161 CCTGTCAGGCCCGCGGCAATGAGAGGCTTACACCCGCGGCAAGCGGCTGCGGAGGCT 2220
Db 2180 CCTGTCAGGCCCGCGGCAATGAGAGGCTTACACCCGCGGCAAGCGGCTGCGGAGGCT 2239

QY 2221 ACTGGGTCGCCAGCACTGGCAGGCCCGCGCTGCTGCTGCATTTCTCACTGGCC 2280
Db 2240 ACTGGGGCCCCACACAGTGGCCAGCCCGCGCTGCTGCTGCATTTCTCACTGGCC 2299
QY 2281 CTTAGCAGCTTCCCGCGGGGCAAGGCTCGGAGCTCAGAGCCGCAATGCTGAGCTCC 2340
Db 2300 CTTAGCAGCTTCCCGCGGGGCAAGGCTCGGAGCTCAGAGCCGCAATGCTGAGCTCC 2359
QY 2341 CTTCCATGGGCTCTGTGGGCCCGAGCTCCCGAGCAGCACCACCCCTGCTCAAG 2400
Db 2360 CTTCCATGGGCTCTGTGGGCCCGAGCTCCCGAGCAGCACCACCCCTGCTCAAG 2419
QY 2401 CGCCCATGCCATGCGACGCAAGGGCTGGAAGTGGGGCGGACGCAACCGGAACTGG 2460
Db 2420 CGCCCATGCCATGCGACGCAAGGGCTGGAAGTGGGGCGGACGCAACCGGAACTGG 2479
QY 2461 CAGGCACTACCCCTGCGAGCCCTGTGCGGATCCAGTGGGTGAAGCAGCTGGGCTCT 2520
Db 2480 CAGGCACTACCCCTGCGAGCCCTGTGCGGATCCAGTGGGTGAAGCAGCTGGGCTCT 2539
QY 2521 GAGTCTGGTGAAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCGTAAATACCAAT 2580
Db 2540 GAGTCTGGTGAAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCGTAAATACCAAT 2599
QY 2581 CAGCAGCCGTGCTAGCTCAGGGTCTGTGAATGCAACCAATCCACACTCTGTATCTAGCT 2640
Db 2600 CAGCAGCCGTGCTAGCTCAGGGTCTGTGAATGCAACCAATCCACACTCTGTATCTAGCT 2659
QY 2641 ACTCTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAATC 2700
Db 2660 ACTCTGATGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAATC 2719
QY 2701 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGCACCCTGTCTAGCTC 2760
Db 2720 GGCACCTGTATCTAGCTCAAGGTTTGTAAACACCAATCAGCACCCTGTCTAGCTC 2779
QY 2761 AGGCTATGTAAATGCAACCAATCGACGTCTGTATCTAGCTCACTTCAATGGGCACTCCGT 2820
Db 2780 AGGCTATGTAAATGCAACCAATCGACGTCTGTATCTAGCTCACTTCAATGGGCACTCCGT 2839
QY 2821 GAAGAGACCAACCAAGGCTTGTGTAGCAATAAAGCTTCTATCACTCGGCGCAGGT 2880
Db 2840 GAAGAGACCAACCAAGGCTTGTGTAGCAATAAAGCTTCTATCACTCGGCGCAGGT 2899
QY 2881 GGGCTGAGTCCGAAGAGAGTCAAGGAGATAAAGGTGGGGCGCTTTTATAGAT 2940
Db 2900 GGGCTGAGTCCGAAGAGAGTCAAGGAGATAAAGGTGGGGCGCTTTTATAGAT 2959
QY 2941 TTGGGTAGTAAAGGAAATTTACAGTCAAGGGGCTTGTCTCTGGCGGGCAGAGTGG 3000
Db 2960 TTGGGTAGTAAAGGAAATTTACAGTCAAGGGGCTTGTCTCTGGCGGGCAGAGTGG 3019
QY 3001 GGGGTGCAAGGTGCTCAGTGGGGGCTTTTGTAGCCAGATGAGCAGGAAAAAGACT 3060
Db 3020 GGGGTGCAAGGTGCTCAGTGGGGGCTTTTGTAGCCAGATGAGCAGGAAAAAGACT 3079
QY 3061 TTCAACAAGTAAATGTCAATTAAGGCAAGAACCCGCATTACACCTTTTGTGTG 3120
Db 3080 TTCAACAAGTAAATGTCAATTAAGGCAAGAACCCGCATTACACCTTTTGTGTG 3139
QY 3121 GAATGTCATAGTTAAGTTGGGGCAGGSCATTTCACTTTTGTGTGATCTTCACTTAC 3180
Db 3140 GAATGTCATAGTTAAGTTGGGGCAGGSCATTTCACTTTTGTGTGATCTTCACTTAC 3199
QY 3181 TTCAAGGCATCTGGGCGTATATGTGCAAGTTACAGGGATGCGATGGCTTGGGCT 3240
Db 3200 TTCAAGGCATCTGGGCGTATATGTGCAAGTTACAGGGATGCGATGGCTTGGGCT 3259
QY 3241 CAAGAGCTTACAGCTACTGTGGTGGGGCTTGGAGATTTTGTGTGACACTCTGTAT 3300
Db 3260 CAAGAGCTTACAGCTACTGTGGTGGGGCTTGGAGATTTTGTGTGACACTCTGTAT 3319
QY 3301 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTCTAGCTCAGGGATTTGTAACGCA 3360

Db 3320 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTCTAGCTCAGGGATTTGTAACGCA 3379
QY 3361 CCAATCAGCGCCCTGTCAAAAAACAGACACTCGGCTTACCAATACAGAGATGTGGTGG 3420
Db 3380 CCAATCAGCGCCCTGTCAAAAAACAGACACTCGGCTTACCAATACAGAGATGTGGTGG 3439
QY 3421 GGGCAGATTAAGAAATTAAGAGCAGCTGCCGAGCCAGCAGGTGCAACGGCACAGTCC 3480
Db 3440 GGGCAGATTAAGAAATTAAGAGCAGCTGCCGAGCCAGCAGGTGCAACGGCACAGTCC 3499
QY 3481 CTATCCAAATATAGGAGCTTTGTCTTGTGCTGTGCAATTAATCTTGTACTGTGCTG 3540
Db 3500 CTATCCAAATATAGGAGCTTTGTCTTGTGCTGTGCAATTAATCTTGTACTGTGCTG 3559
QY 3541 CTTTGTGGTCCACACTGCTTTTATGAGCTGTAACTCAACAGAGTCTGCAAGCTTC 3600
Db 3560 CTTTGTGGTCCACACTGCTTTTATGAGCTGTAACTCAACAGAGTCTGCAAGCTTC 3619
QY 3601 ACTCCTGAAGCCACTAAAGCCAGAGCCACCGGGAGGAATGAACAACTCCGGCGGCT 3660
Db 3620 ACTCCTGAAGCCACTAAAGCCAGAGCCACCGGGAGGAATGAACAACTCCGGCGGCT 3679
QY 3661 GCCTTAAGAGCTATAACACTCACCGGAGAGTCTGCAAGCTTCACTCTCAGCCAGCGAGA 3720
Db 3680 GCCTTAAGAGCTATAACACTCACCGGAGAGTCTGCAAGCTTCACTCTCAGCCAGCGAGA 3739
QY 3721 CCAGGAACCCACAGAGGAAGAAATGCGAACACATCTGAATCAAGAGGAACAAT 3780
Db 3740 CCAGGAACCCACAGAGGAAGAAATGCGAACACATCTGAATCAAGAGGAACAAT 3799
QY 3781 CCAGATCACCACTTAAGAGCTGTAAACTCACTCGGAGGGTCCGGCTTCTCTTGTG 3840
Db 3800 CCAGATCACCACTTAAGAGCTGTAAACTCACTCGGAGGGTCCGGCTTCTCTTGTG 3859
QY 3841 AAGTCAATGAGAACCAACACTCAACAGTTTCGACAAACCCAGGAGTTTGAGATCAGC 3900
Db 3860 AAGTCAATGAGAACCAACACTCAACAGTTTCGACAAACCCAGGAGTTTGAGATCAGC 3919
QY 3901 CTTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAAAATTTACAAAATTTGGCGG 3960
Db 3920 CTTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAAAATTTACAAAATTTGGCGG 3979
QY 3961 AGCATGTGTGCTGCTGCTGTGTGCCAGCTACGCGGAGGCTTAAATGGGAGATGCT 4020
Db 3980 AGCATGTGTGCTGCTGCTGTGTGCCAGCTACGCGGAGGCTTAAATGGGAGATGCT 4039
QY 4021 TGAGCCCTGGGAGGTGAAGACTGCAAGTGTGATTTGTACCAAGCCCTCTAGGCTGGG 4080
Db 4040 TGAGCCCTGGGAGGTGAAGACTGCAAGTGTGATTTGTACCAAGCCCTCTAGGCTGGG 4099
QY 4081 GGACAGACTGAGACCCGTTTCCCTCCGCAAAAAAATTTGCAAAAATGTAAAGAGGT 4140
Db 4100 GGACAGACTGAGACCCGTTTCCCTCCGCAAAAAAATTTGCAAAAATGTAAAGAGGT 4159
QY 4141 GCTGTATATGCTAGGCGCAGTGGCTCATCTGTAAATCCAGCACTTTGGGAAGCCGAG 4200
Db 4160 GCTGTATATGCTAGGCGCAGTGGCTCATCTGTAAATCCAGCACTTTGGGAAGCCGAG 4219
QY 4201 GCGGGCGGGTACCTAAGGTACAGAGTGTAGACCCGCGGCAACATGTGAAAAAGCCC 4260
Db 4220 GCGGGCGGGTACCTAAGGTGTAGAGTGTAGACCAACCTGGGCCAATGTGAAAAAGCCC 4279
QY 4261 ATCTCTTCTAAAAATATACAAAATTAAGCGGCTGTGGGGCGAGTGTGAGCATCTGTAA 4320
Db 4280 ATCTCTTCTAAAAATATACAAAATTAAGCGGCTGTGGGGCGAGTGTGAGCATCTGTAA 4339
QY 4321 TCCAGCTACTCAGAGGCTGTAGGCGAGAGATCTTGAACCCAGAGGCGCGGTTGC 4380
Db 4340 TCCAGCTACTCAGAGGCTGTAGGCGAGAGATCTTGAACCCAGAGGCGCGGTTGC 4399
QY 4381 AGTGAAGCGAGATCGTGCATTTGCACTCCACCCACTCCAGCTGGGCAACAAAGCCAA 4440

Db	4400	AGTAGCCGGAATGTGGCATTTGCATCTCCACCACCTCCAGCTGGGCAACAAGCCAAA	4453
OY	4441	CTGTGTCTTAAAAAAAAAAAAAAAAAGTGCCCTGACATATAAGAGGTGTCAATGCAATAG	4500
Db	4460	CTGTGTCTTAAAAAAAAAAAAAAAAAGCGCTGACATATAAGAGGTGTCAATGCAATAG	4519
OY	4501	TTGGCAGGCAACATGTTTAAGAAATGTGGAGTCTCGCTTTCATATGTCTTAAAAAC	4560
Db	4520	TTGGCAGGCAACATGTTTAAAGATGTGGAGTCTCGCTTTCATATGTCTTAAAAAC	4579
OY	4561	CACCCCTCAAGGCCAGAGTGCAGTGGCTGTATGCTTAATCCAGACCTTTGGGAGGCCGAG	4620
Db	4580	CACCCCTCAAGGCCAGAGTGCAGTGGCTGTATGCTTAATCCAGACCTTTGGGAGGCCGAG	4639
OY	4621	GGGGGTGGATCACTGAGGTGAGGATTTGAGACAGCTGACCAACCAATGGTGAAT	4680
Db	4640	GGGGGTGGATCACTGAGGTGAGGATTTGAGACAGCTGACCAACCAATGGTGAAT	4699
OY	4681	CCCACTCTACTAAAAATACAAATTTAGATAGCATGGTGGTATGCTCTATATCCAC	4740
Db	4700	CCCACTCTACTAAAAATACAAATTTAGATAGCATGGTGGTATGCTCTATATCCAC	4759
OY	4741	CTACTTGGGAGCTGAGGACAGAAAAATCACTATAGAAACAGGGAGCGGAGTGTAGTAG	4800
Db	4760	CTACTTGGGAGCTGAGGACAGAAAAATCACTATAGAAACAGGGAGCGGAGTGTAGTAG	4819
OY	4801	CCGAGATCTGCCCATTTGCATCTCCAGCCTGAGCAATGAGCGAACTCCATCTCAAAAAAC	4860
Db	4820	CCGAGATCTGCCCATTTGCATCTCCAGCCTGAGCAATGAGCGAACTCCATCTCAAAAAAC	4879
OY	4861	AACAACAACAAACCCACCTCTACCTCCACAGGAGCTGGGTACAGAGCTTGGGCCAATCAGT	4920
Db	4880	AACAACAACAAACCCACCTCTACCTCCACAGGAGCTGGGTACAGAGCTTGGGCCAATCAGT	4939
OY	4921	GCAAGGTGCTGAGCCACAGAGACTAAAGGGGAGTGTGACAGACCGGGGACACAGATAACAGTG	4980
Db	4940	GCAAGGTGCTGAGCCACAGAGACTAAAGGGGAGTGTGACAGACCGGGGACACAGATAACAGTG	4999
OY	4981	TGTGAGATCAGTGTGTGAGATCAGACGTCCTGTCATTTGATGACCAACAGGGGGCCCCA	5040
Db	5000	TGTGAGATCAGTGTGTGAGATCAGACGTCCTGTCATTTGATGACCAACAGGGGGCCCCA	5059
OY	5041	AGCACCCAGAGTAGGCCCATTCACATCACCATCTCTCATTCAGAGATGTCTGTTT	5100
Db	5060	AGCACCCAGAGTAGGCCCATTCACATCACCATCTCTCATTCAGAGATGTCTGTTT	5119
OY	5101	CTTGGCAGCGCTGGGGTAAATATAGACAGAAAGTACAGTCTTTGGGTGGTGGCAGCTCAGAC	5160
Db	5120	CTTGGCAGCGCTGGGGTAAATATAGACAGAAAGTACAGTCTTTGGGTGGTGGCAGCTCAGAC	5179
OY	5161	TGCCCCCAGGCGCTTGTGGCGTGTAGAAAAAGTTCAAGGCTTAGGCCGGGACAGGCTGGC	5220
Db	5180	TGCCCCCAGGCGCTTGTGGCGTGTAGAAAAAGTTCAAGGCTTAGGCCGGGACAGGCTGGC	5239
OY	5221	TCAGGCGCTGTAAATCCACAGCAATTTTGGGAGGCCGAGGGGGTGTGATCACGAGGTACGAGA	5280
Db	5240	TCAGGCGCTGTAAATCCACAGCAATTTTGGGAGGCCGAGGGGGTGTGATCACGAGGTACGAGA	5299
OY	5281	TCGTGACCATCTGGCTAAACAGGGTGAACCCCGCTCTATTAATAAATACAAAAAATTTGG	5340
Db	5300	TCGTGACCATCTGGCTAAACAGGGTGAACCCCGCTCTCTACTAAAAATACAAAAAATTTGG	5359
OY	5341	CCGGGCGATGATGGGGGCACTGTATGTTCCAGTACTTCGGGAGGCTGAGGAGAGAGATG	5400
Db	5360	CCGGGCGATGATGGGGGCACTGTATGTTCCAGTACTTCGGGAGGCTGAGGAGAGAGATG	5419
OY	5401	GCGTGAACCCGAGAGGACAGAGTTTGTGACGTAGCCGAGATGCGGCCACTGCATCCAGCT	5460
Db	5420	GCGTGAACCCGAGAGGACAGAGTTTGTGACGTAGCCGAGATGCGGCCACTGCATCCAGCT	5479
OY	5461	GGGGGACAGACAGACATCCATCTGCGAAAAAAGAAAAACGTTCAAGTGTAGGCCAGA	5520
Db	5480	GGGGGACAGACAGACATCCATCTGCGAAAAAAGAAAAACGTTCAAGTGTAGGCCAGA	5539

OY	5521	GGCCCAAGGCTGTAAATCTGTCTACATTACATACCTTGGGCAAGAGACTTCTTCCCTGGC	5588
Db	5540	GGCCCAAGGCTGTAAATCTGTCTACATTACATACCTTGGGCAAGAGACTTCTTCCCTGGC	5599
OY	5581	CCAGTTCACGGGGGTGGGAATCGACATCCAAAGGTCCCTTCACACATTAACGCTGCATGTTC	5640
Db	5600	CCAGTTCACGGGGGTGGGAATCGACATCCAAAGGTCCCTTCACACATTAACGCTGCATGTTC	5659
OY	5641	TAAAGTGAAGAAAGATGGGACAGTTCCCTCTCTCAACCCAGCCCGGTGTCCACTTCAGGT	5700
Db	5660	TAAAGTGAAGAAAGATGGGACAGTTCCCTCTCTCAACCCAGCCCGGTGTCCACTTCAGAGT	5719
OY	5701	GAATACACAGGAAATCGACTGTGCCAATCCCGGACTGCAAAGGCCCTTGGGAGCCCTAC	5760
Db	5720	GAATACACAGGAAATCGACTGTGCCAATCCCGGACTGCAAAGGCCCTTGGGAGCCCTAC	5779
OY	5761	TGTCAAGGTCGTGCACGAGAGGTGAAGTCAGTGAAGCCATGCGCTCGAAGGGCTCTTG	5820
Db	5780	TGTCAAGGTCGTGCACGAGAGGTGAAGTCAGTGAAGCCATGCGCTCGAAGGGCTCTTG	5839
OY	5821	CCCTATTTGGGGACACATCCGGTTTCCCTGCGGCTCTACCGGAAATTCAGAGGGCTTTAGC	5880
Db	5840	CCCTATTTGGGGACACATCCGGTTTCCCTGCGGCTCTACCGGAAATTCAGAGGGCTTTAGC	5899
OY	5881	CGAATGAGTCATGGGGGGGGGGGGGTTCTGGGGGAGTCCCAAGCTAATCAACTTGGGA	5940
Db	5900	CGAATGAGTCATGGGGGGGGGGGGGTTCTGGGGGAGTCCCAAGCTAATCAACTTGGGA	5959
OY	5941	CAGGACACCTGGGAATTCGATGGTGGCTTATCCAAAGTGTGGGGGACAGAGCCCA	6000
Db	5960	CAGGACACCTGGGAATTCGATGGTGGCTTATCCAAAGTGTGGGGGACAGAGCCCA	6019
OY	6001	GACCCAAATGTCTTATCTCAGGTAGGGGCTCAGGAGGCTCCACAGACAGGACGCTCCGG	6060
Db	6020	GACCCAAATGTCTTATCTCAGGTAGGGGCTCAGGAGGCTCCACAGACAGGACGCTCCGG	6079
OY	6061	AGAGTTTGGGGGTAGGAATGGGAGACACAGGCTCTTTTTCCTCTTGAATTTGGG	6120
Db	6080	AGAGTTTGGGGGTAGGAATGGGAGACACAGGCTCTTTTTCCTCTTGAATTTGGG	6139
OY	6121	GGCTTTGGGGGACAGGCTTGAGAAATCCCAAAGAGAGGGGCAAAAGAGCACTCCCCACAAG	6180
Db	6140	GGCTTTGGGGGACAGGCTTGAGAAATCCCAAAGAGAGGGGCAAAAGAGCACTCCCCACAAG	6199
OY	6181	TCTGCCAAGAGAGAGAGAGAGACCCCGACTGAGCTGCACACTTCCCAAGAGGCTT	6235
Db	6200	TCTGCCAAGAGAGAGAGAGAGACCCCGACTGAGCTGCACACTTCCCAAGAGGCTT	6254

```

1  RESULT 3
2  US-09-845-020A-6
3  ; Sequence 6, Application US/09845020A
4  ; Publication No. US20030022850A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Treco, Douglas A.
7  ; APPLICANT: Seiden, Richard F.
8  ; TITLE OF INVENTION: Genomic Sequences for Protein Production
9  ; TITLE OF INVENTION: and Delivery
10 ; FILE REFERENCE: 50010/017003
11 ; CURRENT APPLICATION NUMBER: US/09/845,020A
12 ; CURRENT FILING DATE: 2001-04-27
13 ; PRIOR APPLICATION NUMBER: US 09/305,384
14 ; PRIOR FILING DATE: 1999-05-05
15 ; PRIOR APPLICATION NUMBER: US 60/084,649
16 ; PRIOR FILING DATE: 1998-05-07
17 ; NUMBER OF SEQ ID NOS: 8
18 ; SOFTWARE: FastSeq for Windows Version 4.0
19 ; SEQ ID NO 6
20 ; LENGTH: 2834
21 ; TYPE: DNA
22 ; ORGANISM: Homo sapiens

```

US-09-845-020A-6

Query Match 45.5%; Score 2834; DB 11; Length 2834;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2834; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1890 CCGGACAGTCTCACAAGCCCTGTTGCTCTGCGGCGCTTCCTGCTGGGCTCCGACATTC 1949
Db 1 CCGGACAGTCTCACAAGCCCTGTTGCTCTGCGGCGCTTCCTGCTGGGCTCCGACATTC 60
QY 1950 GGTGGCACTTGAAGAGCCCTTACAGCCACCGCTGCACTGTGGAGAGCCCTTCTCTGGGCTG 2009
Db 61 GGTGGCACTTGAAGAGCCCTTACAGCCACCGCTGCACTGTGGAGAGCCCTTCTCTGGGCTG 120
QY 2010 GCCAAGGCGCAGAGCGGCTCCCTCAGCTTTCAGAGGAGGTGTGAGAGGAGAGGCTTAAGCA 2069
Db 121 GCCAAGGCGCAGAGCGGCTCCCTCAGCTTTCAGAGGAGGTGTGAGAGGAGAGGCTTAAGCA 180
QY 2070 GGAACCCGGGCTGGCGACAGGCGCTTTCGCGGCGCAGCTGGAATTCGCGGTGGGCTGGGCTT 2129
Db 181 GGAACCCGGGCTGGCGACAGGCGCTTTCGCGGCGCAGCTGGAATTCGCGGTGGGCTGGGCTT 240
QY 2130 GGGCGGCGCCGCACTCGAGAGCAGGCGGCGCAGCCCTGCCAGGCGCCCGGCAATGAGAGGCT 2189
Db 241 GGGCGGCGCCGCACTCGAGAGCAGGCGGCGCAGCCCTGCCAGGCGCCCGGCAATGAGAGGCT 300
QY 2190 TAGACCCGGGCGCAGGCGCTGCGGAGGCTGTACTGGGTGTGCGGCGCCGACAGCTGCCAGCGCC 2249
Db 301 TAGACCCGGGCGCAGGCGCTGCGGAGGCTGTACTGGGTGTGCGGCGCCGACAGCTGCCAGCGCC 360
QY 2250 GGGCGCTGTGCTGCTCGATTTTCTCACTGGGCTTTCAGAGCCTTCCCGGCGGCGCAGAGGCTC 2309
Db 361 GGGCGCTGTGCTGCTCGATTTTCTCACTGGGCTTTCAGAGCCTTCCCGGCGGCGCAGAGGCTC 420
QY 2310 GGGACCTTCAGAGCCCGCCATGCTTCGAGCCTTCCCTTCATGAGGCTCTCTGTGCGGCGGAGCC 2369
Db 421 GGGACCTTCAGAGCCCGCCATGCTTCGAGCCTTCCCTTCATGAGGCTCTCTGTGCGGCGGAGCC 480
QY 2370 TCCCGAGAGCAGCAGCCCGCTGCTCCAGAGGCGGCGCAGCCAGCTTCAGAGGAGGAGGCT 2429
Db 481 TCCCGAGAGCAGCAGCCCGCTGCTCCAGAGGCGGCGCAGCCAGCTTCAGAGGAGGAGGCT 540
QY 2430 GAGAAGTGGCGGCGCAGCGGCGCAGGACTGGCAGGAGCCTTACCCTTCAGAGCCTTCGTGCTG 2489
Db 541 GAGAAGTGGCGGCGCAGCGGCGCAGGACTGGCAGGAGCCTTACCCTTCAGAGCCTTCGTGCTG 600
QY 2490 GAATCCACTGGGTGAAGCCAGAGCTGGGCTCTGAGTCTGGGTGGAAGCTTGAAGAACTTTTA 2549
Db 601 GAATCCACTGGGTGAAGCCAGAGCTGGGCTCTGAGTCTGGGTGGAAGCTTGAAGAACTTTTA 660
QY 2550 TGTCTAGCTCAGGGATGTAATATACCAATCAGACCCGCTGTACTGCTAGCTAAGGCTCTGT 2609
Db 661 TGTCTAGCTCAGGGATGTAATATACCAATCAGACCCGCTGTACTGCTAGCTAAGGCTCTGT 720
QY 2610 GAATGCACCAATCCACACTCTGTATCTAGTACTCTGATGGGCGCTTGGAGAACTTTAT 2669
Db 721 GAATGCACCAATCCACACTCTGTATCTAGTACTCTGATGGGCGCTTGGAGAACTTTAT 780
QY 2670 GTCTAGCTCAGGAGTTTAAATATACCAATTCGAGCTCTGTATCTAGCTCAAGGTTTETA 2729
Db 781 GTCTAGCTCAGGAGTTTAAATATACCAATTCGAGCTCTGTATCTAGCTCAAGGTTTETA 840
QY 2730 AACAACCAATCAGACACCCCTGTGTAGCTCAGGCTATGTGAATGCACCAATTCAGAGTTC 2789
Db 841 AACAACCAATCAGACACCCCTGTGTAGCTCAGGCTATGTGAATGCACCAATTCAGAGTTC 900
QY 2790 TGTATCTGCTACTTTTCATGGGCTCCGCTGTGAAGAGAACCAAGGCTTGTGTGA 2849
Db 901 TGTATCTGCTACTTTTCATGGGCTCCGCTGTGAAGAGAACCAAGGCTTGTGTGA 960
QY 2850 GCAATAAAGCTTTCATCACTGGGTGAGGCTGGGCTGAGTCCGAAAAGAGAGTCAAGGAA 2909
Db 961 GCAATAAAGCTTTCATCACTGGGTGAGGCTGGGCTGAGTCCGAAAAGAGAGTCAAGGAA 1020
```

```
QY 2910 GGGAGATTAAGGTGGGCGCGTTTATAGAGATTTGGGTAGCTAAAGGAAATTAACATCA 2969
Db 1021 GGGAGATTAAGGTGGGCGCGTTTATAGAGATTTGGGTAGCTAAAGGAAATTAACATCA 1080
QY 2970 AGGGGCTTGTCTCTCGGGGCGCAGAGTGGGGGCTCCGAAGTGTCTAGTGGGGTGTCT 3029
Db 1081 AGGGGCTTGTCTCTCGGGGCGCAGAGTGGGGGCTCCGAAGTGTCTAGTGGGGTGTCT 1140
QY 3030 TTTTGAAGCAGAGATGAGCCAGGAAAGAAAGACTTTCACAAAGTATGATCAATTAAGGCA 3089
Db 1141 TTTTGAAGCAGAGATGAGCCAGGAAAGAAAGACTTTCACAAAGTATGATCAATTAAGGCA 1200
QY 3090 AGGACCCGCGCATTTACACCTCTTTGTGTGATGTCAATCATGTTAAGTTGGGCGAGGCG 3149
Db 1201 AGGACCCGCGCATTTACACCTCTTTGTGTGATGTCAATCATGTTAAGTTGGGCGAGGCG 1260
QY 3150 ATATTCACCTCTTTTGTGATTTCTCAGTACTTTCAGGCGCATGCGGCGTATATGTGCAAG 3209
Db 1261 ATATTCACCTCTTTTGTGATTTCTCAGTACTTTCAGGCGCATGCGGCGTATATGTGCAAG 1320
QY 3210 TTACAGGGGATGCGATGGCTTGGCTTGGCTCAGAGGCTTTCAGAGCTACTTGTGGGCG 3269
Db 1321 TTACAGGGGATGCGATGGCTTGGCTTGGCTCAGAGGCTTTCAGAGCTACTTGTGGGCG 1380
QY 3270 CTTCGAGAAATGTTTGTGTGACACTCTGTATCTAGTTAATCTAGTGGGAGCTGAGAAC 3329
Db 1381 CTTCGAGAAATGTTTGTGTGACACTCTGTATCTAGTTAATCTAGTGGGAGCTGAGAAC 1440
QY 3330 CTTTGTGCTACCTCAGGAGTTGTAAGCAGCAATCAGCGGCGTGTCAAAACAGACGAC 3389
Db 1441 CTTTGTGCTACCTCAGGAGTTGTAAGCAGCAATCAGCGGCGTGTCAAAACAGACGAC 1500
QY 3390 TCGGCTCTACCAATCAGCAGAGATGTGGGTGGGCGCAGATTAAGATAATAAAGAGGCTC 3449
Db 1501 TCGGCTCTACCAATCAGCAGAGATGTGGGTGGGCGCAGATTAAGATAATAAAGAGGCTC 1560
QY 3450 CCGAGCCAGCAGTGGCAGACGCGCAGAGTCCCTATTCACAAATATGGCAGCTTGTCTTT 3509
Db 1561 CCGAGCCAGCAGTGGCAGACGCGCAGAGTCCCTATTCACAAATATGGCAGCTTGTCTTT 1620
QY 3510 TGCCTGTTTGCATTAATCTTGTACTGCTGCTTGTGCTTGTGGGTGCACAGCTCTTTATAGAC 3569
Db 1621 TGCCTGTTTGCATTAATCTTGTACTGCTGCTTGTGCTTGTGGGTGCACAGCTCTTTATAGAC 1680
QY 3570 TGTAACTCTACACAGAGGCTTCAGAGCTTCACTCTGTGAAGCCACTTAAGACGACGAGCC 3629
Db 1681 TGTAACTCTACACAGAGGCTTCAGAGCTTCACTCTGTGAAGCCACTTAAGACGACGAGCC 1740
QY 3630 ACCGGGAGGATGAACAACCTCGGCGCGGCTGCTTTAAGAGCTATTAACACTCACCGCGAA 3689
Db 1741 ACCGGGAGGATGAACAACCTCGGCGCGGCTGCTTTAAGAGCTATTAACACTCACCGCGAA 1800
QY 3690 GGTTCGAGGCTTCACTCTCAGCGCAGCGAGACCAAGAACCCGCAAGGAGGAAATTCG 3749
Db 1801 GGTTCGAGGCTTCACTCTCAGCGCAGCGAGACCAAGAACCCGCAAGGAGGAAATTCG 1860
QY 3750 GAACACATCTGATCAATCAGAAAGAAACAACCTTCAGATGCACCACTTAAGAGCTGTAA 3809
Db 1861 GAACACATCTGATCAATCAGAAAGAAACAACCTTCAGATGCACCACTTAAGAGCTGTAA 1920
QY 3810 CTCACCTGCGAGGCTCCGCGGCTTCTTGTGAAGTCACTGAGACCAACACACTCACAGTT 3869
Db 1921 CTCACCTGCGAGGCTCCGCGGCTTCTTGTGAAGTCACTGAGACCAACACACTCACAGTT 1980
QY 3870 TCGGACACAAAGCCGAGGAGTTTGAATAGCTGGGCGCAACATGATGAATGCGCTCTG 3929
Db 1981 TCGGACACAAAGCCGAGGAGTTTGAATAGCTGGGCGCAACATGATGAATGCGCTCTG 2040
QY 3930 CAAAAAATTTTCAAAAAATTTGCGGAGGAGATGAGTGGTGGCTGCTGGGCGGAG 3989
Db 2041 CAAAAAATTTTCAAAAAATTTGCGGAGGAGATGAGTGGTGGCTGCTGGGCGGAG 2100
```

```

Oy 3990 CTACGGGAGGCTAAAGTGGAGAGTCCCTTGAGCCCTGGAGGTGAAGACTGCACTGAG 4049
    |||||||
Db 2101 CTACGGGAGGCTAAAGTGGAGAGTCCCTTGAGCCCTGGAGGTGAAGACTGCACTGAG 2160
Oy 4050 CTGTGATGTTACACAGCCCTCTAGGCTGGGGGAGAGACTGAGACCCTGTTTCCCTCCG 4109
    |||||||
Db 2161 CTGTGATGTTACACAGCCCTCTAGGCTGGGGGAGAGACTGAGACCCTGTTTCCCTCCG 2220
Oy 4110 CAAAAAATTTACAAAAATGTAATTAAGAGTGGCTGATGATGCTAGGCGCAGTGGCTCAT 4169
    |||||||
Db 2221 CAAAAAATTTACAAAAATGTAATTAAGAGTGGCTGATGATGCTAGGCGCAGTGGCTCAT 2280
Oy 4170 GCCTGTAATCCACACTTTTGGGAAGCCGAGCGGGCGGTCCACCTAAGATGAGAGTGT 4229
    |||||||
Db 2281 GCCTGTAATCCACACTTTTGGGAAGCCGAGCGGGCGGTCCACCTAAGATGAGAGTGT 2340
Oy 4230 GAGACAGCCCTGGCCAAACATGAGAGAAAGCCCATCTCTTCTAATAATACAAAAATTAGCCGG 4289
    |||||||
Db 2341 GAGACAGCCCTGGCCAAACATGAGAGAAAGCCCATCTCTTCTAATAATACAAAAATTAGCCGG 2400
Oy 4290 CTGTGGGGGAGAGTGGAGAGTCCCTGTAATCCACACTGCTAGAGAGCTGAGAGAGCA 4349
    |||||||
Db 2401 CTGTGGGGGAGAGTGGAGAGTCCCTGTAATCCACACTGCTAGAGAGCTGAGAGAGCA 2460
Oy 4350 GAATCACTTGAACCCAGAGAGCGGGGTGAGTGAAGAGATGCTGCTCATTTGACATCC 4409
    |||||||
Db 2461 GAATCACTTGAACCCAGAGAGCGGGGTGAGTGAAGAGATGCTGCTCATTTGACATCC 2520
Oy 4410 ACCCACTCCAGCTGGGGCAACAGAGCCAACTCTGTCTTAAAAAATTTAAAAAAGTG 4469
    |||||||
Db 2521 ACCCACTCCAGCTGGGGCAACAGAGCCAACTCTGTCTTAAAAAATTTAAAAAAGTG 2580
Oy 4470 CCTGACATTAAGAAGTGTGCAATGATGTCAGAGGCAACATGTTAAAGTAAAGTGTGA 4529
    |||||||
Db 2581 CCTGACATTAAGAAGTGTGCAATGATGTCAGAGGCAACATGTTAAAGTAAAGTGTGA 2640
Oy 4530 GCTCTGCTTCATGTCCTGTTAAAAAACCACCTCAAGCCGAGTGTGAGTGGCTCAT 4589
    |||||||
Db 2641 GCTCTGCTTCATGTCCTGTTAAAAAACCACCTCAAGCCGAGTGTGAGTGGCTCAT 2700
Oy 4590 GCCCTAATATCCAGACACTTTTGGAGCGGAGCGGGGTGATCACCCTGAGGTGAGAGTTC 4649
    |||||||
Db 2701 GCCCTAATATCCAGACACTTTTGGAGCGGAGCGGGGTGATCACCCTGAGGTGAGAGTTC 2760
Oy 4650 GAGACAGCCCTGAGCAGCAGCAATGTTGAATCCCACTCTAATAAATACAAAAATTGAG 4709
    |||||||
Db 2761 GAGACAGCCCTGAGCAGCAGCAATGTTGAATCCCACTCTAATAAATACAAAAATTGAG 2820
Oy 4710 TGAGCATGTGTGTG 4723
    |||||||
Db 2821 TGAGCATGTGTGTG 2834
    |||||||

```

```

RESULT 4
US-09-845-020A-7
: Sequence 7, Application US/09845020A
: Publication No. US20030022850A1
: GENERAL INFORMATION:
: APPLICANT: Treco, Douglas A.
: APPLICANT: Heartlein, Michel W.
: APPLICANT: Seiden, Richard F.
: TITLE OF INVENTION: Genomic Sequences for Protein Production
: FILE REFERENCE: 50010/017003
: CURRENT APPLICATION NUMBER: US/09/845, 020A
: CURRENT FILING DATE: 2001-04-27
: PRIOR APPLICATION NUMBER: US 09/305,384
: PRIOR FILING DATE: 1999-05-05
: PRIOR APPLICATION NUMBER: US 60/084,649
: PRIOR FILING DATE: 1998-05-07
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7

```

```

: LENGTH: 1252
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-845-020A-7

Query Match      20.1%; Score 1252; DB 11; Length 1252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4728 CCTGTAATCCACACTTCTGAGAGCTGAGGCAAGAAATCACTAGAACAGAGGAGCGG 4787
    |||||||
Db 1 CCTGTAATCCACACTTCTGAGAGCTGAGGCAAGAAATCACTAGAACAGAGGAGCGG 60
Oy 4788 AGGTGTGATGAGCCGAGATGCTGCACTTGCACCTCCAGAGCTGAGCAATGAGCGAATCC 4847
    |||||||
Db 61 AGGTGTGATGAGCCGAGATGCTGCACTTGCACCTCCAGAGCTGAGCAATGAGCGAATCC 120
Oy 4848 ATCTCAAAAAAACAACAACAAACCACTCTCTACTCCAGAGAGTGGGTACAGACT 4907
    |||||||
Db 121 ATCTCAAAAAAACAACAACCACTCTCTACTCCAGAGAGCTGGGTACAGACT 180
Oy 4908 GGGCCACATCAGTGCAGAGTGTGAGCCACAGAGCTAAGGCGAGCTGACAGACCGGA 4967
    |||||||
Db 181 GGGCCACATCAGTGCAGAGTGTGAGCCACAGAGCTAAGGCGAGCTGACAGACCGGA 240
Oy 4968 CCAGTATACAGTGTGATGATCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 5027
    |||||||
Db 241 CCAGTATACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Oy 5028 CAGGGGGCCCCCAGCAGCAGAGATGGCCCATCCAGTCCACATCCACTTCTCATCA 5087
    |||||||
Db 301 CAGGGGGCCCCCAGCAGCAGAGATGGCCCATCCAGTCCACATCCACTTCTCATCA 360
Oy 5088 GAGATGTGTTCTTCTGACACGCTGGGTAAATTAAGACAGAGTGAAGTGTGAGTGTG 5147
    |||||||
Db 361 GAGATGTGTTCTTCTGACACGCTGGGTAAATTAAGACAGAGTGAAGTGTGAGTGTG 420
Oy 5148 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5207
    |||||||
Db 421 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Oy 5208 CGGGCAGGTGTGCTACGCTGTATCCAGACTTTTGGAGCGGAGCGGGGTGATCA 5267
    |||||||
Db 481 CGGGCAGGTGTGCTACGCTGTATCCAGACTTTTGGAGCGGAGCGGGGTGATCA 540
Oy 5268 CGAGTGTGAGATGTGATCACTCTGCTTAACACGTTGAACCCCGTCTCTACTAATAA 5327
    |||||||
Db 541 CGAGTGTGAGATGTGATCACTCTGCTTAACACGTTGAACCCCGTCTCTACTAATAA 600
Oy 5328 TACAAAAAATTTGGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5387
    |||||||
Db 601 TACAAAAAATTTGGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Oy 5388 AGCGAGAGAAATGCGGTGAACCCGAGAGGAGAGTTCAGTGAAGCCGAGATCCGCCAC 5447
    |||||||
Db 661 AGCGAGAGAAATGCGGTGAACCCGAGAGGAGAGTTCAGTGAAGCCGAGATCCGCCAC 720
Oy 5448 TGCACCTCAGCTGGGGCAGACAGAGACTCCATCTGAAAAAGAAAAAGAAAGCTTCA 5507
    |||||||
Db 721 TGCACCTCAGCTGGGGCAGACAGAGACTCCATCTGAAAAAGAAAAAGAAAGCTTCA 780
Oy 5508 GGTGTGAGCCAGAGGCGCAGGCTGTAAATCTGTCACTTAACATGACCTTGGGCAAGGAGC 5567
    |||||||
Db 781 GGTGTGAGCCAGAGGCGCAGGCTGTAAATCTGTCACTTAACATGACCTTGGGCAAGGAGC 840
Oy 5568 TTCTCTTCCCTGGCCAGTTCAAGCGGGGTGGAATGCACTCAAGAGTCCCTCCAGATTAA 5627
    |||||||
Db 841 TTCTCTTCCCTGGCCAGTTCAAGCGGGGTGGAATGCACTCAAGAGTCCCTCCAGATTAA 900
Oy 5628 CGCTGCAATGTTCTTAAGATGAGAAAGATGGGCAAGTTTCCCTCTCAACCCAGCCGCTG 5687
    |||||||
Db 901 CGCTGCAATGTTCTTAAGATGAGAAAGATGGGCAAGTTTCCCTCTCAACCCAGCCGCTG 960
    |||||||

```

[illegible]

```

RESULT 5
US-09-954-556-29/C
: Sequence 29, Application US/09954556
: Publication No. US20030078219A1
: GENERAL INFORMATION:
: APPLICANT: Brett P. Monta
: APPLICANT: Susan M. Freiler
: APPLICANT: Scott Cooper
: TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
: FILE REFERENCE: RTS-0250
: CURRENT APPLICATION NUMBER: US/09/954,556
: CURRENT FILING DATE: 2001-09-14
: NUMBER OF SEQ ID NOS: 108
: SEQ ID NO 29
: LENGTH: 36221
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)...(36221)
: OTHER INFORMATION: n = A,T,C or G
US-09-954-556-29

```

	Query Match	16.1%	Score 1002.2	DB 11	Length 36221
	Best Local Similarity	73.8%	Pred. No. 8.3e-25		
	Matches 1515	Conservative 0	Mismatches 338	Indels 200	Gaps 11
QY	1857 GTGATGGCTTGACCCTGAGAGGTGACAGCATGCCGGCAGTCTCTCACAGCCCTGTTCCG				
Db	4120 GGGGCTGTGCTATTACTGAGAGGTGACACGCTGCTGGCAGTCCACAGCCCTGCTTGC				
QY	1917 TCTGGGGGCCCTCTGCTGGGGCTCCACACTTGGGTGGCACTTATGAGAGCCCTTACAG---				
Db	4060 TCTGGGCACTCCCTGCTGGGGCTCCACACTTGGGTGGCACTTATGAGAGCCCTTACAGCC				
QY	1974 -----CCACCGCTGACGTGTGGAGGCCCTTCTGGGGTGGCAGAGGCCAGAGCCGGC				
Db	4000 CCCCCCCCCCACTGACACTGTGGAGCCCTTCTGAGGCTGGCAAGGCTGGAGCCAC				
QY	2028 TCCCTCACTTGCAGGAGGTGTGGAGGAGAGGCTCAAGCAGGACCGGGGCTGGCCAC				
Db	3940 TCCCTCACTTGCAGGAGGTGTGGAGGAGAGGCTGAGAGGGGAAGGGGGGCTGCTCG				
QY	2088 GGCCTTGCGGGGCCAGCTGAGATTCCGGGTGGGGGTGGCTTGGCGGGCCCGGACTCGG				
Db	3880 GGCCTTGCGGGGCCAGCTGAGATTCCGGGTGGGGGTGGCTTGGCAGGCCCCCGACTCGG				
QY	2148 AGCAGCGGGCAGCCCTGCGAGGCCCGGGCAATGAGAGGCTTAGCACCCGGGCGACGG				
Db	3820 AGCAGCGGGCAGCCCTGCGAGGCCCGGGCAATGAGAGGCTTAGCACCCGGGCGACGG				
QY	2208 CTGCGAGAGGTGTACTGGGTGCCCAAGACTGCCAGCCCGCGGCTGCTGCTGCAGA				

[illegible]

[illegible]

QY 2174 CGGGCAATGAGAGGCTTAAAGCACCAGCGGCGAGAGGCTGTAAGTGGTCCCA 2233
|||||
Db 22182 CGGCGAGTGAAGGGCTTAAAGCACCAGCGGCTGGGAG-----GTACCA 22135
QY 2234 GCAATGCCAGCCCGCGGCTGTGTCTGATTTCTCACTGGGCTTACAGCCCTTC 2293
|||||
Db 22134 GCAATGCCAGCCCGCGGCTGTGTCTGATTTCTCACTGGGCTTACAGCCCTTC 22079
QY 2294 CCGGGGGGAGGGGCTCGGGAGCTGAGCCCGCATGCTGAGCTCC-----CTCATG 2348
|||||
Db 222078 CCGAGGGAGGAGGCTCGGGA-CTGACAGCCCGCATGCTGAGCTTCACCCATCCATG 222020
QY 2349 GGCCTGTGTGGGCGCGAGCTCCCGAGCAGCACCACCCCTGCTCCAGAGCCAGT 2408
|||||
Db 222019 GGCCTGTGTGGGCGCGAGCTCCCGAGCAGCACCACCCCTGCTCATAGCTCCAGT 221960
QY 2409 CCCATGACACACGAGAGGGCTGAGAGTGGGGGCGACAGGACCGGAGTGGAGGACG 2468
|||||
Db 221959 CCCATGACACACGAGAGGGCTGAGAGTGGGGGCGACAGGACCGGAGTGGAGGACG 221901
QY 2469 TACCCCTGAGCCCTGTGGGAGTTCACCTGGGTGAAGCCAGCTGGGCTCTGAGTGG 2528
|||||
Db 221900 TCCACTGACAGCCCTGTGGGAGTTCACCTGAAGGAGGAGGCTGGGCTCTGAGTGG 221841
QY 2529 TGGAGACTGGAGAACCTTATGTCTAGCTCAGGAGTGTAAATACACATCAGCACC 2588
|||||
Db 221840 TGGGAGAGTGGAG--TCTTATGTCTAGCTCAGGAGTGTAAATACACATCAGCACC 221783
QY 2589 TGTGTCTAGCTCAGGAGTGTGAATGACACATCAGCTGTATCTAGCTAGTGTAT 2648
|||||
Db 221782 TGTGTCTAGCTCAGGAGTGTGAATGACACATCAGCTGTATCTAGCTAGTGTAT 221723
QY 2649 GGGGCTTGGAGACTTATGTCTAGCTCAGGAGTGTAAATACACATCAGCACCCT 2708
|||||
Db 221722 GGGGCTTGGAGACTTATGTCTAGCTCAGGAG----- 221688
QY 2709 GTATCTAGCTCAGGAGTGTAAACACACATCAGCACCCTGTGTAGCTCAGGAGT 2768
|||||
Db 221687 -----TTGTAAACACACATCAGCACCCTGTGTAGCTCAGGAGT 221644
QY 2769 TGAATGACCAATGACAGTGTGTATCTGCTACTTTCATGAGGAGTCCGTGTGAAGAC 2828
|||||
Db 221643 TGAATGACCAATGACAGTGTGTATCTGCTACTTTCATGAGGAGTCCGTGTGAAGAC 221603
QY 2829 CACCAACAGGCTTGTGTGAGCAATTAAGCTTATCAGCTGGGTGAGGTGGGCTGAG 2888
221602 ----- 221603
QY 2889 TCCGAAAGAGAGTACAGGAGGAGATTAAGGTGGGCGTATTATAGATTGGGTAG 2948
221602 -----GCCTTGGAGAAC 221591
QY 2949 GTAAAGAAATTAACACTCAAGGGGTTTGTCTGTGGCGGAGAGTGGGGGCTGCG 3008
221590 CTTTATGTCTAGCTCAGGAGTGTGTATACACCAATTGAC----- 221551
QY 3009 AAGGTGTCAGTGGGGTGTCTTTTGAAGCAGATGAGCCGAGAAAGACTTTCACAG 3068
221550 -----ACTGTATCTAG 221540
QY 3069 GTATGTCAATTAAGAGCAGGAGCCGCATTTACACCTTTTGTGGTGAATGCA 3128
221539 CTCAAGGTTTGTAAACACACATCAGCACCCTGTGTGTAGCTCAAGTTTGGCAATGCA 221480
QY 3129 TCACTTAAGTTGGGCGAGGGCATTTCACTTTTGTGATTTCTCACTTCAAGGCC 3188
221479 CCAATGCA----- 221472
QY 3189 ATCTGGGCGTATATGTGCAAGTTACAGGAGTGGGATGGCTTGGCTCAGAGGCT 3248
221471 -----CACTGTGT 221464
QY 3249 TGACAGTACTCTGTGGGGCTTGGAGAAATGTTTGTGTGACACTCTGTATCTAATTA 3308

Db 221463 ATCTAGTCTGTGGTGGGCGCTTGAAGAACCTGTGTCAAAACTGTAACTAATTA 221404
QY 3309 TCTAGTGGGAGCGTGGAGAACCTTTGTCTAGCTCAGGAGTGTAAACGACCAATAG 3368
Db 221403 TCTAGTGGGAGCGTGGAGAACCTTTGTCTAGCTCAGGAGTGTAAACGACCAATAG 221344
QY 3369 CGCCCTGTCAAAACAGACACTCGGCTTACCAATCAGAGATGTGGGTGGGCGAGAT 3428
Db 221343 CACCTGTCAAAACAGGAGCTCGCTTACCAATCAGAGATGTGGGTGGGCGAGAT 221284
QY 3429 AAGAAATTAAGAGAGGCTGGCCGAGCAGCAGTGGGCAACGACAGTCCCTATCCAC 3488
221283 AAGAAATTAAGAGAGGCTGGCCGAGCAGCAGTGGGCAACGAGATGTGGGTGGGCGAGAT 221224
QY 3489 AATATGAGCTTGTCTTTTGTCTGTGTGAGTAAATCTTGTACTGTCTGCTTTTGG 3548
221223 ACTGTGAGAGCTCGTCTTGTCTGTGTGAGTAAATCTTGTACTGTCTGCTTTTGG 221164
QY 3549 GTCCAGACTGCTTTATAGCTGTAAACACTCAGCAGAGGCTGACCTTCACTCTGA 3608
221163 GTCCAGCGCTTTTATAGCTGTAAACACTCAGCAGAGGCTGACCTTCACTCTGA 221104
QY 3609 AGCCACTAAGACCAAGAGCCAGCGGAGAGTGAATCAACTCCGCGCTGCTTAAG 3668
221103 GCCAGAGGAGACAGAGAGCCAGTGGAGAGACAGCAACTCCAGAGCGCTGCTTAAG 221044
QY 3669 AGCTAATCACTCAGCCGAGAGTGTGTGAGCTTCACTCTCAGCAGCAGCAGAC 3728
Db 221043 AGCTAATCACTCA-CCGGAAGTGTGTGAGCTTCACTCTCAGCAGCAGCAGAC 220985
QY 3729 CCACAGAGAGAGAACTGGAGACACTGGAACATGGAAGAGCAAACTCCAGATGC 3788
220984 CCACAGAGAGAGAACTGGAGACACTGGAACATGGAAGAGCAAACTCCAGATGC 220925
QY 3789 ACCACTTAAGAGCTGTAAACACTCAGCTGAGAGGTCGCGGCTCTTCTGAAGTCA 3848
220924 GCCAAGTAAAGAGCTGTAAACACTCAGCAGAGGTCGCGCAGCTCATTTCTGAAGTCA 220865
QY 3849 GAGACCAAGACACTCAGCAGTTTCGAGACAA 3879
220864 GAGACCAAGACCACTCAGCAGTTTCGAGACAA 220834
Db 220864 GAGACCAAGACCACTCAGCAGTTTCGAGACAA 220834
RESULT 8
US-10-002-491-10
; Sequence 10, Application US/10002491
; Publication No. US20030109467A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Mont
; TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION
; FILE REFERENCE: RUS-0239
; CURRENT APPLICATION NUMBER: US/10/002,491
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 91000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 73772-74071
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: (576)...(19018)
; LOCATION: (576)...(19018)
; OTHER INFORMATION: Intron 1
; NAME/KEY: Intron
; LOCATION: (19154)...(19785)
; OTHER INFORMATION: Intron 2
; NAME/KEY: Intron
; LOCATION: (19919)...(37293)
; OTHER INFORMATION: Intron 3

```

; NAME/KEY: Intron
; LOCATION: (37660)...(58973)
; OTHER INFORMATION: Intron 4
; NAME/KEY: Intron
; LOCATION: (59115)...(61405)
; OTHER INFORMATION: Intron 5
; NAME/KEY: Intron
; LOCATION: (61540)...(63027)
; OTHER INFORMATION: Intron 6
; NAME/KEY: Intron
; LOCATION: (63127)...(63463)
; OTHER INFORMATION: Intron 7
; NAME/KEY: Intron
; LOCATION: (63564)...(67187)
; OTHER INFORMATION: Intron 8
; NAME/KEY: Intron
; LOCATION: (67335)...(87922)
; OTHER INFORMATION: Intron 9
; NAME/KEY: Intron
; LOCATION: (88037)...(89288)
; OTHER INFORMATION: Intron 10
; US-10-002-491-10
```

Query Match 11.0%; Score 683.2; DB 14; Length 91000;

Best Local Similarity 89.2%; Pred. No. 1.1e-169; Indels 13; Gaps 5;

Matches 796; Conservative 0; Mismatches 83;

```

QY 1873 TGAAGGTGACAGAGTCCGCGAGTCTCTACAGCCCTCGTTCGCTCGCGCCCTCTCT
DB 85237 TGAGAGGTGACAGAGTCTCTGAGTCTCTGAGAGCCCTGCTGCTCGGACCTCTCT
QY 1933 GCCTGGGCTCCCACTTGGTGGGCACTTGAGAGAGCCCTTACAGCCACCGCTCACTG
DB 85297 GCTGGGCTCCCACTTGGGCACTTGAGAGAGCCCTTACAGCCACCTCACTG
QY 1993 AGCCCTTCTGGGCTGGCCAGAGAGCCGCTCCCTAGCTTGAGAGAGGTTGG
DB 85357 AGCCCTTCTGGGCTGGCCAGAGAGCCGCTCCCTAGCTTGAGAGAGGTTGG
QY 2053 AGGAGAGGCTCAAGAGAAACGGGGCTGGCAAGGCGCTTGGGGGCACTGAGTTTC
DB 85417 AGGAGAGAGAGCGAGCGGAAACGGGGCTGGCAAGGCGCTTGGAGGCACTGGAATTC
QY 2113 CGGGTGGGCTGGGCTGGGCGGCGCCGCACTCGGAGAGAGGCGCCAGCTGCGAGCC
DB 85477 CGGGTGGGCTGGGCTGGGCGGCGCCGCACTCGGAGAGAGGCGCTGACTGGGTCCCC
QY 2173 CCGGGCAATGAGAGGCTTAGACACCGGGGCAAGCGGCTGCGGAGAGGTTACTGGTCC
DB 85536 CCGGGTAAATAAGGACTTAGACACCGGGGCAAGTGGTGGAGGTTACTGGGTCCCC
QY 2233 AGAAGTCCAGCCCGCGCGCTGTGCTCGCTGATTTCTCACTGGGCTTAGAGAGCTT
DB 85596 AGCAGTCCAGCCCGCGCGCTGTGCTCGCTGATTTCTCACTGGGCTTAGAGTCC
QY 2293 CCGGCGGGAGAGGCTGGGAGCTGAGAGCCCGGCACTGCTGAGCTTCC-----CTCAT
DB 85652 CCGGAGGGGAGAGGCTGGGAGCTGAGAGCCCGGCACTGAGCTTCCACCCACTCAT
QY 2348 GGGCTCTGTGCGGCGCGAGCTCCCGAGAGCAGCACCCTCGCTCCACAGGCGCAG
DB 85712 GGGCTCTGTGCGGCGCGAGCTTCCCGAGAGCAGCACCCTCGCTCCACAGGCGCAG
QY 2408 TCCCATCGACAGCAGGAGCTGAGAGTGGGCGAGCAGGCAACCGGAGTGGCAGGAGC
DB 85772 TCCCATCGACAGCAGGAGCTGAGAGTGGGCGAGGAGGAGGAGGAGGAGGAGGAG
QY 2468 CTACCCCTGAGCCCTGTGCTGCGGATCTCACTGGGTGAGAGCAGCTGGGCTCTGAGTCTG
DB 85831 CTTCACCTGAGCCCTGTGCTGCGGATCTCACTGAGTGAAGCAGAGCTGGGCTCTGAGTCTG
QY 2528 GTGGAGACTGGAGAACCTTTATGTCTAGTCAAGGAGTCTGTAATTAACCAATAGCAGCC
```

```

DB 85891 GTGGGAGCTGAGAGTCTTTATATCTAGCTCAGGAGTAAACACCAATAGCAGCC
QY 2588 CTGTGTAGCTAGGAGTCTGTGAATGACCAATGACACCTGTATGACTAGCTGTA
DB 85951 CTGTGTAGCTAGGAGTGTGTGAGTGCACCAATGAGACA--CTGTATCTAGTGTCTG
QY 2648 TGGGCGCTTGGAGAACCTTTATGTCTAGCTCAGGAGTGTAAATACCAATGCGCAGTC
DB 86009 TGGGCGCTTGGAGAACCTTTATGCTTACCTCAGGAGTGTAAATACCAATGAGCAGCC
QY 2708 TGTATCTAGCTCAGGAGTGTAAACACCAATGACACCCGCTGTCTAGCT
DB 86069 TGTGTAGCTCAGGAGTGTGTGAATGACCAATGACACCTGTATCTAGCT

RESULT 9
US-10-012-984-14
; Sequence 14, Application US/10012984
; Publication No. US20030118561A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
; FILE REFERENCE: RTS-0334
; CURRENT APPLICATION NUMBER: US/10/012,984
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 14
; LENGTH: 104000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 14992
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 14993
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 14994
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 14995
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 14996
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 14997
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 14998
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 14999
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 15000
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 15001
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 15002
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 15003
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 15004
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 15005
; OTHER INFORMATION: unknown
```

NAME/KEY: unsure
 LOCATION: 15006
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15007
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15008
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15009
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15010
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15011
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15012
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15013
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15014
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15015
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15016
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15017
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15018
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15019
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15020
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15021
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15022
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15023
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15024
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15025
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15026
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15027
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15028
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15029
 OTHER INFORMATION: unknown
 NAME/KEY: unsure

LOCATION: 15030
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15031
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15032
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15033
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15034
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15035
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15036
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15037
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15038
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15039
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15040
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15041
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15042
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15043
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15044
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15045
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15046
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15047
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15048
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15049
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15050
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15051
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15052
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 15053
 OTHER INFORMATION: unknown

Query Match

10.7%; Score 670; DB 14; Length 104000;


```

: APPLICANT: Brenner, Michael B
: APPLICANT: Behar, Samuel M
: TITLE OF INVENTION: Soluble CD1 Compositions and Uses Thereof
: FILE REFERENCE: B00801/70212
: CURRENT APPLICATION NUMBER: US/09/874,470
: PRIOR FILING DATE: 2001-06-05
: PRIOR APPLICATION NUMBER: US 60/209,416
: PRIOR FILING DATE: 2000-06-05
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO: 5
: LENGTH: 10351
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-874-470-5

Query Match      10.5%; Score 652.8; DB 9; Length 10351;
Best Local Similarity 58.4%; Pred. No. 3.4e-162;
Matches 1626; Conservative 0; Mismatches 942; Indels 218; Gaps 19;

73  ATTATGCCGGGCGATGTGGCTCAGCTCTGTAATCCCTGAACTTTGGACATCAAGCAA 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2709  AATCAGCCAGGCGAGGTGGTCACACCCGTAATCCAGCACTTTGGGAAGCCAGGCGAG 2650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
133  GTGATCACTTGAGGTGAGAGTGGAGCTAGCTGCGCGCAACATGTTGAATCCCTATCT 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2649  GGGAA-----TTGAGACACAGCCTTGCCACATGGCGAAACCTGTCT 2607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193  CCACATAAAATATACAAATATATAGCCAGCATGTGGAGCACTGTATCCCGCTACT 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2606  CTACCAAAAAAAGTAAATATATGCGAGTGCATGATGTGCTGTATTTCCAGCTACT 2547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
233  CAGAGGCTGAGGCGAGAGATCACTTGAACCCAGAGGCGGAGGTTCAGTGAAGCTGAG 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2546  CAGGAGGCTGAGGCGAGAGATTCCTTGAGCTTAGAGGTGAGATTCAGAGGAACTGAG 2487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
313  ATCAACCACTGCATCCAGCCTGGGTGTGACAGAGCAAGCTCTATCTCAAAAAATATA 372
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2486  ATTGTCCACGTGTACTACTCTGCTGGCAGAGAGGTGACTGTGTTCAAAAAA 2427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
373  AAAATAAAAAATATAGCCAGGCATGTAGTGACACACTCTAGCTCAGCTCAGAGAG 432
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2426  AAGAGGGAATTTTAAAAATCAATTGGCAAGTAA----- 2392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
433  CTGAGGTGGAGGATCACTTGAACCTGGGGCAGTCAAGGCTACAGTGAAGCAAGATCATG 492
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2391  ----- 2392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
493  CCACATCACTCCAGCTGGGCAACAGAGAGACCCCTGTCTATAAAAAATATAATAT 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2391  -----ATTAAGCAAAATATATTTAGAAATATAAACAATGTGTAT 2350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
553  AAGAGAAAAAAGAGCTGTGTATGTCTCTGTCATCACTACTACTGTATATAGTT 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2349  CCAGAAAAAATTTGCACTTTTATGTAAGTAAAGATTAACACACCTTAGTTTAAATTTTGA 2290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
613  TGCAAATCTCAAGATCAAGATAGTCAATTTTGTAGCTTTGGCCGTGTCTGTCT 672
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2289  GGCTACAGAACTCAAGATTAAGTCAAAATTTACTGAGCAAAAGTAAATTAATCTGACAG 2230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
673  ACAATCACTGTGCGCTGTCTTCTAGCAAAAGCAAGCATATAACATCACTACATGAT 732
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2229  CAACCCCATATCATTAACAAATATATGAAATTCCTTAATTTAAATTAATCCAGAA-- 2172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
733  TTTTATAGACATGAGATTTGAATTTATATGATTTTATATTTTAAATTAATCTTT 792
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2171  ----GATAAATTCAGAAAGAAAAATATATATTTTATTTTGTATATATATATGT 2116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
793  TTTAAAAATTTTCCCTTAACATTTTAAAGTAAAGCGGCGCAGCGCCATCTGTACAG 852
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2115  ACAATTAATTTCTTCTGCTTTACAAAAATTCATCATGTTGGCCAGGCAAGTGGCTCACT 2056
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
853  CCTGTAATTCAGCACTTTGGAGGCTGAGTGGGCAAGTCACTTGAGATCAACAGTTGCG 912
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2055  CCTGTAATCCAGCACTTTGGAGGCGGAGGAGAGATCA--GGAGTCAAGGATGCG 1998
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
913  AGACCAAGCTGGCCCAATAGCAAAACCC-ATTCTACTAAATATAAATTAATTAAGTCTG 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1997  AGACCATCTGCTTAACAGGTGAACCCCTCTACTATAAATACAAAAAATTAATTAAGCAG 1938
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
972  GGCATATGATGTCACACCTGTATCCACTACTTTGGGAGGCTGAGGCGAGGAATCGCT 1031
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1937  GGCATGTTGGCAGCTGCTATGCTGTCACACTATTCAGAACTGAGGCAAGAAATCGCT 1878
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1032  TGAACCTGGGAAGCGAGGTTGACAGGAGCCAAATCAATCACTGCACTCCAGCTGGG 1091
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1877  TGAACCTGGAGGAGAGAGTTGACAGGAGCCAAAGATGTGCGCACTGCACTCCAGCTGGG 1818
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1092  TGAACAGTGAAGCTTGTCTCAACGAAAAAAGTAAAGCCATTCCTAATTCAG 1151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1817  CAACAGAGAAAGCTCGTCTCAAAAAA-----AAAAATATTCATCACTAGTGC 1762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1152  TGTACATCACTGATCACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1761  CTAAACCACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1212  AGAGTGTGCTGGTCAAGAGACATACATTTCCACATTAATTAATTAATTAATTAATTAAT 1271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1701  AATTTCCCTCTTATGTTTCTGAGGCTGCGCCAGTCACTATGCAATCCCTTTTG 1642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1272  ATCCAGAGAGGTTTTTTTTTAAATCTACACTCCCGCAGCAAAATAGAGTTATCTC 1331
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1641  CCAAAACAGAAATATCTCTCAAAACATATTAATTAATTAATTAATTAATTAATTAAT 1589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1332  CAGATCTTTACAAAGATCTTAAGCCAGTACAGATGAAAGAAAGAGAGGAGGAGG 1391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1588  TTAATCTTTCTATGTAAGATTTTATGAGATTAACATTAATTAATTAATTAATTAAT 1529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1392  AAGCTGCCAGCCCTCTACACATGAAGAAATACCTGTAAGAGCTTGATGCTGGAA 1451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1528  ATTTTGTAGTACTTTGTACAAATGTAAGAAATGTTCCATCTGCTAATTTTTCAAA 1469
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1452  GGATGAATTAAGGGGCTCTGTAGAGCTGCGCCCTGTGAGTCACTGTGACTGTGAGGC 1511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1468  GAATTAATTAAGAGATTTATTTCTTTGCTTATTTTCAAGAAAGTATTCATTTCTACA 1409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1512  TCCAGTCACTGTCAGCCCATGCTGATGAGCCAGTGAATTAAGAGCCCTCACTCTGTT 1571
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1408  TACTTAATTTCTGTTTGTATATTAATTAATTAATTAATTAATTAATTAATTAATTTT 1349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1572  TGG---TCTTTATTCCTCCCATGTGGGCTGAAGTGTGATGAGCGCTTATTAAGATG 1628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1348  CAGCTTTAGTGAAGTACAAACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1629  TACAGCTTCTTGACAGAAAGTATGTACAGAAACACAGAGGCTTGGCAAGATGATC 1688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1288  CTGAGCTGTACATTTTAAATATGTAAGTAAATTAATTAATTAATTAATTAATTAAT 1229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1689  TAACTGCAATCTTACCTGCTGCTGAGCCAGCAGTATCTGTGATCTTGAACAAGTTTT 1748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1228  TTTTATTAATTTGGTATTAAGTGCACAAATGATGATATATATATATATATATAC 1169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1749  TCACTTCTGAGGCGCATCCCTGGCTACACACACAGTGGTGAAGGATGAATGA 1808
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1168  TGTGAAGTAAATGCGCACAGTCAAGTATTAATTAATTAATTAATTAATTAATTAAT 1109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1809  CGAAGTCCCTTACACTGTAAATCCAGCACTTTGGAGGCGCAAGGCGGTGA-7GGCTT 1867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1108  TTTCTTTTCTTTTCTTTTGAAGAGATTCACATCTGCAACCCAGGCTGGAGTGCAGT 1049
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1868  GAGCTGAGAGGTGAGAGATGCGGCACTCTCAGAGCCCTGCTGCTGCTGCGGCGCT 1927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1048  GGCATTTAGAGGTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1928  CCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1987
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 989 CTTCTGCTGGCTCCACCTTTGGCAGACTTGAAGAACTTTCAGCCCGCGCTGCAT 930
 QY 1988 GTGGAGAGCCCTTTCTGGGCTGGCCAGAGCCAGCCGCTCCCTACGTTGAGAGAG 2047
 Db 929 GTAGAGAGCCCTTTCTGGGCTGGCCAGAGCCAGCCGCTCCCTACGTTGAGAGAG 870
 QY 2048 TGTGAGAGAGAGGCTTCAACAGAGAGCCGCGCTGGCAGCGGCTTGGCGCCAGCTGG 2107
 Db 869 TGTGAGAGAGAGAGGCTTCAACAGAGAGCCGCGCTGGCAGCGGCTTGGCGCCAGCTGG 818
 QY 2108 AGTTCGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 2167
 Db 817 AGTTCGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 759
 QY 2168 AGGCCCCGGGCAATGAGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 2227
 Db 758 -GGCCCCGAGCAATGAGAGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 700
 QY 2228 GCGCCAGCAATGAGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 2287
 Db 699 CCGCCAGCAATGAGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 644
 QY 2288 GCGCTCCCGGGGGGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 2342
 Db 643 GCGCTCCCGGGGGGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 584
 QY 2343 TCCATAGGCTTCTGTGGGCGGCGGAGGCTTCCGAGAGCAACCCCGCTGCTCCAGCG 2402
 Db 583 TCCATAGGCTTCTGTGGGCGGCGGAGGCTTCCGAGAGCAACCCCGCTGCTCCAGCG 524
 QY 2403 CCGAGTCCCATGAGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 2462
 Db 523 CCGAGTCCCATGAGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 465
 QY 2463 GGCAGTACCCCTGAGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 2522
 Db 464 GGCAGTACCCCTGAGAGGCTTACAGCCGGGCGCAGCGGCTGGGAGGCTTACTGGGT 405
 QY 2523 GTCGTGGAGAGCTTGAAGAACTTATGTCAGCTGAGGAGTGTAAAT 2572
 Db 404 GTCGTGGAGAGCTTGAAGAACTTATGTCAGCTGAGGAGTGTAAAT 345
 QY 2573 -----ACACCAATGAGAGGCTTGTGTAGCTCA 2601
 Db 344 GCATTCGTCTAGCTCAAGGTTTGAACACACCAATGAGAGGCTTGTGTAGCTCA 285
 QY 2602 GGTCTGTGTAATGAGAGGCTTGTGTAGCTCAAGGTTTGAACACACCAATGAGAGG 2661
 Db 284 GGTCTGTGTAATGAGAGGCTTGTGTAGCTCAAGGTTTGAACACACCAATGAGAGG 225
 QY 2662 ACCTTATATGTC-----TACGTGAGGATTTGAATACACCAATGAGAGGCTTGTAT 2712
 Db 224 ACCTTGTGTGTCACACTGTTATCTATCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 165
 QY 2713 CTAGCTCAAGGTTTGAACACACCAATGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGT 2772
 Db 164 CTAGCTCAAGGATTTGAATCTCGCCCAATGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGT 108
 QY 2773 TGCACCAATGAGAGGCTTGT 2798
 Db 107 TCTACCAATGAGAGGATGT 82
 RESULT 11
 US-10-081-327-40
 ; Sequence 40, Application US/10081327
 ; Publication No. US20030129602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huang, Tim
 ; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
 ; FILE REFERENCE: UMO1523
 ; CURRENT APPLICATION NUMBER: US/10/081,327
 ; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 06/120,592
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: 06/118,760
 ; PRIOR FILING DATE: 1999-02-05
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: Patent version 3.0
 ; SEQ ID NO 40
 ; LENGTH: 161652
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens;
 US-10-081-327-40
 Query Match 10.4%; Score 647.2; DB 15; Length 161652;
 Best Local Similarity 62.3%; Pred. No. 5.8e-160;
 Matches 1303; Conservative 0; Mismatches 678; Indels 109; Gaps 14;
 QY 780 TAAATATCTTTTAAATTTTCCCTTAACTTAAAGTAAAGTAAAGCCGCGCAGG 839
 Db 139002 TAAATATCTTTTAAATTTTAAATTTAAACAAATTAACAAACAAATTCAGCCAGG 139061
 QY 840 CGCCATGCTCAGCCTGTAATTCAGCCTTGGAGGCTGAGGTGGGAGATCATTGGA 899
 Db 139062 GAGGTGGGATGCTGCTTATCATAGACCTTGGAGGCCAAAGTGGGAAGATCATTGGA 139121
 QY 900 GATCACAAGTTCGAGACACGCTGGCCACATATAGCAAAACCCATTCTACTAAATTA 959
 Db 139122 GCTCAAGATTGTGAGACACGCTGGCCAAATGATGACACC-----TCTCAAAATTTT 139176
 QY 960 AAAAATATGAGTGGGATAGTGTGTCACACCTGTGATCCGATCTTGGAGGCTGAGGC 1019
 Db 139177 AAAAATATGAGTGGGATAGTGTGTCACACCTGTGATCCGATCTTGGAGGCTGAGGC 139236
 QY 1020 AGGAAATTCGCTTGAACCTGGGAAAGCGGAGTTGAGTGAAGCCATCATGCTGCA 1079
 Db 139237 GGGAAATTCGCTTGAACCTGGGAAAGCGGAGTTGAGTGAAGCCATCATGCTGCA 139296
 QY 1080 CTCACGCTGGGTGACAGAGTGAAGCTTGTCTCAACGAAAAAAGTGTAAAGCCA 1139
 Db 139297 CTCACGCTGGGTGACAGAGTGAAGCTTGTCTCAACGAAAAAAGTGTAAAGCCA 139354
 QY 1140 TTCTTAATTCAGTATACATAGTATCATCTAGCTGCTGCTGCTGCTGCTGAGGCA 1199
 Db 139355 AACCAATGATAGGATTTACTGTATGTCTAAATGCTTGTGCTGATTTTTCATTTAATCT 139414
 QY 1200 TACCTGAGAAATGAGTGTGCTGTCACAGACATATACATTTCCATTTAATGACAC 1259
 Db 139415 T-----TACAGCAGCTGTAAAGAGTGGCATTATATTCATTTATATATGTA 139464
 QY 1260 TACCAATTTGCCATCCAGAGAGGTTTTTTTTTACATCTACACTCCCCCAGCAACAA 1319
 Db 139465 ATGTGAG-----GCAGACAGATTTAAAGAAATTTAAAGCCAGCACGGT 139510
 QY 1320 TGAGAGTATCTCAGATCTTTTAAAGATGCTTAAGCCAGTACAGATGAAACAGG 1379
 Db 139511 GGTCTATGCTGTATATCCCAACACTTTGGAGGCTGAGGGGGAATTCAAAGTCAAG 139570
 QY 1380 AAGTGGAGGGAAGCTGCCAGCCCTTCTAACCATGAAAGAAATACCTGTAGAGCCTTC 1439
 Db 139571 AGATCGAGACCATCTAGCTAATACAGGTTGAACCCCGCTCTCTAATAAATATACAAATA 139630
 QY 1440 TGGATGCTGGAAGATGATTAACGGGGGTCTTGAGAGCTGCCCGCTGTAGATC-ACTG 1498
 Db 139631 AAAATATAAATTAATAAATAATGAGCCAGATGAGTGGGCTGTATGCCAGTACTT 139680
 QY 1499 TGACTCTGAGCCTCCAGTCAGTCAGGCTCCAGTGTGATGAGCCAGATGATATAGCC 1558
 Db 139691 GCGAGGCTGAGTGAAGAGACTGGCGTTAAACCCGAGAGCAGAGGTGCAATTGACCAAGA 139730
 QY 1559 CTCACCTCTGTTTGTCTTATTTCTCCCATGTGGGCTGAGATGTGATGAGCCGTT 1618
 Db 139731 TCGGACACATG-----CACTCAGGCTGGGCGACAG--AGCAAGACTCGCTC 139795
 QY 1619 ATTCAAGATGTACAGCTTTTCTTTCAGAGAAAGTGTGTCAAGAAACAGCAGGCGCTTGG 1678

Db 6911 GTGTGAGAGGAAAGGCGGAGAGCGGGGCTGGCGGCGGCTTGGCGGCGCCCTG 6852
Qy 2107 GATTCGGGCTGGGCTGGGCTTGGCGGCGCCGCACTCGAGACGCGGCGCACCTGTC 2166
Db 6851 GAACTTCGGGCTGGGCTTGGCGGCGCCGCACTCGAGAGAGGAGCGCGCCG--TG 6794
Qy 2167 CAGGCGCGGGGCAATGAGAGCTTAGACCGCGGCGCGCTCGCGGAGGCTGACGCGG 2226
Db 6793 CCGGCGCGGGGCAATGAGAGCTTAGACCGCGGCGCGCTCGCGGAGGCTGACGCGG 6734
Qy 2227 TGGCCGAGAGTGGCGAGCGCGCGGCGGCTTGGCTCGCTGATTTCTACTGGGCTTAC 2286
Db 6733 TCCCGCAGAGTGGCGAGCGCGCGGCGGCTG----CGCTGATTTCTACTGGGCTTAC 6678
Qy 2287 AGCCTTCGCGGCGGCGAGGCTCGGAGCTGACGCGCGGCAATGCTGAGCTCCG---- 2341
Db 6677 TGGCTTCGCGGCGGCGAGGCTCGGAGCTGACGCGCGGCAATGCTGAGCTCCGCA 6618
Qy 2342 CTCGATGGGCTCTGCTGGGCGCGGAGCTCCGAGCAGACACCGCTGCTGACAGC 2401
Db 6617 CTCGATGGGCTCTGCTGGGCGCGGAGCTCCGCAATGAGCTGCTCCGCTGCTGACAGC 6558
Qy 2402 GCCCAGTCCGATGAGACGAGCGGAGGCTGAGAGTGGGCGCGAGCGGAGCTGAGC 2461
Db 6557 GCCCAGTCCGATGAGACGAGCGGAGGCTGAGAGTGGGCGCGAGCGGAGCTGAGC 6499
Qy 2462 AGCAGCTACCCCTGACGAGCGCTGCGGAGTCCACTGAGTGAAGCGAGCTGGGCTCTG 2521
Db 6498 AGCAGCTACCCCTGACGAGCGCTGCGGAGTCCACTGAGTGAAGCGAGCTGGGCTCTG 6439
Qy 2522 AGCTGGTGGAGACTTGTAGACCTTATGTAGCTCAGGAGTGTGAATGCAATACCAATC 2581
Db 6438 AGCTGGTGGAGACTTGTAGACCTTATGTAGCTCAGGAGTGTGAATGCAATACCAATC 6379
Qy 2582 AGCAGCTGTGTAGCTCAGGCTGTGTGAATGCAATACCAATCAGCTGTGTAGCTA 2641
Db 6378 AGCAGCTGTGTAGCTCAGGCTGTGTGAATGCAATACCAATGCAATGCTGTAGCTA 6319
Qy 2642 CTGTGATGGGCGCTTGGAGAACTTTATG-----TGTAGCTCAGGAGTGTAAATA 2692
Db 6318 CTGTGATGGGCGCTTGGAGAACTTTATGCTGTGACACTGTGTATCTATCTGTGTGG 6259
Qy 2693 CACCAATCGGCACTGTGTATCTAGCTCAGCTGTTGTAACACCAATCAGCACTGCT 2751
Db 6258 GAGCTGGAGAACTTTGTGTGTAGCTCAGGAGTGTGAAGGCAACCAATCAGTGGCTGT 6200

RESULT 13

US-10-081-327-38/c
; Sequence 38, Application US/10081327
; Publication No. US20030129602A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Tdm
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/10/081,327
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 06/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 06/118,760
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 128779
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-10-081-327-38

Query Match 9.48; Score 588.6; DB 15; Length 128779;
Best Local Similarity 83.28; Pred. No. 1,9e-144;
Matches 778; Conservative 0; Mismatches 94; Indels 63; Gaps 7;

Qy 1873 TGAGAGGTGACAGATCCCGGCACTCTCACAGCCCTCTGCTCGGCGGCTCTCT 1932
Db 88576 TGAAGATGACAGGTCTGCTGCACTCTCTCAGAGCCCTGCTCGGCGGCTCTCT 88517
Qy 1933 GCGTGGGCTCCCACTTGGTGGGCACTTGAAGAGCCCTTCAAGCCAGCGTGCACCTGAGG 1992
Db 8816 GCGTGGGCTCCCACTTGGGCGCACTTGAAGAGCCCTTCAAGCCAGCGTGCACCTGAGG 88457
Qy 1993 AGCCCTTCTGGGCTGGCCCAAGGCGCAGAGCCGCTCTCTCAGCTTGCAGGAGGTGG 2052
Db 88456 AGCCCTTCTGGGCTGGCCCAAGGCGGAGCCGCTCTCTCAGCTTGCAGGAGGTGG 88397
Qy 2053 AGGAGAGGCTCAAGCAGAAACCGGCGCTCGCAGCGGCTTGGCGGCGCAGCTGAGTTC 2112
Db 88396 AGGAGAGGCTGAGCGGAGAACCGGCGCTCGTGCAGCGGCTTGGCGGCGCAGCTGAGTTC 88337
Qy 2113 CGGCTGGGCTGGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2172
Db 88336 CGGCGAGAGCTGGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 88278
Qy 2173 CCGGCAATGAGAGGCTTACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2232
Db 88277 CCGGCAATGAGAGGACTTACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 88218
Qy 2233 AGCAGTCCAGCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2292
Db 88217 AGCAGTCCAGCTCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 88162
Qy 2293 CCGGCGGAGAGGCTGCGGAGCTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2347
Db 88161 CCGGCGGAGAGGCTGCGGAGCTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 88103
Qy 2348 GGGCTCTGTGGGCGGCGGAGCTTCCCGAGAGACACACCCCTGCTCAGAGCGGCCAG 2407
Db 88102 GGGCTCTGTGGGCGGCGGAGCTTCCCGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 88043
Qy 2408 TCCCATGACACGAGAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2467
Db 88042 TCCCATGACACGAGAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 87984
Qy 2468 CTACCCCTGAGCGCTGCTGCGGAGTCCAGTGGTGAAGGCGGAGCTGCTGAGTCTG 2527
Db 87983 CTACCCCTGAGCGGCGGCGGAGTCCAGTGGTGAAGGCGGAGCTGCTGAGTCTG 87924
Qy 2528 GTGGAGACTTGGAGAACCTTATGTGTAGCTCAGGAGTGTAAAT----- 2572
Db 87923 GTGGGAGCTGGAGAACCTTATGTGTAGCTCAGGAGTGTAAATACCAATCGGCACT 87864
Qy 2573 -----ACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2606
Db 87863 CTGTATCTAGCTCAGAGGTTGTAACACCAATCAGACCCCTGCTGCTGCTGCTGCTGCTGCTG 87804
Qy 2607 TGTGAATGACCAATCCACACTGTGTATCTAGCTGAGTGGGCGCTTGGAGAACCTT 2666
Db 87803 TGTGAATGACCAATGACACTGTGTATCTAGCTGAGTGGGCGCTTGGAGAACCTT 87744
Qy 2667 TATGTAGCTCAGGAGTGTAAATACCAATCGGCA-----CTGTGTATCTAG 2716
Db 87743 TGTGTGAATCTGTGTATCTAGCTAATCTAAGTGGGAGCAATGAGAACCTTGTGTCTAG 87684
Qy 2717 CTCAGGTTGTAAACACCAATCAGACCCCTG 2751
Db 87683 CTCAGGATGTAAACGCAACCAATCAGGCGCTGT 87649

RESULT 14

US-09-764-847-1878/c
; Sequence 1878, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, proteins, and antibodies
; FILE REFERENCE: PC009

; CURRENT APPLICATION NUMBER: US/09/764, 847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1878
; LENGTH: 6766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1878

Query Match 9.4%; Score 583.8; DB 10; Length 6766;
Best Local Similarity 85.3%; Pred. No. 5.8e-144;
Matches 719; Conservative 0; Mismatches 72; Indels 52; Gaps 4;

QY 1873 TGAAGGTGACAGATGCGCGGAGTCTCTACAGCCCTGCTGCTGCGGCGCTCTCT 1932
DB 4597 TGAGAGGTGACAGGCTGCTGACGCTCTACAGCCCTGCTGCTGCGGCGCTCTCT 4538
QY 1933 GCGTGGGCTCCACTTGGTGGGCACTTGAGAGGCGCTTCAAGCCGCTGACCTGAGG 1992
DB 4537 GCGTGGGCTCCACTTGGTGGGCACTTGAGAGGCGCTTCAAGCCGCTGACCTGAGG 4478
QY 1993 AGCCCTTTCTGGGCTGGCCAAAGGCGCAGAGCGGCTCCCTCAGCTTGAGAGGAGTGG 2052
DB 4477 AGCCCTTTCTGGGCTGGCCAAAGGCGCAGAGCGGCTCCCTCAGCTTGAGAGGAGTGG 4418
QY 2053 AGGAGAGGCTCAAGCAGGAACCGGGGCTGGGCAAGCGGCTGGGCGGCGCTGAGTTC 2112
DB 4417 AGGAGAGGCTCAAGCAGGAACCGGGGCTGGGCAAGCGGCTGGGCGGCGCTGAGTTC 4358
QY 2113 GCGTGGGCTGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2172
DB 4357 GCGTGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4300
QY 2173 CCGGGCAATGAGAGGCTTACAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2232
DB 4299 CCGGGCAATGAGAGGCTTACAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4240
QY 2233 AGCAGTGGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2292
DB 4239 AGAAGTGGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4184
QY 2293 CCGCGGGGCGAGGCGGCTGGGCACTGACAGCCCGCATGCGTGAAGCT-----CCCTCAT 2347
DB 4183 CCGCGGGGCGAGGCGGCTGGGCACTGACAGCCCGCATGCGTGAAGCT-----CCCTCAT 4124
QY 2348 GGGCTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2407
DB 4123 GGGCTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4064
QY 2408 TCCCATGAGCAGCAGGAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2467
DB 4063 TCCCATGAGCAGCAGGAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4004
QY 2468 CTACCCCTGAGAGGCGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2527
DB 4003 CTACCCCTGAGAGGCGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3944
QY 2528 GTGAGAGCTTGAGAGGCGGCTTATGTCTAGCTCAGGAGTCTGTAATACACCAATGAGCAGC 2587
DB 3943 GTGAGAGCTTGAGAGGCGGCTTATGTCTAGCTCAGGAGTCTGTAATACACCAATGAGCAGC 3922
QY 2588 CTGTGTCTAGCTCAGGCTGTGTGATGACCAATTCACACTCTGTATCTAGCTACTGTA 2647
DB 3921 ---GTGTAGCTCAGGCTGTGTGATGACCAATTCACACTCTGTATCTAGCTACTGTA 3865
QY 2648 TGGGGCTTGAGAGGAGCTTATGTCTAGCTCAGGAGTCTGTAATACCAATTCAGGAGTCTG 2707
DB 3864 TGGGGAGTGGAGAGGAGCTTGTGTCTAGCTCAGGAGTCTGTAATACCAATTCAGGAGTCTG 3805
QY 2708 TGT 2710
DB 111

DB 3804 TGT 3802

RESULT 15
US-10-092-154-1878/c
; Sequence 1878, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC00901
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1878
; LENGTH: 6766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1878

Query Match 9.4%; Score 583.8; DB 14; Length 6766;
Best Local Similarity 85.3%; Pred. No. 5.8e-144;
Matches 719; Conservative 0; Mismatches 72; Indels 52; Gaps 4;

QY 1873 TGAAGGTGACAGATGCGCGGAGTCTCTACAGCCCTGCTGCTGCGGCGCTCTCT 1932
DB 4597 TGAGAGGTGACAGGCTGCTGACGCTCTACAGCCCTGCTGCTGCGGCGCTCTCT 4538
QY 1933 GCGTGGGCTCCACTTGGTGGGCACTTGAGAGGCGCTTCAAGCCGCTGACCTGAGG 1992
DB 4537 GCGTGGGCTCCACTTGGTGGGCACTTGAGAGGCGCTTCAAGCCGCTGACCTGAGG 4478
QY 1993 AGCCCTTTCTGGGCTGGCCAAAGGCGCAGAGCGGCTCCCTCAGCTTGAGAGGAGTGG 2052
DB 4477 AGCCCTTTCTGGGCTGGCCAAAGGCGCAGAGCGGCTCCCTCAGCTTGAGAGGAGTGG 4418
QY 2053 AGGAGAGGCTCAAGCAGGAACCGGGGCTGGGCAAGCGGCTGGGCGGCGCTGAGTTC 2112
DB 4417 AGGAGAGGCTCAAGCAGGAACCGGGGCTGGGCAAGCGGCTGGGCGGCGCTGAGTTC 4358
QY 2113 GCGTGGGCTGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2172
DB 4357 GCGTGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4300
QY 2173 CCGGGCAATGAGAGGCTTACAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2232
DB 4299 CCGGGCAATGAGAGGCTTACAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4240
QY 2233 AGCAGTGGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2292
DB 4239 AGAAGTGGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4184
QY 2293 CCGCGGGGCGAGGCGGCTGGGCACTGACAGCCCGCATGCGTGAAGCT-----CCCTCAT 2347
DB 4183 CCGCGGGGCGAGGCGGCTGGGCACTGACAGCCCGCATGCGTGAAGCT-----CCCTCAT 4124
QY 2348 GGGCTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2407
DB 4123 GGGCTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4064
QY 2408 TCCCATGAGCAGCAGGAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2467
DB 4063 TCCCATGAGCAGCAGGAGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4004
QY 2468 CTACCCCTGAGAGGCGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2527
DB 4003 CTACCCCTGAGAGGCGGCTGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3944
QY 2528 GTGAGAGCTTGAGAGGCGGCTTATGTCTAGCTCAGGAGTCTGTAATACACCAATGAGCAGC 2587
DB 3943 GTGAGAGCTTGAGAGGCGGCTTATGTCTAGCTCAGGAGTCTGTAATACACCAATGAGCAGC 3922

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2003, 13:22:16 ; Search time 11294 Seconds
(without alignments)
18089.916 Million cell updates/sec

Title: US-09-845-020A-5
Perfect score: 6235
Sequence: 1 gatcacttgagacagtagt.....tgcacattcccccacagcgct 6235

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```
1: Pending_Patents_NA_Main:*
2: /cgn2_6/ptodata/2/pna/PCrus.COMB.seq.*
3: /cgn2_6/ptodata/2/pna/PCrus.COMB.seq.old.*
4: /cgn2_6/ptodata/2/pna/US07.COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US08.COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US081.COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US082.COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US083.COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US084.COMB.seq.*
10: /cgn2_6/ptodata/2/pna/US085.COMB.seq.*
11: /cgn2_6/ptodata/2/pna/US086.COMB.seq.*
12: /cgn2_6/ptodata/2/pna/US087.COMB.seq.*
13: /cgn2_6/ptodata/2/pna/US088.COMB.seq.*
14: /cgn2_6/ptodata/2/pna/US089.COMB.seq.*
15: /cgn2_6/ptodata/2/pna/US090.COMB.seq.*
16: /cgn2_6/ptodata/2/pna/US091.COMB.seq.*
17: /cgn2_6/ptodata/2/pna/US092.COMB.seq.*
18: /cgn2_6/ptodata/2/pna/US093.COMB.seq.*
19: /cgn2_6/ptodata/2/pna/US094.COMB.seq.*
20: /cgn2_6/ptodata/2/pna/US095.COMB.seq.*
21: /cgn2_6/ptodata/2/pna/US096.COMB.seq.*
22: /cgn2_6/ptodata/2/pna/US097.COMB.seq.*
23: /cgn2_6/ptodata/2/pna/US098.COMB.seq.*
24: /cgn2_6/ptodata/2/pna/US099.COMB.seq.*
25: /cgn2_6/ptodata/2/pna/US100.COMB.seq.*
26: /cgn2_6/ptodata/2/pna/US101.COMB.seq.*
27: /cgn2_6/ptodata/2/pna/US102.COMB.seq.*
28: /cgn2_6/ptodata/2/pna/US103.COMB.seq.*
29: /cgn2_6/ptodata/2/pna/US104.COMB.seq.*
30: /cgn2_6/ptodata/2/pna/US105.COMB.seq.*
31: /cgn2_6/ptodata/2/pna/US106.COMB.seq.*
32: /cgn2_6/ptodata/2/pna/US107.COMB.seq.*
33: /cgn2_6/ptodata/2/pna/US108.COMB.seq.*
34: /cgn2_6/ptodata/2/pna/US109.COMB.seq.*
35: /cgn2_6/ptodata/2/pna/US110.COMB.seq.*
36: /cgn2_6/ptodata/2/pna/US111.COMB.seq.*
37: /cgn2_6/ptodata/2/pna/US112.COMB.seq.*
38: /cgn2_6/ptodata/2/pna/US113.COMB.seq.*
39: /cgn2_6/ptodata/2/pna/US114.COMB.seq.*
40: /cgn2_6/ptodata/2/pna/US115.COMB.seq.*
41: /cgn2_6/ptodata/2/pna/US116.COMB.seq.*
42: /cgn2_6/ptodata/2/pna/US117.COMB.seq.*
43: /cgn2_6/ptodata/2/pna/US118.COMB.seq.*
44: /cgn2_6/ptodata/2/pna/US119.COMB.seq.*
45: /cgn2_6/ptodata/2/pna/US120.COMB.seq.*
46: /cgn2_6/ptodata/2/pna/US121.COMB.seq.*
47: /cgn2_6/ptodata/2/pna/US122.COMB.seq.*
48: /cgn2_6/ptodata/2/pna/US123.COMB.seq.*
49: /cgn2_6/ptodata/2/pna/US124.COMB.seq.*
50: /cgn2_6/ptodata/2/pna/US125.COMB.seq.*
51: /cgn2_6/ptodata/2/pna/US126.COMB.seq.*
52: /cgn2_6/ptodata/2/pna/US127.COMB.seq.*
53: /cgn2_6/ptodata/2/pna/US128.COMB.seq.*
54: /cgn2_6/ptodata/2/pna/US129.COMB.seq.*
55: /cgn2_6/ptodata/2/pna/US130.COMB.seq.*
56: /cgn2_6/ptodata/2/pna/US131.COMB.seq.*
57: /cgn2_6/ptodata/2/pna/US132.COMB.seq.*
58: /cgn2_6/ptodata/2/pna/US133.COMB.seq.*
59: /cgn2_6/ptodata/2/pna/US134.COMB.seq.*
60: /cgn2_6/ptodata/2/pna/US135.COMB.seq.*
61: /cgn2_6/ptodata/2/pna/US136.COMB.seq.*
62: /cgn2_6/ptodata/2/pna/US137.COMB.seq.*
63: /cgn2_6/ptodata/2/pna/US138.COMB.seq.*
64: /cgn2_6/ptodata/2/pna/US139.COMB.seq.*
65: /cgn2_6/ptodata/2/pna/US140.COMB.seq.*
66: /cgn2_6/ptodata/2/pna/US141.COMB.seq.*
67: /cgn2_6/ptodata/2/pna/US142.COMB.seq.*
68: /cgn2_6/ptodata/2/pna/US143.COMB.seq.*
69: /cgn2_6/ptodata/2/pna/US144.COMB.seq.*
70: /cgn2_6/ptodata/2/pna/US145.COMB.seq.*
71: /cgn2_6/ptodata/2/pna/US146.COMB.seq.*
72: /cgn2_6/ptodata/2/pna/US147.COMB.seq.*
73: /cgn2_6/ptodata/2/pna/US148.COMB.seq.*
74: /cgn2_6/ptodata/2/pna/US149.COMB.seq.*
75: /cgn2_6/ptodata/2/pna/US150.COMB.seq.*
76: /cgn2_6/ptodata/2/pna/US151.COMB.seq.*
77: /cgn2_6/ptodata/2/pna/US152.COMB.seq.*
78: /cgn2_6/ptodata/2/pna/US153.COMB.seq.*
79: /cgn2_6/ptodata/2/pna/US154.COMB.seq.*
80: /cgn2_6/ptodata/2/pna/US155.COMB.seq.*
81: /cgn2_6/ptodata/2/pna/US156.COMB.seq.*
82: /cgn2_6/ptodata/2/pna/US157.COMB.seq.*
83: /cgn2_6/ptodata/2/pna/US158.COMB.seq.*
84: /cgn2_6/ptodata/2/pna/US159.COMB.seq.*
85: /cgn2_6/ptodata/2/pna/US160.COMB.seq.*
86: /cgn2_6/ptodata/2/pna/US161.COMB.seq.*
87: /cgn2_6/ptodata/2/pna/US162.COMB.seq.*
88: /cgn2_6/ptodata/2/pna/US163.COMB.seq.*
89: /cgn2_6/ptodata/2/pna/US164.COMB.seq.*
90: /cgn2_6/ptodata/2/pna/US165.COMB.seq.*
91: /cgn2_6/ptodata/2/pna/US166.COMB.seq.*
92: /cgn2_6/ptodata/2/pna/US167.COMB.seq.*
93: /cgn2_6/ptodata/2/pna/US168.COMB.seq.*
94: /cgn2_6/ptodata/2/pna/US169.COMB.seq.*
95: /cgn2_6/ptodata/2/pna/US170.COMB.seq.*
96: /cgn2_6/ptodata/2/pna/US171.COMB.seq.*
97: /cgn2_6/ptodata/2/pna/US172.COMB.seq.*
98: /cgn2_6/ptodata/2/pna/US173.COMB.seq.*
99: /cgn2_6/ptodata/2/pna/US174.COMB.seq.*
100: /cgn2_6/ptodata/2/pna/US175.COMB.seq.*
101: /cgn2_6/ptodata/2/pna/US176.COMB.seq.*
102: /cgn2_6/ptodata/2/pna/US177.COMB.seq.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6235	100.0	6235	35	US-09-845-020A-5
2	6235	100.0	6679	35	US-09-845-020A-1
3	6056	97.1	4925599	40	US-09-948-128-259
4	6052.8	97.1	14371	101	US-60-466-412-83872

[illegible]

Qy	661	ATGCTCTGTGCACAAATCACTTGGCCCTGTTCTTTAGCACAANAACAGCATATAAACAAT	720
Dd	661	ATGCTCTGTGCACAAATCACTTGGCCCTGTTCTTTAGCACAANAACAGCATATAAACAAT	720
Qy	721	ACATACATGAATTTTTTAATAGACATGAGATTGAAATTCATATGATTTTTTACATTTTAT	780
Dd	721	ACATACATGAATTTTTTAATAGACATGAGATTGAAATTCATATGATTTTTTACATTTTAT	780
Qy	781	AAAAATATCTTTTTTAAAAAATTTTCCCCTAACCATTTAAAAGSTAAAAACCGGCCAGGCC	840
Dd	781	AAAAATATCTTTTTTAAAAAATTTTCCCCTAACCATTTAAAAGSTAAAAACCGGCCAGGCC	840
Qy	841	GCCATGCTCACGCCCTGTAATTCAGACACTTTGGGAGGCTGAGGTGGCGAGATCACTTGAG	900
Dd	841	GCCATGCTCACGCCCTGTAATTCAGACACTTTGGGAGGCTGAGGTGGCGAGATCACTTGAG	900
Qy	901	ATCAACAGTTTCGAGACCAGCCTGGCCAACATAGCAAACCCCATTTCTCTAAAAATAAA	960
Dd	901	ATCAACAGTTTCGAGACCAGCCTGGCCAACATAGCAAACCCCATTTCTCTAAAAATAAA	960
Qy	961	AAAAATTAGCTGGGCGCATATGATGTGCACAACTGTGATCCACAGTACTTTGGAGAGCTGAGCCA	1020
Dd	961	AAAAATTAGCTGGGCGCATATGATGTGCACAACTGTGATCCACAGTACTTTGGAGAGCTGAGCCA	1020

	Gans	0.
	Dh	0.
6235;	QY	1021 GGGAATCGCTTGAAACCTGGGAAAGCCGAGAGTTGCAGTAGGCCAACATCATGTGCACACTGCAC 1080
	Dd	1021 GGGAATTCGCTTGAACCTGGGAAAGCCGAGAGTTGCAGTAGGCCAACATCATGTGCACACTGCAC 1080


```
QY 1081 TCCAGCTGGGTGACAGAGTGAACCTTGTCTCAACGAAAAAAGTGTAAAGGCAT 1140
    |||
Db 1081 TCCAGCTGGGTGACAGAGTGAACCTTGTCTCAACGAAAAAAGTGTAAAGGCAT 1140
QY 1141 TCCTAATTCAGTGTACATCAGTGTACATCTCAGTGTGCTGCTGAGGCAT 1200
    |||
Db 1141 TCCTAATTCAGTGTACATCAGTGTACATCTCAGTGTGCTGCTGAGGCAT 1200
QY 1201 ACCGTGAGAAATAGAGTGTGCTGGTCAACAGACATACATTTCCACATTAATGACACT 1260
    |||
Db 1201 ACCGTGAGAAATAGAGTGTGCTGGTCAACAGACATACATTTCCACATTAATGACACT 1260
QY 1261 ACCAAGTTCATCCAGAGAGGTGTTTTTTTACAAATCTACATCCCCCAGCAAAAT 1320
    |||
Db 1261 ACCAAGTTCATCCAGAGAGGTGTTTTTTTACAAATCTACATCCCCCAGCAAAAT 1320
QY 1321 GAGAGTTACTCCAGATCTTTTACAAAGATGCTTAAGCCAGTACAGATGAAAAAGGA 1380
    |||
Db 1321 GAGAGTTACTCCAGATCTTTTACAAAGATGCTTAAGCCAGTACAGATGAAAAAGGA 1380
QY 1381 AGTGGGAGGGGAAAGCTGCCAGCCCTCTTAACCATGAAAGAAATACCTGTGTAGAGCTTCT 1440
    |||
Db 1381 AGTGGGAGGGGAAAGCTGCCAGCCCTCTTAACCATGAAAGAAATACCTGTGTAGAGCTTCT 1440
QY 1441 GGATGCTGGAAGATGAATAAACGGGGGTCTGTGGAGGCTGCCCTGTCAAGTCACTGTG 1500
    |||
Db 1441 GGATGCTGGAAGATGAATAAACGGGGGTCTGTGGAGGCTGCCCTGTCAAGTCACTGTG 1500
QY 1501 ACTTCTGAGCCTCCAGTCCAGTCTCAAGCCCATGTGTATGGCCAGTGAATATGAGCCCT 1560
    |||
Db 1501 ACTTCTGAGCCTCCAGTCCAGTCTCAAGCCCATGTGTATGGCCAGTGAATATGAGCCCT 1560
QY 1561 CACTCTGTGTTGGTCTTTATTTCTCCCATAGTGGGGGTGAAGTGTGAATGAGCCGTAT 1620
    |||
Db 1561 CACTCTGTGTTGGTCTTTATTTCTCCCATAGTGGGGGTGAAGTGTGAATGAGCCGTAT 1620
QY 1621 TCAAGATGTACAGCTTCTTGACAGAAATAGTGTACACAGAAACACAGGGGCTTGGCA 1680
    |||
Db 1621 TCAAGATGTACAGCTTCTTGACAGAAATAGTGTACACAGAAACACAGGGGCTTGGCA 1680
QY 1681 AGATGATCTAATCTCAATCTTACCTGTGCTCAGCCAGCAGCTAGTCTGTGATCTTGAAC 1740
    |||
Db 1681 AGATGATCTAATCTCAATCTTACCTGTGCTCAGCCAGCAGCTAGTCTGTGATCTTGAAC 1740
QY 1741 AAGTTTTTCACTTCTGTGAGGCATGCCCTGTGTACAAACACATGTTGTGACAGGA 1800
    |||
Db 1741 AAGTTTTTCACTTCTGTGAGGCATGCCCTGTGTACAAACACATGTTGTGACAGGA 1800
QY 1801 TGAATGTACAGAGTCCCTTACACCTGTATCCAGCACTTGGGAGGCCAAGGGGGGTGG 1860
    |||
Db 1801 TGAATGTACAGAGTCCCTTACACCTGTATCCAGCACTTGGGAGGCCAAGGGGGGTGG 1860
QY 1861 ATGGCTTGAAGCTGTAGAGGTGACAGCATGCCGGCAGTCTCACAGCCCTGTGTGCTCTC 1920
    |||
Db 1861 ATGGCTTGAAGCTGTAGAGGTGACAGCATGCCGGCAGTCTCACAGCCCTGTGTGCTCTC 1920
QY 1921 GGGGGCTCCCTGTGCTGGGCTGCCACTTGGGTGGCACTTGAAGGAGCCCTTCAAGCCACCG 1980
    |||
Db 1921 GGGGGCTCCCTGTGCTGGGCTGCCACTTGGGTGGCACTTGAAGGAGCCCTTCAAGCCACCG 1980
QY 1981 CTGCACTGTGGAGCCCTTCTGAGGTGGCCAAAGGGCAGAGCCGGCTCCCTCAAGCTTGC 2040
    |||
Db 1981 CTGCACTGTGGAGCCCTTCTGAGGTGGCCAAAGGGCAGAGCCGGCTCCCTCAAGCTTGC 2040
QY 2041 AGGAGAGTGTGAGAGGAGGCTCAAGCAGAAACGGGGGTGGCCAGCGGGCTTGGCGGC 2100
    |||
Db 2041 AGGAGAGTGTGAGAGGAGGCTCAAGCAGAAACGGGGGTGGCCAGCGGGCTTGGCGGC 2100
QY 2101 CACGTGAGTTCCGGGGGTGGGCTTGGGGGGCCCGCAGCTCGGAGAGCGGGGCTAG 2160
    |||
Db 2101 CACGTGAGTTCCGGGGGTGGGCTTGGGGGGCCCGCAGCTCGGAGAGCGGGGCTAG 2160
QY 2161 CCCTGGCAGGCCCGGGCAGATGAGAGGCTTAGCACCCGGGCGAGGGCTCGGAGGGTGT 2220
    |||
Db 2161 CCCTGGCAGGCCCGGGCAGATGAGAGGCTTAGCACCCGGGCGAGGGCTCGGAGGGTGT 2220
    |||
QY 2221 ACTGGGTGCCAGACAGTGCAGCCCGCGCGGTGTCTGCTGATTTCTCACTGGGC 2280
    |||
Db 2221 ACTGGGTGCCAGACAGTGCAGCCCGCGCGGTGTCTGCTGATTTCTCACTGGGC 2280
QY 2281 CTTAGCAGCCTTCCCGGGGGGAGGGCTCGGGAGCTCAGCCGCCATGCTGTAGGCTCC 2340
    |||
Db 2281 CTTAGCAGCCTTCCCGGGGGGAGGGCTCGGGAGCTCAGCCGCCATGCTGTAGGCTCC 2340
QY 2341 CCTCCATGGGCTCTGTGGGCGCGGAGCTCCCGGAGAGACACCCCGCTGCACAG 2400
    |||
Db 2341 CCTCCATGGGCTCTGTGGGCGCGGAGCTCCCGGAGAGACACCCCGCTGCACAG 2400
QY 2401 CGCCAGTCCCATGACACAGCAGGGCTGAGAGTGCGGGCGACGGCAGCGGAGCTGG 2460
    |||
Db 2401 CGCCAGTCCCATGACACAGCAGGGCTGAGAGTGCGGGCGACGGCAGCGGAGCTGG 2460
QY 2461 CAGGCAGCTACCCCTGCAAGCCCTGTGGGATCCACTGGGTGAAGCAGCTGGGCTCT 2520
    |||
Db 2461 CAGGCAGCTACCCCTGCAAGCCCTGTGGGATCCACTGGGTGAAGCAGCTGGGCTCT 2520
QY 2521 GAGTCTGTGGAGACTTGGAGAACCTTATGTAGTCAAGGATCGTAAATACACCAAT 2580
    |||
Db 2521 GAGTCTGTGGAGACTTGGAGAACCTTATGTAGTCAAGGATCGTAAATACACCAAT 2580
QY 2581 CAGCACCCTGTGTACTCAGAGGTGTGTAATCCACCAATCCACTGTATCTAGCT 2640
    |||
Db 2581 CAGCACCCTGTGTACTCAGAGGTGTGTAATCCACCAATCCACTGTATCTAGCT 2640
QY 2641 ACTGTGATGGGGCTTGGAGAACCTTATGTAGTCAAGGATCGTAAATACACCAATC 2700
    |||
Db 2641 ACTGTGATGGGGCTTGGAGAACCTTATGTAGTCAAGGATCGTAAATACACCAATC 2700
QY 2701 GGCACCTGTATCTAGCTCAAGGCTTGTAAACACACCAATCAGCACCCTGTCTACTCTC 2760
    |||
Db 2701 GGCACCTGTATCTAGCTCAAGGCTTGTAAACACACCAATCAGCACCCTGTCTACTCTC 2760
QY 2761 AGGCTATGTGAATCACCACCAATCAGACAGTCTGTATCTGTGCTTCAATGGGCAATCCGTGT 2820
    |||
Db 2761 AGGCTATGTGAATCACCACCAATCAGACAGTCTGTATCTGTGCTTCAATGGGCAATCCGTGT 2820
QY 2821 GAAAGACACCAACAGGGCTTGTGTGAGCAATAAAGCTTATACCTGGGGGAGAGCT 2880
    |||
Db 2821 GAAAGACACCAACAGGGCTTGTGTGAGCAATAAAGCTTATACCTGGGGGAGAGCT 2880
QY 2881 GGGCTGAGTCCGAAAGAGAGTCAAGGAGGAGATGAAGGTGGGGCGTTTATAGAT 2940
    |||
Db 2881 GGGCTGAGTCCGAAAGAGAGTCAAGGAGGAGATGAAGGTGGGGCGTTTATAGAT 2940
QY 2941 TTGGGTAGTAAAGAAAAATTTACAGTCAAAAGGGGTTTGTCTGTGGCGGGCAGAGTGG 3000
    |||
Db 2941 TTGGGTAGTAAAGAAAAATTTACAGTCAAAAGGGGTTTGTCTGTGGCGGGCAGAGTGG 3000
QY 3001 GGGGTCCCAAGGTCTCAGTGGGGGTCTTTTATAGCCAGAGATGACGAGAAAAAGACT 3060
    |||
Db 3001 GGGGTCCCAAGGTCTCAGTGGGGGTCTTTTATAGCCAGAGATGACGAGAAAAAGACT 3060
QY 3061 TTCAAGATGATATGATCAATTAAGGAGAGAGCCCGCATTTACACTCTTTGTGTGGTG 3120
    |||
Db 3061 TTCAAGATGATATGATCAATTAAGGAGAGAGCCCGCATTTACACTCTTTGTGTGGTG 3120
QY 3121 GAATGTATCAGTTAAGTGGGCGAGGCAATTTCACTTCTTTGTATCTTCAAGTTAC 3180
    |||
Db 3121 GAATGTATCAGTTAAGTGGGCGAGGCAATTTCACTTCTTTGTATCTTCAAGTTAC 3180
QY 3181 TTGAGGCAATCTGGGCTATATGTGCAAGTTACAGGGGAGTGCATGCTTGGCTGGGCT 3240
    |||
Db 3181 TTGAGGCAATCTGGGCTATATGTGCAAGTTACAGGGGAGTGCATGCTTGGCTGGGCT 3240
QY 3241 CAGAGCTTACAGACTCTCTGTGGGGCTTGAAGATGTTTGTGACACTCTGTAT 3300
    |||
Db 3241 CAGAGCTTACAGACTCTCTGTGGGGCTTGAAGATGTTTGTGACACTCTGTAT 3300
```

Db 3241 CAGAGGCTTGACAGCTACTCTGTGGGCGCTTGGAGAAATGTTTGTGTCCAGCACTCTGTAT 3300
OY 3301 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTAGCTCAGAGGATTTGTAACGCA 3360
Db 3301 CTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTAGCTCAGAGGATTTGTAACGCA 3360
OY 3361 CCAATCAGGCGCTGTCAAAACAGACACTGGCTCTACCAATCAGCAGAGTGGGTGG 3420
Db 3361 CCAATCAGGCGCTGTCAAAACAGACACTGGCTCTACCAATCAGCAGAGTGGGTGG 3420
OY 3421 GGGCAGATAGAGAAATAAAAGGAGGCTGGCCGAGCCAGAGTGGCAACGGCAGAGTGC 3480
Db 3421 GGGCAGATAGAGAAATAAAAGGAGGCTGGCCGAGCCAGAGTGGCAACGGCAGAGTGC 3480
OY 3481 CTATCCACAATATGGCAGCTTTGTTCTTTTGTGTGTGGATTAATCTTGTCTACTGCTG 3540
Db 3481 CTATCCACAATATGGCAGCTTTGTTCTTTTGTGTGTGGATTAATCTTGTCTACTGCTG 3540
OY 3541 CTTTTTGGGTCCACACTGCTTTTATGAGCTGTAACTCACCAGCAAGGCTGTGCAAGCTTC 3600
Db 3541 CTTTTTGGGTCCACACTGCTTTTATGAGCTGTAACTCACCAGCAAGGCTGTGCAAGCTTC 3600
OY 3601 ACTCCTGAAGCCACTAAGACCAACGAGCCGAGGAGATGAACTCCGGCCGCGT 3660
Db 3601 ACTCCTGAAGCCACTAAGACCAACGAGCCGAGGAGATGAACTCCGGCCGCGT 3660
OY 3661 GCGTTAAGACTTAACACTCACCAGGAAAGTGTGCAAGCTTCACTCTCAGCCAGCAGAG 3720
Db 3661 GCGTTAAGACTTAACACTCACCAGGAAAGTGTGCAAGCTTCACTCTCAGCCAGCAGAG 3720
OY 3721 CCACGAAACCCACAGAGAGAAAGAACTGGGAACACTGTGAACATAGAAAGAACAACT 3780
Db 3721 CCACGAAACCCACAGAGAGAAAGAACTGGGAACACTGTGAACATAGAAAGAACAACT 3780
OY 3781 CCAGATGCACCACTTAAGAGCTGTAACTCAGTCCAGAGGTCGCGGCTTCTCTTG 3840
Db 3781 CCAGATGCACCACTTAAGAGCTGTAACTCAGTCCAGAGGTCGCGGCTTCTCTTG 3840
OY 3841 AAGTCAGTGAAGCAACAGCACTCACAGTTTCGACACAAAGCCAGAGATTGAGATCAGC 3900
Db 3841 AAGTCAGTGAAGCAACAGCACTCACAGTTTCGACACAAAGCCAGAGATTGAGATCAGC 3900
OY 3901 CTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCG 3960
Db 3901 CTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCG 3960
OY 3961 AGCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4020
Db 3961 AGCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4020
OY 4021 TGAAGCTGGAGGTGAAGACTGCAAGTGTGATTTGACACAGCCCTTAAGCTGG 4080
Db 4021 TGAAGCTGGAGGTGAAGACTGCAAGTGTGATTTGACACAGCCCTTAAGCTGG 4080
OY 4081 GGAAGACTGAGAGCCCTGTTCCCTCCCAAAAAAATTTGACAAAGTGTAAATAAGGT 4140
Db 4081 GGAAGACTGAGAGCCCTGTTCCCTCCCAAAAAAATTTGACAAAGTGTAAATAAGGT 4140
OY 4141 GCGTGTATGTAGTGAAGGAGTGTGCTCATGCTGTAACTCCAGCACTTTGGGAGCGAG 4200
Db 4141 GCGTGTATGTAGTGAAGGAGTGTGCTCATGCTGTAACTCCAGCACTTTGGGAGCGAG 4200
OY 4201 GCGGCGGCGGTCACTTAAGGTGAGAGTGTGAGACAGCTGGCCAACTGAGAAAGCCC 4260
Db 4201 GCGGCGGCGGTCACTTAAGGTGAGAGTGTGAGACAGCTGGCCAACTGAGAAAGCCC 4260
OY 4261 ATCTCTTTAAAAATTAATAATTTAGCGGCTGTGGGGGCAAGTGTGAGACATGCTGTAA 4320
Db 4261 ATCTCTTTAAAAATTAATAATTTAGCGGCTGTGGGGGCAAGTGTGAGACATGCTGTAA 4320
OY 4321 TCCCAAGCTACTAGAGAGCTGAGGCGAGAGAACTGATGACCCAGAGGAGGCGGCTGTC 4380
Db 4321 TCCCAAGCTACTAGAGAGCTGAGGCGAGAGAACTGATGACCCAGAGGAGGCGGCTGTC 4380

OY 4381 AGTGAACCGAGATCGTGCCATTGCACTCCACCACATCCAGGCTGGGCAACAGAGCCAAA 4440
Db 4381 AGTGAACCGAGATCGTGCCATTGCACTCCACCACATCCAGGCTGGGCAACAGAGCCAAA 4440
OY 4441 CTCTGCTTTAAAAAATTTAAAAAATTTAGGCTGTGATTAAGAGTGTGCAATGCAATAG 4500
Db 4441 CTCTGCTTTAAAAAATTTAAAAAATTTAGGCTGTGATTAAGAGTGTGCAATGCAATAG 4500
OY 4501 TTGCGAGGCAACATGTTTAAAGATGTGAGAGTCTGCTTCCATGGTCTGTTAAAAAC 4560
Db 4501 TTGCGAGGCAACATGTTTAAAGATGTGAGAGTCTGCTTCCATGGTCTGTTAAAAAC 4560
OY 4561 CACCTCAAGGCGAGGTGAGTGTGATGCTATATATCCAGCACTTTGGAGGCGGAG 4620
Db 4561 CACCTCAAGGCGAGGTGAGTGTGATGCTATATATCCAGCACTTTGGAGGCGGAG 4620
OY 4621 GCGGAGTGAATCAGTGAAGTGTGAGAGTGTGAGAGCCGCTGACCAACATGTTAAAT 4680
Db 4621 GCGGAGTGAATCAGTGAAGTGTGAGAGTGTGAGAGCCGCTGACCAACATGTTAAAT 4680
OY 4681 CCCACCTTACTTAAAAATTAATAATTAAGATGATGTGTGATGCTGTATATCCAC 4740
Db 4681 CCCACCTTACTTAAAAATTAATAATTAAGATGATGTGTGATGCTGTATATCCAC 4740
OY 4741 CTACTTGGAGGCTGAGGCGAGAAATACATAGAACAGGAGGCGGAGGTTGTACTGAG 4800
Db 4741 CTACTTGGAGGCTGAGGCGAGAAATACATAGAACAGGAGGCGGAGGTTGTACTGAG 4800
OY 4801 CCGAGATGCGTGCATTCGACTCCAGCTGAGCAATGAGGAAATCTCATCTCAAAAAAAC 4860
Db 4801 CCGAGATGCGTGCATTCGACTCCAGCTGAGCAATGAGGAAATCTCATCTCAAAAAAAC 4860
OY 4861 AACAAACAAAAACCACTCTTACTTCCAGGAGAGTGGGTACAGAGCTGGGCCATCAGT 4920
Db 4861 AACAAACAAAAACCACTCTTACTTCCAGGAGAGTGGGTACAGAGCTGGGCCATCAGT 4920
OY 4921 GCAAGTGTGAGCCACAGAGCTTAAGGCGAGCTGCAAGAGCCGCGACCAAGATTAACGTG 4980
Db 4921 GCAAGTGTGAGCCACAGAGCTTAAGGCGAGCTGCAAGAGCCGCGACCAAGATTAACGTG 4980
OY 4981 TGTGAATGATGATGTGAATATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Db 4981 TGTGAATGATGATGTGAATATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
OY 5041 AGCAGCAGAGATGGCCCCATCCAGTCCAGCAGATCCTCTCATCCAGAGATGCTGTTT 5100
Db 5041 AGCAGCAGAGATGGCCCCATCCAGTCCAGCAGATCCTCTCATCCAGAGATGCTGTTT 5100
OY 5101 CTTGGCAGCTGGGGTAAATTAAGACAGAGGTGACAGTCTTGGGTGCTCAGTACAG 5160
Db 5101 CTTGGCAGCTGGGGTAAATTAAGACAGAGGTGACAGTCTTGGGTGCTCAGTACAG 5160
OY 5161 TGGCCGAGGAGGCGCTTGTGGCTGTGAAGAAAGCTTCAAGGCTTCAAGGCGGCGAGTGGC 5220
Db 5161 TGGCCGAGGAGGCGCTTGTGGCTGTGAAGAAAGCTTCAAGGCTTCAAGGCGGCGAGTGGC 5220
OY 5221 TCACGCTGTAAATCCAGACATTTGGGAGGCGAGGCTGGATGATCAGAGGTGACAGAGA 5280
Db 5221 TCACGCTGTAAATCCAGACATTTGGGAGGCGAGGCTGGATGATCAGAGGTGACAGAGA 5280
OY 5281 TCGTGAACATCTGTGCTAAACAGGTGAAGAACCCCGTCTACTTAAAAATTAATAATTTGG 5340
Db 5281 TCGTGAACATCTGTGCTAAACAGGTGAAGAACCCCGTCTACTTAAAAATTAATAATTTGG 5340
OY 5341 CCGGAGATGTGGCGGCGACCTGTATGTTCACTGAGTGTGAGGAGCTGAGGCGAGAGATG 5400
Db 5341 CCGGAGATGTGGCGGCGACCTGTATGTTCACTGAGTGTGAGGAGCTGAGGCGAGAGATG 5400
OY 5401 GCGTGAACCCGAGAGCAGAGTTTGCAGTGAAGCCGAGATCGGCGCACTGCACTCCAGCTT 5460
Db 5401 GCGTGAACCCGAGAGCAGAGTTTGCAGTGAAGCCGAGATCGGCGCACTGCACTCCAGCTT 5460

QY	5461	GGGGAGACAGAGCAAGACTCCATCTGGAAAAAAGAAAAAAGAAACGTTCAAGGTCTGAGCCAGA	5520
Db	5461	GGGGAGACAGAGCAAGACTCCATCTGGAAAAAAGAAAAAAGAAACGTTCAAGGTCTGAGCCAGA	5520
QY	5521	GGCCACGAGCTGTAATTTCTGTCACTTACCATGACTCTTGGGCAAGGCACTTCCCTCCGAGC	5580
Db	5521	GGCCACGAGCTGTAATTTCTGTCACTTACCATGACTCTTGGGCAAGGCACTTCCCTCCGAGC	5580
QY	5581	CCAGTTACAGGGGTTGGAAATCGACTCCAAAGTCCCTTCCAGCATTTAAAGCTGATGGTTTC	5640
Db	5581	CCAGTTACAGGGGTTGGAAATCGACTCCAAAGTCCCTTCCAGCATTTAAAGCTGATGGTTTC	5640
QY	5641	TAAATATAGAAAGATGGGGACAGTTTCCCTCTCTCCACCCACGCCCCGTCTCCACTTCAAGGT	5700
Db	5641	TAAATATAGAAAGATGGGGACAGTTTCCCTCTCTCCACCCACGCCCCGTCTCCACTTCAAGGT	5700
QY	5701	GAATGACACAGGAAAGTACGCTGTCTCCCAATCCCGACAGTTCCAAAGCCCTTGGGAGCCCTAC	5760
Db	5701	GAATGACACAGGAAAGTACGCTGTCTCCCAATCCCGACAGTTCCAAAGCCCTTGGGAGCCCTAC	5760
QY	5761	TGTCAAGGGTCTGTGCACAGAGAGGTGAAGGTCAAGGTGACCAATGCCCCCTCGAAGGGTCTTG	5820
Db	5761	TGTCAAGGGTCTGTGCACAGAGAGGTGAAGGTGACCAATGCCCCCTCGAAGGGTCTTG	5820
QY	5821	CTTCATTCGGGACACGAATCCGTTTCTCTGTGCTTACCGGGATTTCTAGGGGCTTTAGC	5880
Db	5821	CTTCATTCGGGACACGAATCCGTTTCTCTGTGCTTACCGGGATTTCTAGGGGCTTTAGC	5880
QY	5881	CGAATGATGATAGGAGGGGGGGGGGTTTCTGGGGGAGTTTCCCGACTAATCAATCTTGGGA	5940
Db	5881	CGAATGATGATAGGAGGGGGGGGGGTTTCTGGGGGAGTTTCCCGACTAATCAATCTTGGGA	5940
QY	5941	CAGACAGACCTTGAACATTTTGCATGTGTCCTAATCCAAATGATGGGGTGGGACAGCAGCAA	6000
Db	5941	CAGACAGACCTTGAACATTTTGCATGTGTCCTAATCCAAATGATGGGGTGGGACAGCAGCAA	6000
QY	5941	CAGACAGACCTTGAACATTTTGCATGTGTCCTAATCCAAATGATGGGGTGGGACAGCAGCAA	6000
Db	5941	CAGACAGACCTTGAACATTTTGCATGTGTCCTAATCCAAATGATGGGGTGGGACAGCAGCAA	6000
QY	6001	GACCCCATGTTCCTTATCTCAGGTAGGGGCTCAGAGGTCTCCAGACAGGCAAGCTCCGG	6060
Db	6001	GACCCCATGTTCCTTATCTCAGGTAGGGGCTCAGAGGTCTCCAGACAGGCAAGCTCCGG	6060
QY	6061	AGAGTTTGGGGGTGAGATGGGAGCAACAGGCTTCTTTTCTGTCTTGAATTTGGG	6120
Db	6061	AGAGTTTGGGGGTGAGATGGGAGCAACAGGCTTCTTTTCTGTCTTGAATTTGGG	6120
QY	6121	GGCTTTGGGGGACAGGCTTGAAGATCCCAAAAGAGAGGGGGCAAAAGACACTCCCCACAG	6180
Db	6121	GGCTTTGGGGGACAGGCTTGAAGATCCCAAAAGAGAGGGGGCAAAAGACACTCCCCACAG	6180
QY	6181	TCTGCCAGAGCGAGAGAGAGAGACCCGAGCTCAGCTGCCACTTCCCAAGGCGCT	6235
Db	6181	TCTGCCAGAGCGAGAGAGAGAGACCCGAGCTCAGCTGCCACTTCCCAAGGCGCT	6235

	TYPE: DNA	ORGANISM: Homo sapiens
US-09-845-020A-1		
Query Match	100.0%; Score 6235; DB 35; Length 6679;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 6235; Conservative	0; Mismatches	0; Indels
		0; Gaps
0Y	1 GATCAGCTTGGAGACAGTATGTTCAAGACAGCCTGGGAGCATATGAGGACATGCTCTACG	60
Db	20 GATCAGCTTGGAGACAGTATGTTCAAGACAGCCTGGGAGCATATGAGGACATGCTCTACG	79
0Y	61 AAAAAATCAAAAATATATGCGCGGCGATGGTGGCTACGTCGTGTAATCCCTAACTTTGG	120
Db	80 AAAAAATCAAAAATATATGCGCGGCGATGGTGGCTACGTCGTGTAATCCCTAACTTTGG	139
0Y	121 ACATCAAGGCAAGTGGATCAGTGTGGGTCAGAGAGTTCAGACTGACCTGGGCAACATGGT	180
Db	140 ACATCAAGGCAAGTGGATCAGTGTGGGTCAGAGAGTTCAGACTGACCTGGGCAACATGGT	199
0Y	181 GAAACCCATATCTCCACTTAAAAATACAAAAATTTAGCCAGCATGGTGGCAGGCACTGTA	240
Db	200 GAAACCCATATCTCCACTTAAAAATACAAAAATTTAGCCAGCATGGTGGCAGGCACTGTA	259
0Y	241 ATCCGCGTACTCAGGAGCGTGGCAGGAGATCATTGAACCCAGAGCGGAGTTG	300
Db	260 ATCCGCGTACTCAGGAGCGTGGCAGGAGATCATTGAACCCAGAGCGGAGTTG	319
0Y	301 CAGTAGCGTAGATCACACCACTGCATCCAGCCCTGGGTGACAGAGCAAGACTATCTC	360
Db	320 CAGTAGCGTAGATCACACCACTGCATCCAGCCCTGGGTGACAGAGCAAGACTATCTC	379
0Y	361 AAAAAAATPAAAAAATPAAAAAATTTAGCCAGGCACTGGTAGTGCACACCTGTACTCAG	420
Db	380 AAAAAAATPAAAAAATPAAAAAATTTAGCCAGGCACTGGTAGTGCACACCTGTACTCAG	439
0Y	421 CTACTCAGAGGCTGAGGTGGAGGATCATTGAACCTGGGGCACTAAGGCTACAGTA	480
Db	440 CTACTCAGAGGCTGAGGTGGAGGATCATTGAACCTGGGGCACTAAGGCTACAGTA	499
0Y	481 GCCAAGATCATGCCCCTACCTCCAGCCCTGGGCAACAGAGAGACCCCTGCTCTAAAA	540
Db	500 GCCAAGATCATGCCCCTACCTCCAGCCCTGGGCAACAGAGAGACCCCTGCTCTAAAA	559
0Y	541 AATAATTAATTAATTAAGAAAAAACAAGCTCTGTTTATGCTCTGCTGCATACATCTACT	600
Db	560 AATAATTAATTAATTAAGAAAAAACAAGCTCTGTTTATGCTCTGCTGCATACATCTACT	619
0Y	601 ATGTATATAGTTTGCAAACTCAAGATCCAGATAGTCAATTTTTAGGCTTGTGGCCGT	660
Db	620 ATGTATATAGTTTGCAAACTCAAGATCCAGATAGTCAATTTTTAGGCTTGTGGCCGT	679
0Y	661 ATGCTCTGTGCACAACTACCTGTGCCCTGCTTTTACACAAAAAGCACTATAACAAT	720
Db	680 ATGCTCTGTGCACAACTACCTGTGCCCTGCTTTTCTACACAAAAAGCACTATAACAAT	739
0Y	721 ACATCAAGAAATTTTTATAGACATCGAGATTTGAATTTCAATGATTTTTTAACTTTAT	780
Db	740 ACATCAAGAAATTTTTATAGACATCGAGATTTGAATTTCAATGATTTTTTAACTTTAT	799
0Y	781 AAAATAAATCTTTTAAAAAATTTTCCCTCAACCATTTAAAGTGTAAAAAGCCGCGCAGCG	840
Db	800 AAAATAAATCTTTTAAAAAATTTTCCCTCAACCATTTAAAGTGTAAAAAGCCGCGCAGCG	859
0Y	841 GCCATCGTACGCGCTGTAAATTCACAGCACTTTGGAGGCTGAGGTGGCAGATCACTTGA	900
Db	860 GCCATCGTACGCGCTGTAAATTCACAGCACTTTGGAGGCTGAGGTGGCAGATCACTTGA	919
0Y	901 ATCAACAATTTGGAGGCAAGCCTGGCAACATATGCAAAACCCCATTTCTACTAAAAATAAA	960
Db	920 ATCAACAATTTGGAGGCAAGCCTGGCAACATATGCAAAACCCCATTTCTACTAAAAATAAA	979
0Y	961 AAAATTAATCTGGGCAATAGTGTGCACACCTGTGATCCAGCTACTTTGGAGGCTGAGCA	1020

Db 980 AAAATTGCTGGGATGATGCTGACACCTGTGATCCAGCTACTTGGAGGCTGAGGCA 1039
QY 1021 GGAGAAATCGCTTGAACTGTGGAGCGGAGGTTGGAGTGAGGCCAATCATCTGCATGCAC 1080
Db 1040 GGAGAAATCGCTTGAACTGTGGAGCGGAGGTTGGAGTGAGGCCAATCATCTGCATGCAC 1099
QY 1081 TTCAGCCTGGGTGACAGATGAGACTTCGTCTCAACGAAAAAAGTGTAAAAAGCAT 1140
Db 1100 TTCAGCCTGGGTGACAGATGAGACTTCGTCTCAACGAAAAAAGTGTAAAAAGCAT 1159
QY 1141 TCCATAATTCAGTGTACATCAGTGTACATCTCAGGTCTGCTACTCCGTCTGAGGCAT 1200
Db 1160 TCCATAATTCAGTGTACATCAGTGTACATCTCAGGTCTGCTACTCCGTCTGAGGCAT 1219
QY 1201 ACCTGAGAGTGAAGTGTGCTGTGACAGACATACACATTTCCACATTAACATGAGACT 1260
Db 1220 ACCGAGAGTGAAGTGTGCTGTGACAGACATACACATTTCCACATTAACATGAGACT 1279
QY 1261 ACCAAGTTGCAATCCAGAGAGGTTTTTTTTTACAAATCTACACTCCCGCCGCAACAAT 1320
Db 1280 ACCAAGTTGCAATCCAGAGAGGTTTTTTTTTACAAATCTACACTCCCGCCGCAACAAT 1339
QY 1321 GAGAGTTACTCCAGATCTTCTTACAAAGATGCTTAAGCCCGAGTACAGATGAAGAACAGA 1380
Db 1340 GAGAGTTACTCCAGATCTTCTTACAAAGATGCTTAAGCCCGAGTACAGATGAAGAACAGA 1399
QY 1381 AGTGGAGGGGAGAGCTGCGACGCCCTTCTTAACATGAAGAAATACCTGTGAGACCTTCT 1440
Db 1400 AGTGGAGGGGAGAGCTGCGACGCCCTTCTTAACATGAAGAAATACCTGTGTGAGACCTTCT 1459
QY 1441 GGATGCTGGAAGGATGAATAACGGGGGCTCTGAGAGCTGCCCTGTGCAGATACAGTGTG 1500
Db 1460 GGATGCTGGAAGGATGAATAACGGGGGCTCTGAGAGCTGCCCTGTGCAGATACAGTGTG 1519
QY 1501 ACTTCTGAGCCTCCAGTCCAGTCTCAGCCCCCATGTGTATGCCCCAGTATGATGAGCCCT 1560
Db 1520 ACTTCTGAGCCTCCAGTCCAGTCTCAGCCCCCATGTGTATGCCCCAGTATGATGAGCCCT 1579
QY 1561 CACTCTGTGTTGGTCTTTATTTCTCCCATGTGGGGCTGAAGTGTGGAATGAGCCGTAT 1620
Db 1580 CACTCTGTGTTGGTCTTTATTTCTCCCATGTGGGGCTGAAGTGTGGAATGAGCCGTAT 1639
QY 1621 TCAAGATGTACAGCTTCTTGACAGGAAAGTGTGACAGAAACACAGAGGCTTGGCA 1680
Db 1640 TCAAGATGTACAGCTTCTTGACAGGAAAGTGTGACAGAAACACAGAGGCTTGGCA 1699
QY 1681 AGATGATCTAATCTCAATCTCAATCTGCTCAGCCACAGCTAGTCTGTGATCTTGAAC 1740
Db 1700 AGATGATCTAATCTCAATCTCAATCTGCTCAGCCACAGCTAGTCTGTGATCTTGAAC 1759
QY 1741 AAGTTTTTCACTTCTGTGAGGCCATCCCTGGCTACACACACAGATTGGTGTGACAGA 1800
Db 1760 AAGTTTTTCACTTCTGTGAGGCCATCCCTGGCTACACACACAGATTGGTGTGACAGA 1819
QY 1801 TGAATATACCAAGATGCTTACACTGTAAATCCACAGCACTTTGGAGGCCAAAGGGGTGG 1860
Db 1820 TGAATATACCAAGATGCTTACACTGTAAATCCACAGCACTTTGGAGGCCAAAGGGGTGG 1879
QY 1861 ATGGCTTGAGCTGAGAGGTGACAGATGCGGGCAGTCCACAGCCCTGTGGCTGCCTC 1920
Db 1880 ATGGCTTGAGCTGAGAGGTGACAGATGCGGGCAGTCCACAGCCCTGTGGCTGCCTC 1939
QY 1921 GGGGCTCTCTGTGCTGGGCTCCCACTTGGTGGCACATTGAGAGGCCCTTCAAGCCACCG 1980
Db 1940 GGGGCTCTCTGTGCTGGGCTCCCACTTGGTGGCACATTGAGAGGCCCTTCAAGCCACCG 1999
QY 1981 CTGACACTGTGGAGGCCCTTTCTGGGTGGCCAAAGGCCAAGCGCGGCTCCCTCAGCTTGC 2040
Db 2000 CTGACACTGTGGAGGCCCTTTCTGGGTGGCCAAAGGCCAAGCGCGGCTCCCTCAGCTTGC 2059
QY 2041 AGGAGAGTGTGAGGGAGGAGGCTCAAGCAGGAACCGGGGCTGGCCACGGGGCTTGGCGGC 2100

Db 2060 AGGAGAGTGTGAGGGAGAGAGGCTCAAGCAGGAACCGGGGCTGGCCAGGGGCTTGGCGGC 2119
QY 2101 CAGCTGAGATTCGCGGTGGGCGTGGGCTTGGCGGGGCCCGCACTGGAGAGCAGCGGGCAG 2160
Db 2120 CAGCTGAGATTCGCGGTGGGCGTGGGCTTGGCGGGGCCCGCACTGGAGAGCAGCGGGCAG 2179
QY 2161 CCCCTGCCAGGGCCCCGGGCAATGAGAGGCTTATGACACCCGGGGCCACGGGCTGGGAGGCTGT 2220
Db 2180 CCCCTGCCAGGGCCCCGGGCAATGAGAGGCTTATGACACCCGGGGCCACGGGCTGGGAGGCTGT 2239
QY 2221 ACTGGGTGCCCCACAGTGCAGGCCCGGGCGGTGTGCTGTGATTTCTCACTGAGGC 2280
Db 2240 ACTGGGTGCCCCACAGTGCAGGCCCGGGCGGTGTGCTGTGATTTCTCACTGAGGC 2299
QY 2281 CTTAGCAGCCCTTCCCGGGGAGGAGGCTCGGGACCTCGAGCCGCCATGCTGAGCCCTCC 2340
Db 2300 CTTAGCAGCCCTTCCCGGGGAGGAGGCTCGGGACCTCGAGCCGCCATGCTGAGCCCTCC 2359
QY 2341 CCTTCATGAGGCTCCTGTGCGGGCCGAGGCTCTCCCGAGAGCAGCAACCCCTGTCCACAG 2400
Db 2360 CCTTCATGAGGCTCCTGTGCGGGCCGAGGCTCTCCCGAGAGCAGCAACCCCTGTCCACAG 2419
QY 2401 CGCCAGTCCCATGAGCAGCAGAGGAGGCTGAGAGTGCGGGGCGAGCGGACCGGAGCTGG 2460
Db 2420 CGCCAGTCCCATGAGCAGCAGAGGAGGCTGAGAGTGCGGGGCGAGCGGACCGGAGCTGG 2479
QY 2461 CAGGAGCTACCCCTCGACGCCCTGTGTGCGGAATCACTGGGTGAAGCAGCTGGGCTCT 2520
Db 2480 CAGGAGCTACCCCTCGACGCCCTGTGTGCGGAATCACTGGGTGAAGCAGCTGGGCTCT 2539
QY 2521 GAGTCTGTGAGAGCTTGGAGAACCTTATGCTAGCTCAGAGGATCGTAATTAACCAAT 2580
Db 2540 GAGTCTGTGAGAGCTTGGAGAACCTTATGCTAGCTCAGAGGATCGTAATTAACCAAT 2599
QY 2581 CAGCAGCCCTGTGTAGCTCAGGCTGTGTGAATCAGCAATCCACACTGTATATAGCT 2640
Db 2600 CAGCAGCCCTGTGTAGCTCAGGCTGTGTGAATCAGCAATCCACACTGTATATAGCT 2659
QY 2641 ACTGTATGAGGCGCTTGGAGAACCTTATGCTAGCTCAGAGGATCGTAATTAACCAAT 2700
Db 2660 ACTGTATGAGGCGCTTGGAGAACCTTATGCTAGCTCAGAGGATCGTAATTAACCAAT 2719
QY 2701 GGCACCTGTATCTAGCTCAAGGTTGTAAACACACCAATAGCAGCCCTGTGTAGCTC 2760
Db 2720 GGCACCTGTATCTAGCTCAAGGTTGTAAACACACCAATAGCAGCCCTGTGTAGCTC 2779
QY 2761 AGGATATGTGAATCAGCAATCGACAGCTGTATCTGCTTCAATGGGCATCCGCT 2820
Db 2780 AGGATATGTGAATCAGCAATCGACAGCTGTATCTGCTTCAATGGGCATCCGCT 2839
QY 2821 GAAGAGACACCAACAGAGGCTTGTGTGAGCAATTAAGCTTCACTACCTGGGTGACAGT 2880
Db 2840 GAAGAGACACCAACAGAGGCTTGTGTGAGCAATTAAGCTTCACTACCTGGGTGACAGT 2899
QY 2881 GGGCTGAGTCCGAAAGAGAGTCAAGCAAGGAGATTAAGGTTGGGCGCTTTATAGAT 2940
Db 2900 GGGCTGAGTCCGAAAGAGAGTCAAGCAAGGAGATTAAGGTTGGGCGCTTTATAGAT 2959
QY 2941 TTGGGTAGGTAAAGAAATTTACAGTCAAGGGGCTTGTCTCTGCGGGGACAGAGTGG 3000
Db 2960 TTGGGTAGGTAAAGAAATTTACAGTCAAGGGGCTTGTCTCTGCGGGGACAGAGTGG 3019
QY 3001 GGGGTGCAAGGTCTCAGTGGGGGCTTTTATAGCCAGAGATGAGCGAGAAAGAGCT 3060
Db 3020 GGGGTGCAAGGTCTCAGTGGGGGCTTTTATAGCCAGAGATGAGCGAGAAAGAGCT 3079
QY 3061 TTCAAGATTAATGTATCAATTAAGCAAGAGACCGGCATTAACACTCTTTTGTGTTG 3120
Db 3080 TTCAAGATTAATGTATCAATTAAGCAAGAGACCGGCATTAACACTCTTTTGTGTTG 3139
QY 3121 GAATGTATCAGTTAATTTGGGGAGGAGCATTTCACTCTTTTGTGATTTCTCAGTTAC 3180
Db 3140 GAATGTATCAGTTAATTTGGGGAGGAGCATTTCACTCTTTTGTGATTTCTCAGTTAC 3199

OY	3181	TTCAAGCCATCTGGGCGGTATATGTGCAAGTTACAGGGGATGCCATGGCTTGCGTGGGCT	3240
Db	3200	TTTCAGGCCATCTGGGCGGTATATGTGCAAGTTACAGGGGATGCCATGGCTTGCGTGGGCT	3259
OY	3241	CAGAGGCTTGACACTACTCTGGTGGGGCCCTTGAGAGATGTTATGTGCGACACTCTAT	3300
Db	3260	CAGAGGCTTGACACTACTCTGGTGGGGCCCTTGAGAGATGTTATGTGCGACACTCTAT	3319
OY	3301	CTAGTTAATCTAGTGGGACGTGGAGAACCTTTTGTCCTAGCTCAGGGATTTGTAAACGA	3360
Db	3320	CTAGTTAATCTAGTGGGACGTGGAGAACCTTTTGTCCTAGCTCAGGGATTTGTAAACGA	3379
OY	3361	CCAAATCAGCGCCCTGTCAAAAACACACCACCTGGCTCTACCAATATAGAGATGTGGGTGG	3420
Db	3380	CCAAATCAGCGCCCTGTCAAAAACACACCACCTGGCTCTACCAATATAGAGATGTGGGTGG	3439
OY	3421	GGCCAGATTAAGAGAAATAAAAGCAGGCTGCCGACCCAGAGTGGCAACGGCAACAGCTCC	3480
Db	3440	GGCCAGATTAAGAGAAATAAAAGCAGGCTGCCGACCCAGAGTGGCAACGGCAACAGCTCC	3499
OY	3481	CTATCCAAATATGGCAGCTTGTGTTCTTTTGTGCTGTTTGCATTAATCTTGCTACTGCTCG	3540
Db	3500	CTATCCAAATATGGCAGCTTGTGTTCTTTTGTGCTGTTTGCATTAATCTTGCTACTGCTCG	3559
OY	3541	CTTTTGGGCTCCACACTGCTTTTATGAGCTGTACACTCCACACGAAAGGTCTGACGTTCC	3600
Db	3560	CTTTTGGGCTCCACACTGCTTTTATGAGCTGTACACTCCACACGAAAGGTCTGACGTTCC	3619
OY	3601	ACTCCTGAGGACACTAAGACACGACGACCCACCGGGAGAAATGAACAATCCCGCGGCGCT	3660
Db	3620	ACTCCTGAGGACACTAAGACACGACGACCCACCGGGAGAAATGAACAATCCCGCGGCGCT	3679
OY	3661	GCCTTAAGAGCTATTAACAATCACCAGGAGGTCTGCAAGCTTCACTCCTCAGCCAGGAGA	3720
Db	3680	GCCTTAAGAGCTATTAACAATCACCAGGAGGTCTGCAAGCTTCACTCCTCAGCCAGGAGA	3739
OY	3721	CCACGAAACCCACGAAAGGAAACCTGCGAAACACATCTGAACATCGAAAGGAACAACAT	3780
Db	3740	CCACGAAACCCACGAAAGGAAACCTGCGAAACACATCTGAACATCGAAAGGAACAACAT	3799
OY	3781	CCAGATGCAACCCTTAAGACCTGTAAACACTCACTGCGAGGGTCCGGGCTTCTCTTTTG	3840
Db	3800	CCAGATGCAACCCTTAAGACCTGTAAACACTCACTGCGAGGGTCCGGGCTTCTCTTTTG	3859
OY	3841	AAGTCAGTGAAGACCAAGCATCACCAATTCGACACAAAGCCGAGGATTGTGAAATCAGC	3900
Db	3860	AAGTCAGTGAAGACCAAGCATCACCAATTCGACACAAAGCCGAGGATTGTGAAATCAGC	3919
OY	3901	CTGGGCAACATGATGAATAATGCCCTCTCTGCAAAAAAAAATAATCAAAAATTTGGCGG	3960
Db	3920	CTGGGCAACATGATGAATAATGCCCTCTCTGCAAAAAAAAATAATCAAAAATTTGGCGG	3979
OY	3961	AGCATGTGTGCTCCCTGCTGTGTGTCACAGCTACGCGGAGGCTAAAGTGGAGATCGCT	4020
Db	3980	AGCATGTGTGCTCCCTGCTGTGTGTCACAGCTACGCGGAGGCTAAAGTGGAGATCGCT	4039
OY	4021	TGACCTTGGAAGTGAAGACTGACAGTGAAGCTGTATTGTACCAAGCCCTTACGCTGGG	4080
Db	4040	TGACCTTGGAAGTGAAGACTGACAGTGAAGCTGTATTGTACCAAGCCCTTACGCTGGG	4099
OY	4081	GGACAGACTGAGACCTGTATTTCCCTCCGCAAAAAAATTGACAAAACTGTAAATTAAGAGT	4140
Db	4100	GGACAGACTGAGACCTGTATTTCCCTCCGCAAAAAAATTGACAAAACTGTAAATTAAGAGT	4159
OY	4141	GCCGTGATATGGCTTAGCGGCAAGTGGCTCATGCTGTAAATCCAGCACTTTGGGAACCGAG	4200
Db	4160	GCCGTGATATGGCTTAGCGGCAAGTGGCTCATGCTGTAAATCCAGCACTTTGGGAACCGAG	4219
OY	4201	GCGGGCGGAGTACCTTAAGTCAAGAGATGTGAGACACCTGGGCCCAATATGGAGAAACCC	4260
Db	4220	GCGGGCGGAGTACCTTAAGTCAAGAGATGTGAGACACCTGGGCCCAATATGGAGAAACCC	4279

QY	4261	ATCTCTTCTAAAAATACAAATATTAACCGGGCTGTGGGGCACTGGTGGAGCATGCTGTAA	43220
Db	4280	ATCTCTTCTAAAAATACAAATATTAACCGGGCTGTGGGGCACTGGTGGAGCATGCTGTAA	4339
QY	4321	TCCCAAGCTACATCAGGAGGCTAGAGGAGAGATCACTTGAACCCAGAGAGCGGGCTGTG	4380
Db	4340	TCCCAAGCTACTCAGGAGGCTAGAGGAGAGATCACTTGAACCCAGAGAGCGGGCTGTG	4399
QY	4381	AGTAGCCGAGATCTGTGCATTGTGCACCTCCACCCACCTCAGCCCTGGGCACAAAGCCAAA	4440
Db	4400	AGTAGCCGAGATCTGTGCATTGTGCACCTCCACCCACCTCAGCCCTGGGCACAAAGCCAAA	4459
QY	4441	CTCTGTCTTAAAAAATAAAAAATAGTCCCTGACATTTAAAGGTGTGCATGCAATAG	4500
Db	4460	CTCTGTCTTAAAAAATAAAAAATAGTCCCTGACATTTAAAGGTGTGCATGCAATAG	4519
QY	4501	TTGGCAGGCAACATGTTTAAGAAATGTGAGTCCCTGCTTCATGATGTCCTTTAAAAAC	4560
Db	4520	TTGGCAGGCAACATGTTTAAGAAATGTGAGTCCCTGCTTCATGATGTCCTTTAAAAAC	4579
QY	4561	CACCCCTCAAGGCGAGGTGCAGTGGCTCATGCTATTAATCCAGCATTTGGGAGCCGAG	4620
Db	4580	CACCCCTCAAGGCGAGGTGCAGTGGCTCATGCTATTAATCCAGCATTTGGGAGCCGAG	4639
QY	4621	GGGGTGGATCACTCTGAGGTACGAGAGCTTCGAGACCAAGCTTCACCAACAATGTGTAAT	4680
Db	4640	GGGGTGGATCACTCTGAGGTACGAGAGCTTCGAGACCAAGCTTCACCAACAATGTGTAAT	4699
QY	4681	CCCACTCTCTACTAAAAATACAAATTTAATAGATAGCTGGTGGATGGCTCTATATCCAC	4740
Db	4700	CCCACTCTCTACTAAAAATACAAATTTAATAGATAGCTGGTGGATGGCTCTATATCCAC	4759
QY	4741	CTACTTGGGAGGCTGAGGCGAGAAATACTATGAACACAGGAGGCGAGAGCTTGTAGTGAG	4800
Db	4760	CTACTTGGGAGGCTGAGGCGAGAAATACTATGAACACAGGAGGCGAGAGCTTGTAGTGAG	4819
QY	4801	CCGAGATCGTGCATTGCTGCATCTCCAGCCTGAGCAATGAGCGAACTCCATCTCAAAAAAC	4860
Db	4820	CCGAGATCGTGCATTGCTGCATCTCCAGCCTGAGCAATGAGCGAACTCCATCTCAAAAAAC	4879
QY	4861	AACAACAACAAACCCCACTCTCAATCCCGAGGAGTGGGTACAGAGCTGGGCGACATCAGT	4920
Db	4880	AACAACAACAAACCCCACTCTCAATCCCGAGGAGTGGGTACAGAGCTGGGCGACATCAGT	4939
QY	4921	GCAAGGTCTGAGCCACAGAGCTAAAGGCGGAGCTGCAGAGACCGCGGACAGATTAACAGTG	4980
Db	4940	GCAAGGTCTGAGCCACAGAGCTAAAGGCGGAGCTGCAGAGACCGCGGACAGATTAACAGTG	4999
QY	4981	TGTGAGATCATGTGTGTGAGATCAGACGTCCTGCCATTGTGGTACCAAGGGGCCCCCA	5040
Db	5000	TGTGAGATCATGTGTGTGAGATCAGACGTCCTGCCATTGTGGTACCAAGGGGCCCCCA	5059
QY	5041	AGCACACAGATGGGCCCATCCATCCAGCACACATCCACTTCATCCAGAGATGTCTGTTT	5100
Db	5060	AGCACACAGATGGGCCCATCCATCCAGCACACATCCACTTCATCCAGAGATGTCTGTTT	5119
QY	5101	CTTGGCAGCGTGGGGTAAATTAAGACACAAAGGTGCANCTTGGGTGTGGTCACTGACAG	5160
Db	5120	CTTGGCAGCGTGGGGTAAATTAAGACACAAAGGTGCANCTTGGGTGTGGTCACTGACAG	5179
QY	5161	TGCCCCAGGACAGGCTGTGTGGCTGTGTAGAAAACGTTACAGGCTTAGGCGGGGCACGGTGC	5220
Db	5180	TGCCCCAGGACAGGCTGTGTGGCTGTGTAGAAAACGTTACAGGCTTAGGCGGGGCACGGTGC	5239
QY	5221	TCAGGCTCTGTATCCACGACATTTTGGGAGGCGGAGGGGTGTGATCACGAGGTCAAGAGA	5280
Db	5240	TCAGGCTCTGTATCCACGACATTTTGGGAGGCGGAGGGGTGTGATCACGAGGTCAAGAGA	5299
QY	5281	TCGTGACATCTGTGGCTTAACACGGGTAACCCCGTCTCTACTTAAAAAATACAAAAATTTGG	5340
Db	5300	TCGTGACATCTGTGGCTTAACACGGGTAACCCCGTCTCTACTTAAAAAATACAAAAATTTGG	5359
QY	5341	CCGGGCAATGATGGGGGACCTGTATGTTCCAGTACTTCGGGAGGCTGAGGCAAGAGATG	5400

Db	1721827	GAGATTCACAGTTTGACACACGCTGGCCAACTAGAAAAACCCATTCTTCTTAATAAT	1721886
Qy	958	AAAAAATTAGCTGGGCAATAGTGGTGCACACCTGTGTATCCAGCTACTTGGGAGGCTGAG	1017
Db	1721887	AAAAAATTAGCTGGGCAATAGTGGTGCACACCTGTGTATCCAGCTACTTGGGAGGCTGAG	1721946
Qy	1018	GCAGGAAATCGCTTGAACCTGGGAGCGGAGGTTGCGAGTGAAGCAATCATGCCACTG	1077
Db	1721947	GCAGGAAATCGCTTGAACCTGGGAGCGGAGGTTGCGAGTGAAGCAATCATGCCACTG	1722006
Qy	1078	CACGCCAGCGGTGGACAGTGAAGTCTGCTCAACGAAAAAAGTGTAAAGC	1137
Db	1722007	CACGCCAGCGGTGGACAGTGAAGTCTGCTCAACGAAAAAAGTGTAAAGC	1722066
Qy	1138	CATTCTTAATTCAGTGTACATCAGTGTACTACAGGTCTGGCTACTCCTGCTGAG	1197
Db	1722067	CATTCTTAATTCAGTGTACATCAGTGTACTACAGGTCTGGCTACTCCTGCTGAG	1722126
Qy	1198	CATACCTGAGAAGTAGAGTTGCTTGGTGCACAGACATATACATTTCCATTAATAGAC	1257
Db	1722127	CATACCTGAGAAGTAGAGTTGCTTGGTGCACAGACATATACATTTCCATTAATAGAC	1722186
Qy	1258	ACTACCAAGTTGGCATCCAGAGAGG - TTTT TTTT TTTT TTTT TTTT TTTT TTTT	1316
Db	1722187	ACTACCAAGTTGGCATCCAGAGAGGTTT TTTT TTTT TTTT TTTT TTTT TTTT	1722246
Qy	1317	AAATGAGAGTTTACTCCAGATCTCTTTACAAAGATGCTGTAAAGCCAGTACAGATGAAGC	1376
Db	1722247	AAATGAGAGTTTACTCCAGATCTCTTTACAAAGATGCTGTAAAGCCAGTACAGATGAAGC	1722306
Qy	1377	AGGAATGGGAGGGGGAAGCTGCAGCCCTCTTAACCATGAAGAAATACCTGGTAGACC	1436
Db	1722307	AGGAATGGGAGGGGGAAGCTGCAGCCCTCTTAACCATGAAGAAATACCTGGTAGACC	1722366
Qy	1437	TTCTGAGATGCTGGAAGGATGAATTAACGGGGGTCTCTGGAGACCTGCCCTGTATGATCAC	1496
Db	1722367	TTCTGAGATGCTGGAAGGATGAATTAACGGGGGTCTCTGGAGACCTGCCCTGTATGATCAC	1722426
Qy	1497	TGTGACTTCTGAGCCCTCAGTCCAGTCCAGTCCAGCCCATGTGTACATGGCCAGTGAATGAG	1556
Db	1722427	TGTGACTTCTGAGCCCTCAGTCCAGTCCAGTCCAGCCCATGTGTACATGGCCAGTGAATGAG	1722485
Qy	1557	CCCTCACTCTCTGTTGGTCTTATATCT - CCCCATGTGGGGCTGAAGTGTGATGAGCC	1615
Db	1722486	CCCTCACTCTCTGTTGGTCTTATATCTCCCCCATGTGGGGCTGAAGTGTGATGAGCC	1722545
Qy	1616	GTTATTTCAAGATGTACAGCTTTTCTTGACAGGAAAGTATGTCTACAGAAACAGCAGGGGCT	1675
Db	1722546	GTTATTTCAAGATGTACAGCTTTTCTTGACAGGAAAGTATGTCTACAGAAACAGCAGGGGCT	1722605
Qy	1676	TGCGAAGATGATCTAACTGCAAAATCCATCTGGCTCAGCCACAGGAGTGTGTATCT	1735
Db	1722606	TGCGAAGATGATCTAACTGCAAAATCCATCTGGCTCAGCCACAGGAGTGTGTATCT	1722665
Qy	1736	TGAACAAGTTTCTTCACTTCTCTGAGGCAATCCCTGGCTACAAACACACAGTTGGTGA	1795
Db	1722666	TGAACAAGTTTCTTCACTTCTCTGAGGCAATCCCTGGCTACAAACACACAGTTGGTGA	1722725
Qy	1796	CAGGATTAATTAAGAG - AAGTCCCTTACACCTGTATATCCAGCACTTTGGAGGCCAAGC	1854
Db	1722726	CAGGATTAATTAAGAGAAAGTGCCTTACACCTGTATATCCAGCACTTTGGAGGCCAAGC	1722785
Qy	1855	GGGTGATGGCTTGAGCTGAGAGGTGACAGCATGGCGGAGATCCACAGCCCTGTTTC	1914
Db	1722786	GGGTGATGGCTTGAGCTGAGAGGTGACAGCATGGCGGAGATCCACAGCCCTGTTTC	1722845
Qy	1915	GCTCTGGGCGCTCTCTGCTGGGCTCCCACTTGGTGGACATTGAGAGGCCCTTACAG	1974
Db	1722846	GCTCTGGGCGCTCTCTGCTGGGCTCCCACTTGGTGGACATTGAGAGGCCCTTACAG	1722905
Qy	1975	CCACCGCTGCACGTGGGAGCCCTTCTTGCTGGCTGGCCAAAGCCAGCCGCTCCCTCA	2034
Db	1722906	CCACCGCTGCACGTGGGAGCCCTTCTTGCTGGCTGGCCAAAGCCAGCCGCTCCCTCA	1722965
Qy	2035	GCTTGCAGGAGGTGTGAGGAGAGAGGCTCAAGCAGAAACCGGGCTGTGCACGGCGCTT	2094
Db	1722966	GCTTGCAGGAGGTGTGAGGAGAGAGGCTCAAGCAGAAACCGGGCTGTGCACGGCGCTT	1723025
Qy	2095	GGGGGCACTGGAGTTCCGGGTGGGGCTTGGGGCTTGGGGGCCCCGACCTGGAGCAGC	2154
Db	1723026	GGGGGCACTGGAGTTCCGGGTGGGGCTTGGGGCTTGGGGGCCCCGACCTGGAGCAGC	1723085
Qy	2155	GGCCACCGCTGGCAGGCCCCGGGGCAATGAGAGGCTTAGACCCGGGGCCAGGGGCTGGGA	2214
Db	1723086	GGCCACCGCTGGCAGGCCCCGGGGCAATGAGAGGCTTAGACCCGGGGCCAGGGGCTGGGA	1723145
Qy	2215	GGGTGACTAGGGTGGCCCCAGAGTGCACAGCCCGGGCGCTGGCTGCATTTCTCA	2274
Db	1723146	GGGTGACTAGGGTGGCCCCAGAGTGCACAGCCCGGGCGCTGGCTGCATTTCTCA	1723205
Qy	2275	CTGGGCTTACAGAGCTTCCCGCGGGGAGGGCTCGGGACCTGACGCCCATGCTGA	2334
Db	1723206	CTGGGCTTACAGAGCTTCCCGCGGGGAGGGCTCGGGACCTGACGCCCATGCTGA	1723265
Qy	2335	GCTCCCTTCATGGGCTCTCTGTGGGGCCCGGACCTCCCCAGCAGCACACCCCTGCT	2394
Db	1723266	GCTCCCTTCATGGGCTCTCTGTGGGGCCCGGACCTCCCCAGCAGCACACCCCTGCT	1723325
Qy	2395	CCACAGCGCCAGTCCATCCATCGACACAGCAAGGGCTGAGAAAGTGGGGGCGACGGACGG	2454
Db	1723326	CCACAGCGCCAGTCCATCCATCGACACAGCAAGGGCTGAGAAAGTGGGGGCGACGGACGG	1723385
Qy	2455	GACTGGCAGGACAGTACCCCTCAGCCCTGATGGGAAATCCACTGGGTGAACCCAGCTGG	2514
Db	1723386	GACTGGCAGGACAGTACCCCTCAGCCCTGATGGGAAATCCACTGGGTGAACCCAGCTGG	1723445
Qy	2515	GCTCCTGAGTCTGGGAGACACTTGGAGAACTTTATGCTTACTAGGATGTGTAATAC	2574
Db	1723446	GCTCCTGAGTCTGGGAGACACTTGGAGAACTTTATGCTTACTAGGATGTGTAATAC	1723505
Qy	2575	ACCAATCAGCACCCCTGTGTCTAGCTCAGAGGTTGTGAATGACCAATCCACCTCTGTAT	2634
Db	1723506	ACCAATCAGCACCCCTGTGTCTAGCTCAGAGGTTGTGAATGACCAATCCACCTCTGTAT	1723565
Qy	2635	CTAGCTACTGTATGGGGGCTTGGAGAACTTTATGTCTAGCTCAGGATGTGTAATACA	2694
Db	1723566	CTAGCTACTGTATGGGGGCTTGGAGAACTTTATGTCTAGCTCAGGATGTGTAATACA	1723625
Qy	2695	CCAATGGCAGCTGTATCTACTCAAGTTGTGAACACACCAATTCAGCACCTGTCTC	2754
Db	1723626	CCAATGGCAGCTGTATCTACTCAAGTTGTGAACACACCAATTCAGCACCTGTCTC	1723685
Qy	2755	TAGCTCAGGAGTATGGAATGACCAATGCACAGTGTGTATCTGGCTACTTTCAATGGGAT	2814
Db	1723686	TAGCTCAGGAGTATGGAATGACCAATGCACAGTGTGTATCTGGCTACTTTCAATGGGAT	1723745
Qy	2815	CCGTGTGAAGAGACCAACCAACAGGCTTGTGTGACATTAAGCTTCTATCACCTGGGT	2874
Db	1723746	CCGTGTGAAGAGACCAACCAACAGGCTTGTGTGACATTAAGCTTCTATCACCTGGGT	1723805
Qy	2875	GCAGGTGGGCTGAGTCCGAAAAGAGAGTGCAGGAAGGAGATAGGGTGGGGCGTTTGA	2934
Db	1723806	GCAGGTGGGCTGAGTCCGAAAAGAGAGTGCAGGAAGGAGATAGGGTGGGGCGTTTGA	1723865
Qy	2935	TAGGATTTGGTAGAGTAAAGGAAATTTACAGTCAAAAGGGGGTTTCTCTGGCGGGAG	2994
Db	1723866	TAGGATTTGGTAGAGTAAAGGAAATTTACAGTCAAAAGGGGGTTTCTCTGGCGGGAG	1723925
Qy	2995	GAGTGGGGGCTGCAGAGGTCTCACTGGGGGTCTTTTGTGACCGAGATGAGCCAGAAA	3054
Db	1723926	GAGTGGGGGCTGCAGAGGTCTCACTGGGGGTCTTTTGTGACCGAGATGAGCCAGAAA	1723985
Qy	3055	AGGACTTTTACAGGTAATGTATCATATTAAGACAGGACCCGCATTTTACACTCTTTT	3114
Db	1723986	AGGACTTTTACAGGTAATGTATCATATTAAGACAGGACCCGCATTTTACACTCTTTT	1724045

QY	3115	GTGGTGAAGTATCATCACTAAGTTGGGGCAGGGCATATTCATTCTTTTGTGATTCCTC	3174
Db	1724046	GTGGTGAAGTATCATCACTAAGTTGGGGCAGGGCATATTCATTCTTTTGTGATTCCTC	1724105
QY	3175	AGTTACTTCAGGGCATCTGGGCGTATATATGTCCAAAGTTACAGGGGATCGAATGGATTTGGCT	3234
Db	1724106	AGTTACTTCAGGGCATCTGGGCGTATATATGTCCAAAGTTACAGGGGATCGAATGGCTTTGGCT	1724155
QY	3235	TGGGCTCAGAGGCTTGACAGCTACTCTGTGTGGGGCCTTGGAGAAATGTTTGTGTGACACT	3294
Db	1724166	TGGGCTCAGAGGCTTGACAGCTACTCTGTGTGGGGCCTTGGAGAAATGTTTGTGTGACACT	1724225
QY	3295	CTGATATCAGTTAATCTATGTGGGGACGGGGAACCTTTGTGTCTACTCAGGGATTTGTA	3354
Db	1724226	CTGATATCAGTTAATCTATGTGGGGACGGGGAACCTTTGTGTCTACTCAGGGATTTGTA	1724285
QY	3355	AACGCACCAATCAGGGCCCTGTCAAAACAGACACTGGGCTCTACCAATCAGCAGATGT	3414
Db	1724286	AACGCACCAATCAGGGCCCTGTCAAAACAGACACTGGGCTCTACCAATCAGCAGATGT	1724345
QY	3415	GGGTGGGGCCAGTATTAAGAAATTAAGCAGGCTGCGGAGCCAGCAGTGGCAACGGCCAC	3474
Db	1724346	GGGTGGGGCCAGTATTAAGAAATTAAGCAGGCTGCGGAGCCAGCAGTGGCAACGGCCAC	1724405
QY	3475	AGGTCCCTATCTCACATATATGGCAGCTTTGTTCTTTGGCTGTTTGCATTAATCTTGGTAC	3534
Db	1724406	AGGTCCCTATCTCACATATATGGCAGCTTTGTTCTTTGGCTGTTTGCATTAATCTTGGTAC	1724465
QY	3535	TGCTGCTTTTGGGTCCACACTGCTTTTATATAGCTGTATACACTCACACGAGAGTGTGC	3594
Db	1724466	TGCTGCTTTTGGGTCCACACTGCTTTTATATAGCTGTATACACTCACACGAGAGTGTGC	1724525
QY	3595	AGCTTCATCTCTGAAGCCACTTAAGACCAACGAGCCACCGGGAGGAATGAACATCCGGCC	3654
Db	1724526	AGCTTCATCTCTGAAGCCACTTAAGACCAACGAGCCACCGGGAGGAATGAACATCCGGCC	1724585
QY	3655	CGCGCTGCTTTAAGAGCTATTAACACTCAGCGAGAGGTCTGACGCTTCACTCTCAGACCA	3714
Db	1724586	CGCGCTGCTTTAAGAGCTATTAACACTCAGCGAGAGGTCTGACGCTTCACTCTCAGACCA	1724645
QY	3715	GCGAGACACGACAAACCACACAGAGAGAAACTGGAAACATCTGSAACATCAGAGAA	3774
Db	1724646	GCGAGACACGACAAACCACACAGAGAGAAACTGGAAACATCTGSAACATCAGAGAA	1724705
QY	3775	CAAACTCCAGATGCACACACTTAAGAGCTGTAAACACTCACTGCGAGGGTCCGCGCTTCC	3834
Db	1724706	CAAACTCCAGATGCACACACTTAAGAGCTGTAAACACTCACTGCGAGGGTCCGCGCTTCC	1724765
QY	3835	TTCTTGAAGTCAATGAGAACCAAGCACTCACAGTTTGGGACACAAAGCCAGAGATTGAG	3894
Db	1724766	TTCTTGAAGTCAATGAGAACCAAGCACTCACAGTTTGGGACACAAAGCCAGAGATTGAG	1724825
QY	3895	ATCAGCCCTGGGCAACATGATGAATAATGCCCTCTGCAAAAAAATAAATAATTTACAAAAAT	3954
Db	1724826	ATCAGCCCTGGGCAACATGATGAATAATGCCCTCTGCAAAAAAATAAATAATTTACAAAAAT	1724885
QY	3955	TGGCGAGACATGATGTGCTGCTGTGTGTCCACACTACCGGGAGGCTTAAGTGGAGG	4014
Db	1724886	TGGCGAGACATGATGTGCTGCTGTGTGTCCACACTACCGGGAGGCTTAAGTGGAGG	1724945
QY	4015	ATGCGTTTGAAGCTGGGAGGTGAACACGTGAGCTGTGATTTGTACCACAGCCCTCTAG	4074
Db	1724946	ATGCGTTTGAAGCTGGGAGGTGAACACGTGAGCTGTGATTTGTACCACAGCCCTCTAG	1725005
QY	4075	GCTGGGGGACAGACTGAGACCCCTTTTCCCTCCGCAAAAAAATAATTTGACAAAGGTATATA	4134
Db	1725006	GCTGGGGGACAGACTGAGACCCCTTTTCCCTCCGCAAAAAAATAATTTGACAAAGGTATATA	1725065
QY	4135	AGAGTGCCTTATATATGCTAGGGCCAGTGGCTCATGCCCTGTATATCCAGACATTTGGGAA	4194
Db	1725066	AGAGTGCCTTATATATGCTAGGGCCAGTGGCTCATGCCCTGTATATCCAGACATTTGGGAA	1725125

OY	4195	GCCGAGCGGGGGGTCACTTAAGTGAAGAAGTGAGACCAAGCCTGGCCAATGTGAGA	4254
Db	1725126	GCCGAGCGGGGGGGGTCACTTAAGTGAAGAAGTGAGACCAAGCCTGGCCAATGTGAGA	1725185
OY	4255	AAGCCACTCTCTTTAAAAAATACAATAATTACC GGCGCTGTGGGGCAGAGGTGGAGCATGC	4314
Db	1725186	AAGCCACTCTCTTTAAAAAATACAATAATTACC GGCGCTGTGGGGCAGAGGTGGAGCATGC	1725245
OY	4315	CTGTAAATCCACAGTCTACTCAGGAGGCTGAGGAGGAGNAATCACTTGAACCCAGAGGGGCG	4374
Db	1725246	CTGTAAATCCACAGTCTACTCAGGAGGCTGAGGAGGAGNAATCACTTGAACCCAGAGGGGCG	1725305
OY	4375	GGTTTCAGTAGAGCCGAGATCGTGCCATTGCACTCCACCCTCCAGCCTGGGGCAACAGA	4434
Db	1725306	GGTTTCAGTAGAGCCGAGATCGTGCCATTGCACTCCACCCTCCAGCCTGGGGCAACAGA	1725365
OY	4435	GCCAAACTCTGTCTTTAAAAAAAAAAAAAAAAAGGCGCTGACATTAATTAAGAGGTGGCAATG	4494
Db	1725366	GCCAAACTCTGTCTTTAAAAAAAAAAAAAAAAAGGCGCTGACATTAATTAAGAGGTGGCAATG	1725424
OY	4495	CAATAGTTGCACAGGCAACATGTTTTAAGAATGTGAGACTCGTCCCTTCATGGTCTCTGTA	4554
Db	1725425	CAATAGTTGCACAGGCAACATGTTTTAAGAATGTGAGACTCGTCCCTTCATGGTCTCTGTA	1725484
OY	4555	AAAACCCACCTCAAGGCCAGGTGCACTGAGCTCATGCTATTAATCCACGACTTTGGAG	4614
Db	1725485	AAAACCCACCTCAAGGCCAGGTGCACTGAGCTCATGCTATTAATCCACGACTTTGGAG	1725544
OY	4615	GCCGAGGGGGGGGATCACTGAGGTGAGGAGTTGAGAACCAAGCCTGACCAACAAATGG	4674
Db	1725545	GCCGAGGGGGGGGATCACTGAGGTGAGGAGTTGAGAACCAAGCCTGACCAACAAATGG	1725604
OY	4675	TGAATATCCCACCTCTACTTAAAAAATCAAAAAATTAGATGAGCATGTGGTGCACTGCCTGAA	4734
Db	1725605	TGAATATCCCACCTCTACTTAAAAAATCAAAAAATTAGATGAGCATGTGGTGCACTGCCTGAA	1725664
OY	4735	TCCCACTTACTTTGGAGGCTGAGGAGGAAAAATCACTAAGAACGAGGAGCGGAGTTGT	4794
Db	1725665	TCCCACTTACTTTGGAGGCTGAGGAGGAAAAATCACTAAGAACGAGGAGCGGAGTTGT	1725724
OY	4795	AGTGAGCGGAGATCGTGCCATTGGCACTCCAGCCTGAGCAATGAGGGAATCCATTCCTCAA	4854
Db	1725725	AGTGAGCGGAGATCGTGCCATTGGCACTCCAGCCTGAGCAATGAGGGAATCCATTCCTCAA	1725784
OY	4855	AAAAACAACAACAAAAACCACTCTCTACTCCAGGAGGAGTGGGTACAGACTGGGCGAC	4914
Db	1725785	AAAAACAACAACAAAAACCACTCTCTACTCCAGGAGGAGTGGGTACAGACTGGGCGAC	1725844
OY	4915	ATCAGTGCAGGTGCTGAGCCACAGAGCTAAAGCGGAGCTCAGAGCCGGCACAGATA	4974
Db	1725845	ATCAGTGCAGGTGCTGAGCCACAGAGCTAAAGCGGAGCTCAGAGCCGGCACAGATA	1725904
OY	4975	ACAGTGTGTGAGATTCAGTGTGTGAGATTCAGACGTCCCTGCAATTTGTGTACACAGGGGG	5034
Db	1725905	ACAGTGTGTGAGATTCAGTGTGTGAGATTCAGACGTCCCTGCAATTTGTGTACACAGGGGG	1725964
OY	5035	CCCCCAACACAGAGATGAGCCCAATCCAGACACACATCCACTTTCATCCAGAGATGT	5094
Db	1725965	CCCCCAACACAGAGATGAGCCCAATCCAGACACACATCCACTTTCATCCAGAGATGT	1726024
OY	5095	CTGTTTCTTGGCAGCGCTGGGGTAAATTAGACAGAAAGGTGACAGTCTTGGGTGTGTGACG	5154
Db	1726025	CTGTTTCTTGGCAGCGCTGGGGTAAATTAGACAGAAAGGTGACAGTCTTGGGTGTGTGACG	1726084
OY	5155	TCAGACTGCCCGAGGAGGCTTGTGGCTGTAGAAAAAGTTACAGGCTGAGGCCGGGCGAC	5214
Db	1726085	TCAGACTGCCCGAGGAGGCTTGTGGCTGTAGAAAAAGTTACAGGCTGAGGCCGGGCGAC	1726144
OY	5215	GGTGGCTCAGCGCTGTATAATCCACAGCACTTTTGGAGGGCCGAGCGGGTGTCAAGAGTCT	5274
Db	1726145	GGTGGCTCAGCGCTGTATAATCCACAGCACTTTTGGAGGGCCGAGCGGGTGTCAAGAGTCT	1726204
OY	5275	AGGAGATGTATACATCTCTGGCTTAACAGAGGTGAACCCGCTCTTACTAAAAAATACAAA	5334

```

Db 1726205 AGGAGATGTCACCATCTGCTAAGACGAGTGAACCCCGTCTACTAAAAATACAAA 1726264
QY 5335 AATTGGCCGGGACATGTTGGCGGACCTGTAGTTCCTACTCTCGGAGGCTGAGCGACG 5394
Db 1726265 AATTGGCCGGGACATGTTGGCGGACCTGTAGTTCCTACTCTCGGAGGCTGAGCGACG 1726324
QY 5395 AGAATGGCTGAACCCGAGAGGACGATTTGACGAGCCGAGATCGGCGCACCTGACATC 5454
Db 1726325 AGAATGGCTGAACCCGAGAGGACGATTTGACGAGCCGAGATCGGCGCACCTGACATC 1726384
QY 5455 CAGCTGGGACAGAGACGACATCTGATGAAAAAGAAAAAGAAAGCTTCAGGTCTGA 5514
Db 1726385 CAGCTGGGACAGAGACGACATCTGATGAAAAAGAAAAAGAAAGCTTCAGGTCTGA 1726444
QY 5515 GCCAGAGGCGCAGGCTGTAAATTCCTGACCTTACATGACCTTTGGGACAGGACCTTC 5574
Db 1726445 GCCAGAGGCGCAGGCTGTAAATTCCTGACCTTACATGACCTTTGGGACAGGACCTTC 1726504
QY 5575 CCTGGCCCAATTCAGGCGGTTGGAATGACCTCAAGGTCCTTCAGCATTAAGCCTGCA 5634
Db 1726505 CCTGGCCCAATTCAGGCGGTTGGAATGACCTCAAGGTCCTTCAGCATTAAGCCTGCA 1726564
QY 5635 TGGTCTTAAGATGAGAAAGATGGGCGAGTTTCCCTCTCTCAAGCCGCGGTCTCACTT 5694
Db 1726565 TGGTCTTAAGATGAGAAAGATGGGCGAGTTTCCCTCTCTCAAGCCGCGGTCTCACTT 1726624
QY 5695 CAAGCTGAATACCAAGGAGATCAGCTGTCCCAATCCCGAGTTCCAAAGCCCTTTGGGGA 5754
Db 1726625 CAAGCTGAATACCAAGGAGATCAGCTGTCCCAATCCCGAGTTCCAAAGCCCTTTGGGGA 1726684
QY 5755 CCCACTGTCAGGCGCTGACAGGAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 5814
Db 1726685 CCCACTGTCAGGCGCTGACAGGAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1726744
QY 5815 GTCCTGCTCATTCGCGGACAGACATCCGTTTCCCTCTGCTACCGGATTTCTAGGGGC 5874
Db 1726745 GTCCTGCTCATTCGCGGACAGACATCCGTTTCCCTCTGCTACCGGATTTCTAGGGGC 1726804
QY 5875 TTTAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5934
Db 1726805 TTTAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726864
QY 5935 TTTGAGACAGGACGACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 5994
Db 1726865 TTTGAGACAGGACGACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1726924
QY 5995 AGCCAAAGACCCCAATGCTTATCTCAGGTAGAGGCTCAGAGGCTCCAGACAGGACG 6054
Db 1726925 AGCCAAAGACCCCAATGCTTATCTCAGGTAGAGGCTCAGAGGCTCCAGACAGGACG 1726984
QY 6055 CTCGGGAGAGTTTGGGGGTAGGATGAGGACAGGACAGGCTTTCTTTCTCTCTAGAA 6114
Db 1726985 CTCGGGAGAGTTTGGGGGTAGGATGAGGACAGGACAGGCTTTCTTTCTCTCTAGAA 1727043
QY 6115 TTTGGGGCTGGGGGACAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 6173
Db 1727044 TTTGGGGCTGGGGGACAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1727103
QY 6174 CCACAGTCTGACAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6233
Db 1727104 CCACAGTCTGACAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1727162

```

```

RESULT 4
US-60-466-412-83872
; Sequence 83872, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CI001466

```

```

; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 83872
; LENGTH: 14371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-466-412-83872

Query Match      97.1%; Score 6052.8; DB 101; Length 14371;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 6196; Conservative 8; Mismatches 20; Indels 16; Gaps 12:

QY 1 GATCATTGAGACAGTACTTGAAGACAGGCTGGGACAGTATGAGGAGACTCTCTACG 60
Db 2575 GATCATTGAGACAGTACTTGAAGACAGGCTGGGACAGTATGAGGAGACTCTCTACG 2634
QY 61 AAAAAATCAAAAAATATGCGCGGATGCTGCTACGCTGATGATGATGATGATGATGATGATGAT 120
Db 2635 AAAAAATCAAAAAATATGCGCGGATGCTGCTACGCTGATGATGATGATGATGATGATGATGAT 2694
QY 121 ACATCAAGGCAAGTGGATCACTTGAAGTCAAGGATTCAGACTAGCTGGCCAGCATGAT 180
Db 2695 ACATCAAGGCAAGTGGATCACTTGAAGTCAAGGATTCAGACTAGCTGGCCAGCATGAT 2754
QY 181 GAACCCCTATCTCCACTAAAAATATCAAAAAATTTAGCCAGGATGTTGGCAGCCCTGTA 240
Db 2755 GAACCCCTATCTCTACT-AAAAATCAAAAAATTTAGCCAGGATGTTGGCAGGACCTGTA 2813
QY 241 ATCCGGGCTACTCAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 2814 ATCCGGGCTACTCAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2873
QY 301 CAGTAGCTGAGATACACACACTGCTCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 2874 CAGTAGCTGAGATACACACACTGCTCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2933
QY 361 AAAAAAATAAAAAATAAAAAATTTAGCCAGGATGTTGGCAGCCCTGATGCTCAG 420
Db 2934 AAAAAAATAAAAAATAAAAAATTTAGCCAGGATGTTGGCAGCCCTGATGCTCAG 2993
QY 421 CTACTCAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 2994 CTACTCAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3052
QY 481 GCCAAGATCATGCCACTACACTCCAGCCTGGGCAACAGAGAGAGACCTGTCTTAATAA 540
Db 3053 GCCAAGATCATGCCACTACACTCCAGCCTGGGCAACAGAGAGAGACCTGTCTTAATAA 3112
QY 541 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 600
Db 3113 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 3169
QY 601 ATGTATATAGTTTGAACCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 3170 ATGTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 3229
QY 661 ATGGTCTGTGACATCACTCTGCTGCTCTTCTAGACAAAGAGAGCTATTAACAT 720
Db 3230 ATGGTCTGTGACATCACTCTGCTGCTCTTCTAGACAAAGAGAGCTATTAACAT 3289
QY 721 ACATACATGATATTTTATAGACATGAGATTTGATTTGATTTGATTTGATTTGATTTGATTT 780
Db 3290 ACATACATGATATTTTATAGACATGAGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3349
QY 781 AAAAAATCTTTTAAAAATTTTCCCTAACATTTAAAGTAAAGCCGGCA- - -G 837
Db 3350 AAAAAATCTTTTAAAAATTTTCCCTAACATTTAAAGTAAAGCCGGCAAGGCG 3409
QY 838 CGCGCCATGTCACGCTGTATATTCACAGCTTTGGAGGCTGAGTGGGACGATCACTT 897
Db 3410 CGCGCCATGTCACGCTGTATATTCACAGCTTTGGAGGCTGAGTGGGACGATCACTT 3469

```

QY 898 GAGATCAACAGTTTCGAGACCAAGCTTGCCAAATAGCAAAAACCCATTTCTACTAAAAAT 957
 Db 3470 GAGATCAACAGTTTCGAGACCAAGCTTGCCAAATAGCAAAAACCCATTTCTACTAAAAAT 3529
 QY 958 AAAAAATTTAGCTGGGCGATAGTGTGACACCTGTGTATCCAGCTACTTTGGAGGCTGAG 1017
 Db 3530 AAAAAATTTAGCTGGGCGATAGTGTGACACCTGTGTATCCAGCTACTTTGGAGGCTGAG 3589
 QY 1018 GCAGAGAAATCGCTTGAACCTTGAGAAAGGAGGTTGAGTGCAGCAATCATGCCACTG 1077
 Db 3590 GCAGAGAAATCGCTTGAACCTTGAGAAAGGAGGTTGAGTGCAGCAATCATGCCACTG 3649
 QY 1078 CACTCCAGCTGGGTGACAGAGTGAAGCTTCTCTCAACGAAAAAAGTGTAAAAAGC 1137
 Db 3650 CACTCCAGCTGGGTGACAGAGTGAAGCTTCTCTCAACGAAAAAAGTGTAAAAAGC 3709
 QY 1138 CATTCCTAATTCAGTGTACATGATGTACATCTCAAGGTTGGTGGTCTGCTGAGG 1197
 Db 3710 CATTCCTAATTCAGTGTACATGATGTACATCTCAAGGTTGGTGGTCTGCTGAGG 3769
 QY 1198 CATACCTGAGAAATAGAGTGTGTGTACAGAGACATACATTTCCATTTAACTAGAC 1257
 Db 3770 CATACCTGAGAAATAGAGTGTGTGTGTACAGAGACATACATTTCCATTTAACTAGAC 3829
 QY 1258 ACTACCAAGTGGCATCCAAAGAGG--TTTTTTTTTACAATCTTACACTCCCCCAGCAAC 1316
 Db 3830 ACTACCAAGTGGCATCCAAAGAGGTTTTTTTTTTTACAATCTTACACTCCCCCAGCAAC 3889
 QY 1317 AATGAGAGTTACTCCAGATCTTTACAAGATGCTCTAAGCCAGTACAGATGAAAC 1376
 Db 3890 AATGAGAGTTACTCCAGATCTTTACAAGATGCTCTAAGCCAGTACAGATGAAAC 3949
 QY 1377 AGGAACTGGAGGGGAAAGCTGCCAGCCCTTCTAACCATGAGAAATACCTGGTAGAGCC 1436
 Db 3950 AGGAACTGGAGGGGAAAGCTGCCAGCCCTTCTAACCATGAGAAATACCTGGTAGAGCC 4009
 QY 1437 TTCTGATGTGTGAAGAGTAATTAAGGGGGTCTGTGAGACCTGCCCTCTGATGATCAC 1496
 Db 4010 TTCTGATGTGTGAAGAGTAATTAAGGGGGTCTGTGAGACCTGCCCTCTGATGATCAC 4069
 QY 1497 TGTGACTTTCGAGCCTCCAGTCCAGTCTCAGCCCATGCTGATGAGGCAATGATGATGAG 1556
 Db 4070 TGTGACTTTCGAGCCTCCAGTCCAGTCTCAGCCCATGCTGATGAGGCAATGATGATGAG 4128
 QY 1557 CCCTGACTCTCTTTGGTCTTATCTT--CCCCATGTGGGGCTGAAGTGTGATGAGCC 1615
 Db 4129 CCCTGACTCTCTTTGGTCTTATCTTCTCCCATGTGGGGCTGAAGTGTGATGAGCC 4188
 QY 1616 GTTATTCAGATGTACAGCTTCTGTGACAGAAAGTAGTGTCAACAGAAAGAGAGGGCT 1675
 Db 4189 GTTATTCAGATGTACAGCTTCTGTGACAGAAAGTAGTGTCAACAGAAAGAGAGGGCT 4248
 QY 1676 TGGCAAGATGATTAATCTGCAAAATCTTACCTGGCTCAGCCACCAAGTATGCTGTGATCT 1735
 Db 4249 TGGCAAGATGATTAATCTGCAAAATCTTACCTGGCTCAGCCACCAAGTATGCTGTGATCT 4308
 QY 1736 TGAACAAGTTTTTTCACCTTCTGAGGCCATCCCTTGGCTTACAACACAGAGTGTGTA 1795
 Db 4309 TGAACAAGTTTTTTCACCTTCTGAGGCCATCCCTTGGCTTACAACACAGAGTGTGTA 4368
 QY 1796 CAGGATGAATGACG--AAGTCCCTTACCTGTAAATCCGACACTTTGGAGGCCAAAGGC 1854
 Db 4369 CAGGATGAATGACGAAAGTGCCTTACACTGTAAATCCGACACTTTGGAGGCCAAAGGC 4428
 QY 1855 GGGTGGATGGCTTGAAGCTGAGAGGTGACAGATGCGGCGAGTCTCACAGCCCTGCTTC 1914
 Db 4429 GGGTGGATGGCTTGAAGCTGAGAGGTGACAGATGCGGCGAGTCTCACAGCCCTGCTTC 4488
 QY 1915 GCTCTGGGCGCTCTCTGCTGCTGGGCTCCCACTTGGTGGCACTTGAAGAAGCCCTTACGC 1974
 Db 4489 GCTCTGGGCGCTCTCTGCTGCTGGGCTCCCACTTGGTGGCACTTGAAGAAGCCCTTACGC 4548

QY 1975 CCAACGCTGCACTGTGGAGAGCCCTTTCTGGCTGGCCAAAGGCCAGAGCCGCTCCTCA 2034
 Db 4549 CCAACGCTGCACTGTGGAGAGCCCTTTCTGGCTGGCCAAAGGCCAGAGCCGCTCCTCA 4608
 QY 2035 GCTTGCAGGAGAGTGTGGAGGAGAGGCTCAAGCAGAAACCGGGGCTTGCAGCGGCTT 2094
 Db 4609 GCTTGCAGGAGAGTGTGGAGGAGAGGCTCAAGCAGAAACCGGGGCTTGCAGCGGCTT 4668
 QY 2095 GCGGGCCAGCTGGAGTTCGCGGGTGGGGTGGGCTTGGCGGGGCCCGACTCGAGAGAGC 2154
 Db 4669 GCGGGCCAGCTGGAGTTCGCGGGTGGGGTGGGCTTGGCGGGGCCCGACTCGAGAGAGC 4728
 QY 2155 GGGCAGCCCTGCGCAGAGCCCGGGGCAATGAGAGGCTTGAACCCGGGCGACCGGCTGGGA 2214
 Db 4729 GGGCAGCCCTGCGCAGAGCCCGGGGCAATGAGAGGCTTGAACCCGGGCGACCGGCTGGGA 4788
 QY 2215 GGGGTACTGGGTGGGCCCCACAGAGCCCGGCGGCGGCTGTGCTGCTGATTTCTCA 2274
 Db 4789 GGGGTACTGGGTGGGCCCCACAGAGCCCGGCGGCGGCTGTGCTGCTGATTTCTCA 4848
 QY 2275 CTGGGCTTGAAGAGCTTCCCGGGGCAAGGCTCGGAGCTGAGCCCGCATGCTGA 2334
 Db 4849 CTGGGCTTGAAGAGCTTCCCGGGGCAAGGCTCGGAGCTGAGCCCGCATGCTGA 4908
 QY 2335 GCTTCCCTCATGAGGCTCTCTGCGGCGGAGGCTTCCCGAGCAGACACACCCCTGCT 2394
 Db 4909 GCTTCCCTCATGAGGCTCTCTGCGGCGGAGGCTTCCCGAGCAGACACACCCCTGCT 4968
 QY 2395 CCACAGGCGCCAGTCCCATGAGCAGCAGCAAGGGCTGGAAGTGGGGGCGACGGCAGCCG 2454
 Db 4969 CCACAGGCGCCAGTCCCATGAGCAGCAGCAGGCTGGAAGTGGGGGCGACGGCAGCCG 5028
 QY 2455 GACTGGCAGGAGCTTACCCCTGCGAGCCCTGGTGGGAATCCACTGGGTGAAGCCAGCTGG 2514
 Db 5029 GACTGGCAGGAGCTTACCCCTGCGAGCCCTGGTGGGAATCCACTGGGTGAAGCCAGCTGG 5088
 QY 2515 GCTTCTGAGTGTGTGGAGAGCTTGAAGAACTTTATGTCTAGCTCAGAGATGATTAATAC 2574
 Db 5089 GCTTCTGAGTGTGTGGAGAGCTTGAAGAACTTTATGTCTAGCTCAGAGATGATTAATAC 5148
 QY 2575 ACCAATGAGACCTGTGTAGCTCAGGGTGTGTAATCAGCAATCCACACTCTGAT 2634
 Db 5149 ACCAATGAGACCTGTGTAGCTCAGGGTGTGTAATCAGCAATCCACACTCTGAT 5208
 QY 2635 CTAGCTACTGTATGGGCTTGGAGAACTTTATGTCTAGCTCAGAGATGATTAATAC 2694
 Db 5209 CTAGCTACTGTATGGGCTTGGAGAACTTTATGTCTAGCTCAGAGATGATTAATAC 5268
 QY 2695 CCAATGGCAGCTGTGTATGCTCAAGGTTTGTAAACACACCAATCAGACCTGTGTC 2754
 Db 5269 CCAATGGCAGCTGTGTATGCTCAAGGTTTGTAAACACACCAATCAGACCTGTGTC 5328
 QY 2755 TAGCTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2814
 Db 5329 TAGCTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5388
 QY 2815 CCGTGTGAAGAGACCAACCAAGGCTTGTGTGAGCAATTAAGCTTCTATCAGCTGGGT 2874
 Db 5389 CCGTGTGAAGAGACCAACCAAGGCTTGTGTGAGCAATTAAGCTTCTATCAGCTGGGT 5448
 QY 2875 GCAAGTGGGCTGAGTCCGAAAGAGAGTCAAGGAGAGATTAAGGTTGGGGCTTTTGA 2934
 Db 5449 GCAAGTGGGCTGAGTCCGAAAGAGAGTCAAGGAGAGATTAAGGTTGGGGCTTTTGA 5508
 QY 2935 TAGGATTTTGGGTAGTAAAGGAAATTTACAGTCAAAAGGGGTTTGTCTTGGCGGGCAG 2994
 Db 5509 TAGGATTTTGGGTAGTAAAGGAAATTTACAGTCAAAAGGGGTTTGTCTTGGCGGGCAG 5568
 QY 2995 GAGTGGGGGTTCGAAGGTGCTCAGTGGGGGTCTTTTGAAGCAGAGATGAGCAGGAAA 3054
 Db 5569 GAGTGGGGGTTCGAAGGTGCTCAGTGGGGGTCTTTTGAAGCAGAGATGAGCAGGAAA 5628
 QY 3055 AGGACTTTTCAAAAGTATATGATCAATTTAAGCAAGAGACCCGCAATTTACACTCTTTT 3114

|||||
Db 5629 AGGACTTTACAAAGGTATGTCATCAATTAAGGCAAGACCGCCATTTACACCTCTTT 5688
Oy 3115 GTGGTGAATGTATAGTTAGTTGGGGAGGGCATATTCACCTCTTTGTGATTTCTC 3174
Db 5689 GTGGTGAATGTATAGTTAGTTGGGGAGGGCATATTCACCTCTTTGTGATTTCTC 5748
Oy 3175 AGTTACTTCAGGCCATCTGGGCGCTATATGTGCAAGTTACAGGGGATGCGATGGCT 3234
Db 5749 AGTTACTTCAGGCCATCTGGGCGCTATATGTGCAAGTTACAGGGGATGCGATGGCT 5808
Oy 3235 TGGGCTTCAGAGGCTTGACAGCTACTGTGTGGGCGCTTGAGAAATGTTTGTGACACT 3294
Db 5809 TGGGCTTCAGAGGCTTGACAGCTACTGTGTGGGCGCTTGAGAAATGTTTGTGACACT 5868
Oy 3295 CTGTATCTAGTTATCTAGTGGGAGCTGGAGAACTTTGTGTACTCTCAGGATGTA 3354
Db 5869 CTGTATCTAGTTATCTAGTGGGAGCTGGAGAACTTTGTGTACTCTCAGGATGTA 5928
Oy 3355 AAGGCACCAATCAGCGCCCTGTCAAAACAGACACCTGGCTCTACCAATCAGAGATGT 3414
Db 5929 AAGGCACCAATCAGCGCCCTGTCAAAACAGACACCTGGCTCTACCAATCAGAGATGT 5988
Oy 3415 GGGTGGGGCAGATAGAGATAAAGCAGGCTGCCAGGACAGCAGTGGCAACGCCAC 3474
Db 5989 GGGTGGGGCAGATAGAGATAAAGCAGGCTGCCAGGACAGCAGTGGCAACGCCAC 6048
Oy 3475 AGGTCCCTATCCACAAATATGGAGCTTGTCTTTCTGTCTGTAATATCTTGTCTAC 3534
Db 6049 AGGTCCCTATCCACAAATATGGAGCTTGTCTTTCTGTCTGTAATATCTTGTCTAC 6108
Oy 3535 TGGTCCGTTTTGGGTGCACACCTGTTTATAGCTGTAAACACTCACACGAAAGTCTGC 3594
Db 6109 TGGTCCGTTTTGGGTGCACACCTGTTTATAGCTGTAAACACTCACACGAAAGTCTGC 6168
Oy 3595 AGCTTCACTCTTGAAGCCACTAAGACACAGCCACCGGAGGAATGAACAACTCCGGC 3654
Db 6169 AGCTTCACTCTTGAAGCCACTAAGACACAGCCACCGGAGGAATGAACAACTCCGGC 6228
Oy 3655 CGGCTGCCCTTAAGAGCTATTAACACTACCGGAAAGTGTGACCTTCACTCTCAGCCA 3714
Db 6229 CGGCTGCCCTTAAGAGCTATTAACACTACCGGAAAGTGTGACCTTCACTCTCAGCCA 6288
Oy 3715 GCGAGACCAAGAACCCACGAAGGAAGAACTGCAACATGTGAACANTCAGAAGAA 3774
Db 6289 GCGAGACCAAGAACCCACGAAGGAAGAACTGCAACATGTGAACANTCAGAAGAA 6348
Oy 3775 CAAACTCCAGATGCACCACTTAAGAGCTGTAAACACTACCTGCGAGGCTCCGGCTTCC 3834
Db 6349 CAAACTCCAGATGCACCACTTAAGAGCTGTAAACACTACCTGCGAGGCTCCGGCTTCC 6408
Oy 3835 TTCTTGAAGTCAGTAGAGACCAAGCACTACCAAGTTTGGACACAAAGCCAGAGTTTGA 3894
Db 6409 TTCTTGAAGTCAGTAGAGACCAAGCACTACCAAGTTTGGACACAAAGCCAGAGTTTGA 6468
Oy 3895 ATCAGCTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAATTTACAAAAT 3954
Db 6469 ATCAGCTGGGCAACATGATGAATGCCCTCTCTGCAAAAAAATTTACAAAAT 6528
Oy 3955 TGGCGAGCATGTGTGCTCGCTGTGTGCCAGTACGCGGAGGCTAAAGTGGGAG 4014
Db 6529 TGGCGAGCATGTGTGCTCGCTGTGTGCCAGTACGCGGAGGCTAAAGTGGGAG 6588
Oy 4015 ATGCTTGAAGCTTGGAGGTGAAGACTGCAAGTGTGATTTGTACACAGCCCTTAG 4074
Db 6589 ATGCTTGAAGCTTGGAGGTGAAGACTGCAAGTGTGATTTGTACACAGCCCTTAG 6648
Oy 4075 GCTGGGGAGCAGACTGAGACCTGTTCCCTCGCAAAAAAATTTGCAAAAGTATATA 4134
Db 6649 GCTGGGGAGCAGACTGAGACCTGTTCCCTCGCAAAAAAATTTGCAAAAGTATATA 6708
Oy 4135 AGAGGTGCCATATGTGCTAGGGCAGTGGCTCATGTGCTTAATCCAGCACTTTGGAA 4194
|||||

Db 6709 AGAGGTGCCATATGTGCTAGGCGAGTGGCTCATGTGCTTAATCCAGCACTTTGGAA 6768
Oy 4195 GCCGAGGGGGGGGTACCTAAGGTGAGAGTGTGAGAACAGCCTGGCCAAAGTGA 4254
Db 6769 GCCGAGGGGGGGGTACCTAAGGTGAGAGTGTGAGAACAGCCTGGCCAAAGTGA 6828
Oy 4255 AAGCCATCTCTTTAAATAATACAAATAATACCCGCTGTGGGGCAGTGTGAGCAGTC 4314
Db 6829 AAGCCATCTCTTTAAATAATACAAATAATACCCGCTGTGGGGCAGTGTGAGCAGTC 6888
Oy 4315 CTGTATCCAGCTACTCAGAGGCTGAGGCAAGAAATCACTTGAACCCAGAGGGCCG 4374
Db 6889 CTGTATCCAGCTACTCAGAGGCTGAGGCAAGAAATCACTTGAACCCAGAGGGCCG 6948
Oy 4375 GGTGACGTGAGCGAGATGCGCATGACCTCACCACCTCAGCCTGGGCAACAGA 4434
Db 6949 GGTGACGTGAGCGAGATGCGCATGACCTCACCACCTCAGCCTGGGCAACAGA 7008
Oy 4435 GCCAAACTCTCTTTAAAAAAGTCCCTGACATATTAAGGTGTGCAATG 4494
Db 7009 GCCAAACTCTCTTT -AAAAAAGTCCCTGACATATTAAGGTGTGCAATG 7067
Oy 4495 CAATAGTTCAGGCAACATGTTAAGATGTGAGCTCTGCTTCCATGCTCTGTTA 4554
Db 7068 CAATAGTTCAGGCAACATGTTAAGATGTGAGCTCTGCTTCCATGCTCTGTTA 7127
Oy 4555 AAAACCCACCTCAAGGCGAGTGCATGCTCATGCTTATATCCAGCACTTTGGAG 4614
Db 7128 AAAACCCACCTCAAGGCGAGTGCATGCTCATGCTTATATCCAGCACTTTGGAG 7187
Oy 4615 GCCGAGGGGGGTGATCACTGAGGTGAGAGTTCGAGACAGCCTGCACCAACATAG 4674
Db 7188 GCCGAGGGGGGTGATCACTGAGGTGAGAGTTCGAGAGTTCGAGACAGCCTGCACCAACATAG 7247
Oy 4675 TGAATCCACCTCTACTAAAAATACAAATTTAGTAGAGATGTGTGATGCTGTAA 4734
Db 7248 TGAATCCACCTCTACTAAAAATACAAATTTAGTAGAGATGTGTGATGCTGTAA 7307
Oy 4735 TCCCACTACTTGGGAGGCTGAGGCAAGAAATCACTTGAACAGGAGGGGAGTGTGT 4794
Db 7308 TCCCACTACTTGGGAGGCTGAGGCAAGAAATCACTTGAACAGGAGGGGAGTGTGT 7367
Oy 4795 AGTGAGCGAGATGTGCTCATTTGACACTGCACCTGAGCAATGAGGAAACTGCATCTCAA 4854
Db 7368 AGTGAGCGAGATGTGCTCATTTGACACTGCACCTGAGCAATGAGGAAACTGCATCTCAA 7427
Oy 4855 AAAAACAACAACAAACCCACTCTACTCCCAAGGAGTGTGTACAGAGCTGGGCCAC 4914
Db 7428 AAAAACAACAACAAACCCACTCTACTCCCAAGGAGTGTGTGTACAGAGCTGGGCCAC 7487
Oy 4915 ATCAGTGCAGGTGCTGAGCCACAGAGCTTAAGCGGAGCTGCAGAGCCGGGACCATTA 4974
Db 7488 ATCAGTGCAGGTGCTGAGCTGAGCTTAAGCGGAGCTGCAGAGCCGGGACCATTA 7547
Oy 4975 ACAGTGTGAGTACAGTGTGAGTACAGACGTCCTGCAATGTGTACACCAAGGGG 5034
Db 7548 ACAGTGTGAGTACAGTGTGAGTACAGACGTCCTGCAATGTGTGTACACCAAGGGG 7607
Oy 5035 CCCCAGACACACAGATGAGCCCATCCAGTACACACATCCATCTTCATCAAGATGT 5094
Db 7608 CCCCAGACACACAGATGAGCCCATCCAGTACACACATCCATCTTCATCAAGATGT 7667
Oy 5095 CTGTTTCTTGGCAGCTGGGGTAAATTAAGACAGAGTGCACAGTCTTGGGTGTGTCAG 5154
Db 7668 CTGTTTCTTGGCAGCTGGGGTAAATTAAGACAGAGTGCACAGTCTTGGGTGTGTCAG 7727
Oy 5155 TCAGACTGCCAGGAGGCTTGTGCTGTATAAAAAGTTCAAGGCTTAGCGGGGAC 5214
Db 7728 TCAGACTGCCAGGAGGCTTGTGCTGTGTATAAAAAGTTCAAGGCTTAGCGGGGAC 7787
Oy 5215 GGTGCTTCAGGCTGTATATCCACACTTTTGGAGGCGGAGGCGGTGTGATCAGAGGTC 5274
Db 7788 GGTGCTTCAGGCTGTATATCCACACTTTTGGAGGCGGAGGCGGTGTGATCAGAGGTC 7847

QY	5275	GGGAGTCGTACCATCTCGCTTAACAGCGGGAACCCCGCTCTACTAAAAATACAAA	5334
Db	7848	AGGAGATCGTACCATCTCGCTTAACAGCGGGAACCCCGCTCTACTAAAAATACAAA	7907
QY	5335	AATTGGCCGGGCATGTGTGGCGGGCACCTGTAGTTCCAGCTACTCGGGAGGCTGAGGCA	5394
Db	7908	AATTGGCCGGGATATGTGTGGCGGGCACCTGTAGTTCCAGCTACTCGGGAGGCTGAGGCA	7967
QY	5395	AGAAATGGCGTAAACCCGAGAGGCAAGATTTCAGTGAAGCCGAGATCGCGCCATGCATC	5454
Db	7968	AGAAATGGCGTAAACCCGAGAGGCAAGATTTCAGTGAAGCCGAGATCGCGCCATGCATC	8027
QY	5455	CAGCTTGGGGGCACAGAGCANAGATCCATCTGTGAAAAGAAAAGAAAGCTCAGCTCGA	5514
Db	8028	CAGCTTGGGGGCACAGAGCANAGATCCATCTGTGAAAAGAAAAGAAAGCTCAGCTCGA	8087
QY	5515	GCCAGAGGCCGAGAGCTGTAAATTCGTCACTTACCATGACTTGTGGGCAAGGACTTCCCT	5574
Db	8088	GCCAGAGGCCGAGAGCTGTAAATTCGTCACTTACCATGACTTGTGGGCAAGGACTTCCCT	8147
QY	5575	CTTGCGCCAGTTCAAGGGGTTGGATGCATCCAAAGTCCCTTCAGGACTTAAACGTGCA	5634
Db	8148	CCTTGCGCCAGTTCAAGGGGTTGGATGCATCCAAAGTCCCTTCAGGACTTAAACGTGCA	8207
QY	5635	TGTTTCTAAGATGAGAAGATGGGGCAGTTTCCCTCTCAACCCAGCCCTGTCCACTT	5694
Db	8208	TGTTTCTAAGATGAGAAGATGGGGCAGTTTCCCTCTCAACCCAGCCCTGTCCACTT	8267
QY	5695	CAAGGTGAATGACACAGGGAAGTCAACGTGTCCCAATCCCGCAGTTCCAAAGCCCTTGGGA	5754
Db	8268	CAAGGTGAATGACACAGGGAAGTCAACGTGTCCCAATCCCGCAGTTCCAAAGCCCTTGGGA	8327
QY	5755	CCCTACTGTACAGGTCGTGCACGAGAGAGTGAAGTCAAGTGAAGCCAAATGCGCTGAAAG	5814
Db	8328	CCCTACTGTACAGGTCGTGCACGAGAGAGTGAAGTCAAGTGAAGCCAAATGCGCTGAAAG	8387
QY	5815	GTCCTTGGCTCTTGTGGGACACANATCCGGGTTCCCTCTGCGCTCAACCGGGAATTCAGAGGC	5874
Db	8388	GTCCTTGGCTCTTGTGGGACACANATCCGGGTTCCCTCTGCGCTCAACCGGGAATTCAGAGGC	8447
QY	5875	TTTATGCCGAATGATCATGTGGGGGCGGGGGCGGTTCTTGGGGGAATTCACACCTTAATCAAC	5934
Db	8448	TTTATGCCGAATGATCATGTGGGGGCGGGGGCGGTTCTTGGGGGAATTCACACCTTAATCAAC	8507
QY	5935	TTGGGACAGCAGACCTTGGAACCTTCATGTGTGCTATCCAAAGTGTGGGGTGGGCACAGC	5994
Db	8508	TTGGGACAGCAGACCTTGGAACCTTCATGTGTGCTATCCAAAGTGTGGGGTGGGCACAGC	8567
QY	5995	AGCCAAACACCAATGTGCTTATCTCAGGTAGGGGCTCAGAGAGTCTCCACAGCAGCAGC	6054
Db	8568	AGCCAAACACCAATGTGCTTATCTCAGGTAGGGGCTCAGAGAGTCTCCACAGCAGCAGC	8627
QY	6055	CTCCGAGAGTTTGTGGGTAAGAAATGGAGCAACACGAGCTCTTTTTCCTCTTATGAA	6114
Db	8628	CTCCGAGAGTTTGTGGGTAAGAAATGGAGCAACCA -GCTTCTTTTTCCTCTTATGAA	8686
QY	6115	TTTGGGGGCTTGGGGGACAGGCTTGAGAAATCCAAAGAGAGGGGCAAAAGGACACT -CC	6173
Db	8687	TTTGGGGGCTTGGGGGACAGGCTTGAGAAATCCAAAGAGAGGGGCAAAAGGACACTGCC	8746
QY	6174	CCAAACAATCTGCGAG	6233
Db	8747	CCGGAAGCTGTCCACAGAGC -AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	8805

RESULT 5
US-60-465-241-52636
: Sequence 52636, Application US/60465241
: GENERAL INFORMATION:
: APPLICANT: CARCILL, Michele
: APPLICANT: BEOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```

: TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CU001468
:
: CURRENT APPLICATION NUMBER: US/60/465,241
:
: CURRENT FILING DATE: 2003-04-23
:
: NUMBER OF SEQ ID NOS: 258418
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 52636
:
: LENGTH: 14381
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-60-465-241-52636

```

Query Match	88.78;	Score 5532.6;	DB 101;	Length 14381;
-------------	--------	---------------	---------	---------------

Matches 5655; Conservative 0; Mismatches 14; Indels 14; Gaps 10;

QY	558	AAAAAAGAGCTGTTTATGTCTCGTGCATCATCATCATATGATATGATGGA	617
Db	1	AAAAAAGAGCTGTTTATGTCTCGTGCATCATCATCATATGATATGATGGA	57
QY	618	ACTCAAGAGTCAGATAGTCAATTTTTAGGCTGTGGCCGTATGTCTGTCAAT	677
Db	58	ACTCAAGAGTCAGATAGTCAATTTTTAGGCTGTGGCCGTATGTCTGTCAAT	117
QY	678	CAGCTCGCCCTGTTCTTCTAGCAGAAAAGAGCTATTAACATCATCATGATTTT	737
Db	118	CAGCTCGCCCTGTTCTTCTAGCAGAAAAGAGCTATTAACATCATCATGATTTT	177
QY	738	ATAGACATCGAGATTTGAATTTTCATATGATTTTTACATTTATTAATAATCTTTTAA	797
Db	178	ATAGACATCGAGATTTGAATTTTCATATGATTTTTACATTTATTAATAATCTTTTAA	237
QY	798	AATTTTCCCCTACCACTTTAAAGTGTAAAGCCGGCCA---GGCCGCATCTACGCC	854
Db	238	AATTTTCCCCTACCACTTTAAAGTGTAAAGCCGGCCAAGCCGCCATGGCTACGCC	297
QY	855	TGTATATTCAGACATTTGGAGGCGTGAAGTGGGAGATCAGTTGATCAACAGTTTCAG	914
Db	298	TGTATATTCAGACATTTGGAGGCGTGAAGTGGGAGATCAGTTGATCAACAGTTTCAG	357
QY	915	ACGAGCCTGGCCAAATAGCAAAACCCCATTTCTACTAAAAATAAAAAATTAAGTGGGC	974
Db	358	ACGAGCCTGGCCAAATAGCAAAACCCCATTTCTACTAAAAATAAAAAATTAAGTGGGC	417
QY	975	ATATGTGTGACACACTGTGATCCAGCAGTCTTGGAGGCTAGAGCAGAGAAATGCTTGA	1033
Db	418	ATATGTGTGACACACTGTGATCCAGCAGTCTTGGAGGCTAGAGCAGAGAAATGCTTGA	477
QY	1035	ACCTGGGAAGGGAGTGTGAGTAGAGCCAAATCATGACATGACCTGCACCTCGTGCTGA	1094
Db	478	ACCTGGGAAGGGAGTGTGAGTAGAGCCAAATCATGACATGACCTGCACCTCGTGCTGA	537
QY	1095	CAGAGTAGACTTGCTCTCAACGAAAAAAAAGTGTAAAGCCATTTCTTAATTCAGTGT	1155
Db	538	CAGAGTAGACTTGCTCTCAACGAAAAAAAAGTGTAAAGCCATTTCTTAATTCAGTGT	597
QY	1155	ACATCAGTGTATCACTCAGGTCTGCGACTACCTGCTGTGAGGCTACTCTGAGAACTGTA	1214
Db	598	ACATCAGTGTATCACTCAGGTCTGCGACTACCTGCTGTGAGGCTACTCTGAGAACTGTA	657
QY	1215	GTTGCTTGGTCACAGACATACACATTTCCACATTAACATAGACACTACCAAGTTGCCATC	1274
Db	658	GTTGCTTGGTCACAGACATACACATTTCCACATTAACATAGACACTACCAAGTTGCCATC	717
QY	1275	CAAGGAGG-TTTTTTTTTTTACAAATCTACCTCCCCCAGCAAAATGAGAGTTACTTCA	1333
Db	718	CAAGGAGGTTTTTTTTTTTACAAATCTACCTCCCCCAGCAAAATGAGAGTTACTTCA	777
QY	1334	GATCCTTTACAAAGATGCTCTTAAGCCCAAGTACAGATGAAAAAGAAAGTGGAGGGGAA	1393
Db	778	GATCCTTTACAAAGATGCTCTTAAGCCCAAGTACAGATGAAAAAGAAAGTGGAGGGGAA	837
QY	1394	GCTGCCAGCCCTTCTAACCAATGAAGAAATACCTGTAGAGCCCTTGTGATGCTGGAAG	1453

|||||
Db 838 GCTGCCAGCCCTTCTAACCATGAAATACTGTAAGAGCCTTGTGATGCTGGAAAG 897
OY 1454 ATGAATACGGGGGCTCTGTGAGCTGCCCTGTCAAGATCATGTGACTTTCAGGCTC 1513
Db 898 ATGAATACGGGGGCTCTGTGAGCTGCCCTGTCAAGATCATGTGACTTTCAGGCTC 957
OY 1514 CAGCCAGTCTCAGCCCCATGTGCATAGGCCAGTAATAGGCCCTCAGCTCTGTG 1573
Db 958 CAGTCACG-CTCAGCCCCATGTGCATAGGCCAGTAATAGGCCCTCAGCTCTGTG 1016
OY 1574 GCTTTATTCY-CCCCATGTGGGCTGAAGTCTGATTTGAGCCGTTATTCAGATGACA 1632
Db 1017 GCTTTATTCYCCCCATGTGGGCTGAAGTCTGATTTGAGCCGTTATTCAGATGACA 1076
OY 1633 GCTTTCTTGACAGGAAGTGTGTACAGAAACAGCAGGGGCTTGGCAAGTATCTAAC 1692
Db 1077 GCTTTCTTGACAGGAAGTGTGTGTACAGAAACAGCAGGGGCTTGGCAAGTATCTAAC 1136
OY 1693 TGCATACTCTACCTGGCTCAGCCACAGCTAGTCTGTGATCTTGAACAGTTTTCAC 1752
Db 1137 TGCATACTCTACCTGGCTCAGCCACAGCTAGTCTGTGATCTTGAACAGTTTTCAC 1196
OY 1753 TTTCTGAGGCCATCCCTGGCTACAAACACACAGTTTGTGACAGATGAATGACG-A 1811
Db 1197 TTTCTGAGGCCATCCCTGGCTACAAACACACAGTTTGTGACAGATGAATGACGAA 1256
OY 1812 AGTCCCTTACACCTGTATCCACAGACTTTGGAGGCCAAGGGGCTGATGCTTGAC 1871
Db 1257 AGTCCCTTACACCTGTATCCACAGACTTTGGAGGCCAAGGGGCTGATGCTTGAC 1316
OY 1872 CTGAGAGGTGACAGCATGCCGGCAGTCTCTACAGCCCTGCTGCTCGCCGCTCTC 1931
Db 1317 CTGAGAGGTGACAGCATGCCGGCAGTCTCTACAGCCCTGCTGCTCGCCGCTCTC 1376
OY 1932 TGCTGGGCTCCCACTTCGTGTGAGCACTTGAAGAGCCCTTACGCCACCGCTGCACTGG 1991
Db 1377 TGCTGGGCTCCCACTTCGTGTGAGCACTTGAAGAGCCCTTACGCCACCGCTGCACTGG 1436
OY 1992 GAGCCCTTCTGTGGGCTTGCGCAGGCCAAGCCGCTCCCTACGCTTGCAGGAGGTG 2051
Db 1437 GAGCCCTTCTGTGGGCTTGCGCAGGCCAAGCCGCTCCCTACGCTTGCAGGAGGTG 1496
OY 2052 GAGGAGAGGCTCAAGCAGGAACCGGGCTGCGCAGCGGCTTCGCGGCCAGCTGGAATT 2111
Db 1497 GAGGAGAGGCTCAAGCAGGAACCGGGCTGCGCAGCGGCTTCGCGGCCAGCTGGAATT 1556
OY 2112 CCGGGTGGGCTTGCGGCTTGCGCAGCTGCGACCTGCGAGCAGCGGCCAGCCCTGCAAGC 2171
Db 1557 CCGGGTGGGCTTGCGGCTTGCGGCGCCCGCAGCTGCGAGCAGCGGCCAGCCCTGCAAGC 1616
OY 2172 CCGGGCAATGAGAGCTTACACCCGCGGCCAGCGGCTGCGAGGCTGACTGGGTGCC 2231
Db 1617 CCGGGCAATGAGAGCTTACACCCGCGGCCAGCGGCTGCGAGGCTGACTGGGTGCC 1676
OY 2232 CAGGAGTGCAGCCCGCGGCTGTGCTGCTGATTTCTCATGTGGGCTTACAGAGCT 2291
Db 1677 CAGGAGTGCAGCCCGCGGCTGTGCTGCTGATTTCTCATGTGGGCTTACAGAGCT 1736
OY 2292 TCCCGCGGGCAGGCTGCGGACCTGAGCCCGCATGCTGAGAGCTCCCTTCATGGG 2351
Db 1737 TCCCGCGGGCAGGCTGCGGACCTGAGCCCGCATGCTGAGAGCTCCCTTCATGGG 1796
OY 2352 TCTGTGTGGCCGAGCTTCCCGAGAGCAGCACCCCTGCTCACAGCGCCAGTCCC 2411
Db 1797 TCTGTGTGGCCGAGCTTCCCGAGAGCAGCACCCCTGCTCACAGCGCCAGTCCC 1856
OY 2412 ATGACACGAGAGGCTGAGAAATGGGGGCGACCGGCACTGGGACTGGGAGGCTAC 2471
Db 1857 ATGACACGAGAGGCTGAGAAATGGGGGCGACCGGCACTGGGAGGCTAC 1916
OY 2472 CCGTGCAGCCCTGTGGGAATCAGTGGGTGAAGCCAGCTGGGCTCCTGAGTGGGTG 2531
|||||

Db 1917 CCTTCAGCCCTGCTGAGGAATCCACTGGGTGAAGCCAGTGGGCTCCTGAGTCTGTGG 1976
OY 2532 AGACTTGAGAACTTTATGTCTAGCTCAGGGATGTAATATACCAATTCAGACCCCTGT 2591
Db 1977 AGACTTGAGAACTTTATGTCTAGCTCAGGGATGTAATATACCAATTCAGACCCCTGT 2036
OY 2592 GCTTACGTCAGGGCTGTGAATGACCAATCCACTCTGTATCTAGCTCTGATGG 2651
Db 2037 GCTTACGTCAGGGCTGTGAATGACCAATCCACTCTGTATCTAGCTCTGATGG 2096
OY 2652 GCTTGGAGAACCTTTATGTCTAGCTCAGGGATTTGTAATACCAATTCGACCTCTGTA 2711
Db 2097 GCTTGGAGAACCTTTATGTCTAGCTCAGGGATTTGTAATACCAATTCGACCTCTGTA 2156
OY 2712 TCTAGCTAAGTTTGTAAACACACCAATCAGACACCCTGTGTCTAGCTCAGGGTATGTA 2771
Db 2157 TCTAGCTAAGTTTGTAAACACACCAATCAGACACCCTGTGTCTAGCTCAGGGTATGTA 2216
OY 2772 ATGCACAATGCAGCTGTATCTGGCTACTTTCATGGGCTCCGCTGAAGAGCAC 2831
Db 2217 ATGCACAATGCAGCTGTATCTGGCTACTTTCATGGGCTCCGCTGAAGAGCAC 2276
OY 2832 CAACAGGCTTTGTGTGAGCAATAAAGCTTATCAGCTGGGTGAGGTGGCTGATCC 2891
Db 2277 CAACAGGCTTTGTGTGAGCAATAAAGCTTATCAGCTGGGTGAGGTGGCTGATCC 2336
OY 2892 GAAAGAGAGTCAGGAAGGAGATAAAGGGGGCCCTTTATAGATTTGGATGTA 2951
Db 2337 GAAAGAGAGTCAGGAAGGAGATAAAGGGGGCCCTTTATAGATTTGGATGTA 2396
OY 2952 AAGGAAATTCAGTCAAGGGGCTTTGCTCTGGGGCAGAGTGGGGGTGCAAG 3011
Db 2397 AAGGAAATTCAGTCAAGGGGCTTTGCTCTGGGGCAGAGTGGGGGTGCAAG 2456
OY 3012 GTGCTAGTGGGGGTCTTTTGTAGCCAGATGAGCCAGAAAGACTTTCACAAGTA 3071
Db 2457 GTGCTAGTGGGGGTCTTTTGTAGCCAGATGAGCCAGAAAGACTTTCACAAGTA 2516
OY 3072 ATGTATCAATTAAGGCAAGACCCGCAATTTACACTCTTTTGTGTGGAATGTATCA 3131
Db 2517 ATGTATCAATTAAGGCAAGACCCGCAATTTACACTCTTTTGTGTGGAATGTATCA 2576
OY 3132 GTTAAGTTGGGCAAGGATATCACTCTTTTGTGATTTCTCACTTACTTACAGGCATC 3191
Db 2577 GTTAAGTTGGGCAAGGATATCACTCTTTTGTGATTTCTCACTTACTTACAGGCATC 2636
OY 3192 TGGGCTATATGTGCAAGTTACAGGGGATGCGATGGCTTGGGCTCAGAGGCTTGA 3251
Db 2637 TGGGCTATATGTGCAAGTTACAGGGGATGCGATGGCTTGGGCTCAGAGGCTTGA 2696
OY 3252 CAGCTACTGTGGGCTTGGAGATTTGTGTGACACTGTATCTAGTTAATCT 3311
Db 2697 CAGCTACTGTGGGCTTGGAGATTTGTGTGACACTGTATCTAGTTAATCT 2756
OY 3312 AGTGGGAGCTGGAGAACTTTGTGTGAGCTCAGAGGATTTGTAAGCAGCAATAGGGC 3371
Db 2757 AGTGGGAGCTGGAGAACTTTGTGTGAGCTCAGAGGATTTGTAAGCAGCAATAGGGC 2816
OY 3372 CCTGTCAAAAGAGCACTCGGCTTACCAATTCAGACAGATGTGGGTGGGCGAGATAG 3431
Db 2817 CCTGTCAAAAGAGCACTCGGCTTACCAATTCAGACAGATGTGGGTGGGCGAGATAG 2876
OY 3432 AGAATAAAGAGGCTGCCGAGCCAGAGTGGCAGCGCAGCAGGTCCCATTCACAAAT 3491
Db 2937 AGAATAAAGAGGCTGCCGAGCCAGAGTGGCAGCGCAGCAGGTCCCATTCACAAAT 2936
OY 3492 ATGCAAGCTTTGCTTTGTGCTTTGTGGAATTAATCTGTCACTGCTGCTTTGGGTC 3551
Db 2937 ATGCAAGCTTTGCTTTGTGCTTTGTGGAATTAATCTGTCACTGCTGCTTTGGGTC 2996
OY 3552 CACACTGCTTTATGAGCTGTAACTACACAGAAAGTGTGACACTTCACTCTGAAGC 3611
Db 2997 CACACTGCTTTATGAGCTGTAACTACACAGAAAGTGTGACACTTCACTCTGAAGC 3056
|||||

[illegible]

QY	4692	TAATAATACAAAATTATGATGACGATGGTGGTCAATGCCGTATATCCACACTTGGAG	475
Db	4136	TAATAATACAAAATTATGATGACATGGTGGTCAATGCCGTATATCCACACTTGGAG	4199
QY	4752	GGCGAGGCGAGAAAATCATACAAACGAGGAGCGGAGAGTTGTATGAGCCGATCGTG	481
Db	4196	GGCGAGGCGAGAAAATCATACAAACGAGGAGCGGAGAGTTGTATGAGCCGATCGTG	4255
QY	4812	CCATTGCACATCCAGGCTGAGCAATGAGCAAAATCTCATTCGAAAAAACACACAAAA	487
Db	4256	CCATTGCACATCCAGGCTGAGCAATGAGCAAAATCTCATTCGAAAAAACACACAAAA	4311
QY	4872	CCCACTCTCTACTCCCAAGGAGCTGGGTACAGAGCTGGGGCCACATCACTGCAAGGTGCTG	4933
Db	4316	CCCACTCTCTACTCCCAAGGAGCTGGGTACAGAGCTGGGGCCACATCACTGCAAGGTGCTG	4377
QY	4932	AAGCCACAGAGCTAAAGGCGGAGCTGCAGAGACCGCGGACACAGATAACAGTGTGAGATCAG	499
Db	4376	AAGCCACAGAGCTAAAGGCGGAGCTGCAGAGACCGCGGACACAGATAACAGTGTGAGATCAG	4433
QY	4992	TGTGTGAGATTCAGAGCTGCCCTGCCATTTGGTGTGCACACGAGGGGGCCCCAAGACACAGAG	505
Db	4436	TGTGTGAGATTCAGAGCTGCCCTGCCATTTGGTGTGCACACGAGGGGGCCCCAAGACACAGAG	4499
QY	5052	TGGCCCATTCACAGTCACACACATCACTTCTCATCCAGAGATGTCTGTTCTTGGCAAGCT	5111
Db	4496	TGGCCCATTCACAGTCACACACATCACTTCTCATCCAGAGATGTCTGTTCTTGGCAAGCT	4555
QY	5112	GGGGTAAATTAGAGACAGAAAGGTGACAGTCTTGGGTGTGCTCAGTCACTGCCCCAGGCA	5177
Db	4556	GGGGTAAATTAGAGACAGAAAGGTGACAGTCTTGGGTGTGCTCAGTCACTGCCCCAGGCA	4611
QY	5172	GGCCCTTGTGGCCTTATGAGAAAAGTTCAGGGCCATAGGCGGGGACGGTGGCTCAACGCTCTA	5233
Db	4616	GGCCCTTGTGGCCTTATGAGAAAAGTTCAGGGCCATAGGCGGGGACGGTGGCTCAACGCTCTA	4677
QY	5232	ATCCACAGACATTTGGGAGGCGGAGGCGGGGTGGATTCACGAGGTCAAGAAATCGTGACATC	5291
Db	4676	ATCCACAGACATTTGGGAGGCGGAGGCGGGGTGGATTCACGAGGTCAAGAAATCGTGACATC	4733
QY	5292	CTGGCTAACAGGGTGAACCCCGCTCTACTATAAAATACAAAAAATTGGCCGGCAGTGT	5351
Db	4736	CTGGCTAACAGGGTGAACCCCGCTCTACTATAAAATACAAAAAATTGGCCGGCAGTGT	4799
QY	5352	GGCGGGACCTGTATGTTCCAGCTACTCGGGAGGGCTGAGGACGAGGAATGGGCTGAACCG	5411
Db	4796	GGCGGGACCTGTATGTTCCAGCTACTCGGGAGGGCTGAGGACGAGGAATGGGCTGAACCG	4855
QY	5412	AGAGGACAGATTTGCACTGAGCCGAGATCGCGCCACTGTCCAGCTTGGGCGACAGAG	5471
Db	4856	AGAGGACAGATTTGCACTGAGCCGAGATCGCGCCACTGTCCAGCTTGGGCGACAGAG	4915
QY	5472	CAAGACATCATCTGGAAAAAGAAAAAGAAACGTTCAAGTCTGAGCCAGAGGCCACGCTG	5531
Db	4916	CAAGACATCATCTGGAAAAAGAAAAAGAAACGTTCAAGTCTGAGCCAGAGGCCACGCTG	4975
QY	5532	TAATTTCTGTCACTTACCATGACCTTGGGCAAGGACACTTCCCTGCGCCAGTTCAAGG	5591
Db	4976	TAATTTCTGTCACTTACCATGACCTTGGGCAAGGACACTTCCCTGCGCCAGTTCAAGG	5035
QY	5592	GGTTTGAATGACATCCAAAGTCCCTTCACAGATTTAACGCTGTCAAGTGTCTTAAGATGAGAA	5651
Db	5036	GGTTTGAATGACATCCAAAGTCCCTTCACAGATTTAACGCTGTCAAGTGTCTTAAGATGAGAA	5095
QY	5652	GATGGGGCAGTTTCCCTCTCTCAACCCAGCCGCTGTCACTTCAAGGTGAATGACAGG	5711
Db	5096	GATGGGGCAGTTTCCCTCTCTCAACCCAGCCGCTGTCACTTCAAGGTGAATGACAGG	5155
QY	5712	GAATGTACAGTGTCCCAATCCCGGAGTTCCAAAGCCCTTGGGGAGCCCTTACGTCAAGGCTG	5771
Db	5156	GAATGTACAGTGTCCCAATCCCGGAGTTCCAAAGCCCTTGGGGAGCCCTTACGTCAAGGCTG	5215
QY	5772	TGCACGAGGAGTGAAGGTCAAGTGAACCAATCGCCTGAAAGGATCTTGGCTCATTCGCG	5831

D	b	238	AATTTTCCCTAACCATTTTAAAAAGTATAAACCCGGCCAGGGGCCCATGGCTCACGCC	297
Q	y	855	TGTAATTCACACACTTTGGGAGGCTGAGGTGGGCAGATCACTTGAGATCAACAGTTGAG	914
D	b	298	TGTAATTCACAGACTTTGGGAGGCTGAGGTGGGCAGATCACTTGAGATCAACAGTTGAG	357
Q	y	915	ACCAAGCTTGGCCACATAGCAAAACCCCTTTCTACTAAAAATAAAAAATTTAGCTGGGC	974
D	b	358	ACCAAGCTTGGCCACATAGCAAAACCCCTTTCTACTAAAAATAAAAAATTTAGCTGGGC	417
Q	y	975	ATAGAGGTGACACACTGTGATCCAGCTACTTGGGAGGCTGAGAGCGAGAAATCGCTTGA	1034
D	b	418	ATAGAGGTGACACACTGTGATCCAGCTACTTGGGAGGCTGAGAGCGAGAAATCGCTTGA	477
Q	y	1035	ACCTGGAGAGGGAGGTTGCTGAGTGAAGCCATCATGCCACTGCACTCCAGCTGGGTGA	1094
D	b	478	ACCTGGAGAGGGAGGTTGCTGAGTGAAGCCATCATGCCACTGCACTCCAGCTGGGTGA	537
Q	y	1095	CAGAGTGAAGCTTGTCTTCACGAAAAAAGTATAAAGCATTTCTTAATTCAGTGT	1154
D	b	538	CAGAGTGAAGCTTGTCTTCACGAAAAAAGTATAAAGCATTTCTTAATTCAGTGT	597
Q	y	1155	ACATAGAGTACATCTGAGGTCTGGGTGCTGCTGCTGAGAGCAATCCGAGAAAGTGA	1214
D	b	598	ACATAGAGTACATCTGAGGTCTGGGTGCTGCTGCTGAGAGCAATCCGAGAAAGTGA	657
Q	y	1215	GTTGGTGGTGCAGAGACATACATATTCACATTAACATAGACACTACCAAGTTGCCATC	1274
D	b	658	GTTGGTGGTGCAGAGACATACATATTCACATTAACATAGACACTACCAAGTTGCCATC	717
Q	y	1275	CAAGGAG-TTTTTTTTTTACAATCTACACTCCCCCAGCACAAATGAGAGTTACTCCA	1333
D	b	718	CAAGGAGGTTTTTTTTTTACAATCTACACTCCCCCAGCACAAATGAGAGTTACTCCA	777
Q	y	1334	GATCCTTTACAAAGATGCTCTAAGCCCACTACAGATGAGAAACAGAAAGTGGAGGGAA	1393
D	b	778	GATCCTTTACAAAGATGCTCTAAGCCCACTACAGATGAGAAACAGAAAGTGGAGGGAA	837
Q	y	1394	GCTGCCAGCCCCCTTTAAACCATGAGAAATACCTGGTAGAGCCTTCTGATGCTGGAAG	1453
D	b	838	GCTGCCAGCCCCCTTTAAACCATGAGAAATACCTGGTAGAGCCTTCTGATGCTGGAAG	897
Q	y	1454	ATGAATACGGGGGCTCTGGAAGCCTCCCCCTGTAGATCACTGTGACTTCTGAGGCTC	1513
D	b	898	ATGAATACGGGGGCTCTGGAAGCCTCCCCCTGTAGATCACTGTGACTTCTGAGGCTC	957
Q	y	1514	CAGTCCATGTCAGCCCCCATGATGTCATGAGCCAGTGATTAATGAGCCCTCATCTCTGTTTG	1573
D	b	958	CAGTCCATGTCAGCCCCCATGATGTCATGAGCCAGTGATTAATGAGCCCTCATCTCTGTTTG	1016
Q	y	1574	GTCCTTATTCCT-CCCCATGTGGGGCTGAAGTCTGATTAAGCCGTTATTCAAAATGTACA	1632
D	b	1017	GTCCTTATTCCTCCCATGTGGGGCTGAAGTCTGATTAAGCCGTTATTCAAAATGTACA	1076
Q	y	1633	GCTTTCCTTGACAGAAAGTAGTGTACACAGAAAAACAGAGGGGCTTGGCAAGATGATTAAC	1692
D	b	1077	GCTTTCCTTGACAGAAAGTAGTGTACACAGAAAAACAGAGGGGCTTGGCAAGATGATTAAC	1136
Q	y	1693	TGCAAAATCCTACCTGTGGCTCAGCCACACAGCTAATTCTGTATCTTGAACAAATTTTTCAC	1752
D	b	1137	TGCAAAATCCTACCTGTGGCTCAGCCACACAGCTAATTCTGTATCTTGAACAAATTTTTCAC	1196
Q	y	1753	TTTCTGTGAGGCATCCCTTGGCTACAAACACAGTTGGTTGACAGATGAATGAGC-A	1811
D	b	1197	TTTCTGTGAGGCATCCCTTGGCTACAAACACAGTTGGTTGACAGATGAATGAGAA	1256
Q	y	1812	AGTCCCTTACACCTGTAAATCCACAGCACTTGGGAGGCCAAGGCGGGTGTGATGCTTGAGC	1871
D	b	1257	AGTCCCTTACACCTGTAAATCCACAGCACTTGGGAGGCCAAGGCGGGTGTGATGCTTGAGC	1316
Q	y	1872	CTGAGAGGTGACAGCATCCGGCAGTCTCACAGCCCTCTGTTGCTCTCTGGGGCCTCTCTC	1931
D	b	1317	CTGAGAGGTGACAGCATCCGGCAGTCTCACAGCCCTCTGTTGCTCTCTGGGGCCTCTCTC	1376

OY	1932	TGCTGGGGCTCCCACTTGGTGGGCACTGAGAGGCGCTTCAAGCCCAACCGGTCGACTGTGG	1991
Db	1377	TGCTTGGGCTCCCACTTGGTGGGCACTGAGAGGCGCTTCAAGCCCAACCGGTCGACTGTGG	1436
OY	1992	GAGCCCTTTTCTGGGCTGGCCAAAGCCAGAGCCGGGCTCCCTCAGCTTGCAGAGAGGTGTG	2051
Db	1437	GAGCCCTTTTCTGGGCTGGCCAAAGCCAGAGCCGGGCTCCCTCAGCTTGCAGAGAGGTGTG	1496
OY	2052	GAGGAGAGGCTCAAGCAGAGAACCGGGGCTCGCAGACGGGCTTGGGGCCAGCTGAGATT	2111
Db	1497	GAGGAGAGGCTCAAGCAGAGAACCGGGGCTCGCAGACGGGCTTGGGGCCAGCTGAGATT	1556
OY	2112	CCGGGTGGGCTTGGGCTTGGGGGGCCCGGCACTGGAGACAGCGGGCCAGCCCTGCCAAGC	2171
Db	1557	CCGGGTGGGCTTGGGCTTGGGGGGCCCGGCACTGGAGACAGCGGGCCAGCCCTGCCAAGC	1616
OY	2172	CCCGGGCAATGAGAGGCTTACACACCGGGCCAGCGGCTGGGAGGCTTACTGGGTGCC	2231
Db	1617	CCCGGGCAATGAGAGGCTTACACACCGGGCCAGCGGCTGGGAGGCTTACTGGGTGCC	1676
OY	2232	CAGCAGTGGCAGCGCCCGCGGCTGTGCTGCTGATTTCTCAGTTGGGCTTACAGGCT	2291
Db	1677	CAGCAGTGGCAGCGCCCGCGGCTGTGCTGCTGATTTCTCAGTTGGGCTTACAGGCT	1736
OY	2292	TCCCGGGGAGGAGGCTCGGGACCTGGACCGCGGCATGCGCTGAGCCTCCCTCCATGGGC	2351
Db	1737	TCCCGGGGAGGAGGCTCGGGACCTGGACCGCGGCATGCGCTGAGCCTCCCTCCATGGGC	1796
OY	2352	TCTGTGCGGCGCCAGGCTCCCGACAGACACACACCCCTGCTCACAGCGCCAGTCCC	2411
Db	1797	TCTGTGCGGCGCCAGGCTCCCGACAGACACACACCCCTGCTCACAGCGCCAGTCCC	1856
OY	2412	ATGCACCAACGAGGCTGAGAGTGGGGGCGCACGGCACCGGAGCTGGCAGGAGCTAC	2471
Db	1857	ATGCACCAACGAGGCTGAGAGTGGGGGCGCACGGCACCGGAGCTGGCAGGAGCTAC	1916
OY	2472	CCCTGCAGCCCTGGTGGGGAATCCACTGGGTGAAGCCAGCTGGGCTCTGATGTGGTG	2531
Db	1917	CCCTGCAGCCCTGGTGGGGAATCCACTGGGTGAAGCCAGCTGGGCTCTGATGTGGTG	1976
OY	2532	AGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCTTAATATACCAATCGACACCTGT	2591
Db	1977	AGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCTTAATATACCAATCGACACCTGT	2036
OY	2592	GTCAGCTCAGGGCTGTGATGACCAATCCACACTCTGTATCTACTACTGTATGGG	2651
Db	2037	GTCAGCTCAGGGCTGTGATGATGACCAATCCACACTCTGTATCTACTACTGTATGGG	2096
OY	2652	GCCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAATCGGCACTGTCTA	2711
Db	2097	GCCTTGGAGAACCTTTATGTCTAGCTCAGGGATGTAAATACCAATCGGCACTGTCTA	2156
OY	2712	TCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTGTAGCTCAGGATGTGA	2771
Db	2157	TCTAGCTCAAGGTTTGTAAACACACCAATCAGACCCCTGTGTAGCTCAGGATGTGA	2216
OY	2772	ATGCACCAATCGACAGCTGTATCTGCTACTTTTATGAGGATCCGTGTGAAGACAC	2831
Db	2217	ATGCACCAATCGACAGCTGTATCTGCTACTTTTATGAGGATCCGTGTGAAGACAC	2276
OY	2832	CAACAAGGCTTGTGTAGCAATTAAGCTTCTATCATCTGGTGCAGGTGGGCTGAGTCC	2891
Db	2277	CAACAAGGCTTGTGTAGCAATTAAGCTTCTATCACCCTGGGTGCAGGTGGGCTGAGTCC	2336
OY	2892	GAAAAGAGTCAAGCGAAGGAGATTAAGGTGGGCGCTTTTATAGATTGGGTAGTA	2951
Db	2337	GAAAAGAGTCAAGCGAAGGAGATTAAGGTGGGCGCTTTTATAGATTGGGTAGTA	2396
OY	2952	AAAGAAATTAAGCTCAAAAGGGGTTGTCTCTGGGCGCAGAGTGGGGGTCCGCAAG	3011
Db	2397	AAAGAAATTAAGCTCAAAAGGGGTTGTCTCTGGGCGCAGAGTGGGGGTCCGCAAG	2456

OY	3012	GTGCTCACTGGGGGCTTTTTTGAACCAAGATGAGCCAGAGAAAGGACTTTCACAAGTA	3071
Db	2457	GTGCTCACTGGGGGCTTTTTTGAACCAAGATGAGCCAGAGAAAGGACTTTCACAAGTA	2516
OY	3072	ATGTCATCAATTAAGCAAGGACCCGCCATTTACACCTCTTTTGGGTGAGATGCATCA	3131
Db	2517	ATGTCATCAATTAAGCAAGGACCCGCCATTTACACCTCTTTTGGGTGAGATGCATCA	2576
OY	3132	GTTAAGTTGGGGCAGGCAATTCACCTTCTTTTGTGATCTTTCAGTACTTCAAGGCATC	3191
Db	2577	GTTAAGTTGGGGCAGGCAATTCACCTTCTTTTGTGATCTTTCAGTACTTCAAGGCATC	2636
OY	3192	TGGGGCTATATGTGCAATTACAGGGGATGCGATGTGCTTGGCTTCAGAGGCTTGA	3251
Db	2637	TGGGGCTATATGTGCAATTACAGGGGATGCGATGTGCTTGGCTTCAGAGGCTTGA	2696
OY	3252	CAGCTACTCTGTGGGGCTTGGAGAAATTTGTGTGACACTGTATCTAATCAATCT	3311
Db	2697	CAGCTACTCTGTGGGGCTTGGAGAAATTTGTGTGACACTGTATCTAATCAATCT	2756
OY	3312	AGTGGGACGTGGAGAACCTTGTGTAGCTCAGGGATTTGTAAACGACCAATCAGCGC	3371
Db	2757	AGTGGGACGTGGAGAACCTTGTGTAGCTCAGGGATTTGTAAACGACCAATCAGCGC	2816
OY	3372	CCTGTCAAAACAGACACTCGGCTCTACCAATCAGCAGAGTGTGGGTGGCCAGATTAAG	3431
Db	2817	CCTGTCAAAACAGACACTCGGCTCTACCAATCAGCAGAGTGTGGGTGGCCAGATTAAG	2876
OY	3432	AGAATTAAGAGAGGCTGCCAGCAGCAGAGGAGGCAAGCGACAGGCTCCATCCACANT	3491
Db	2877	AGAATTAAGAGAGGCTGCCAGCAGCAGAGGAGGCAAGCGACAGGCTCCATCCACANT	2936
OY	3492	ATGGCAGCTTGTCTTTTGTGTGGATTAATCTTGTACTGCTCGCTTTTGGGTC	3551
Db	2937	ATGGCAGCTTGTCTTTTGTGTGGATTAATCTTGTACTGCTCGCTTTTGGGTC	2996
OY	3552	CACACTGCTTTTATGAGCTGTAAACATCACCAGCAAGGCTGTGACGCTTCACTCTGAAGC	3611
Db	2997	CACACTGCTTTTATGAGCTGTAAACATCACCAGCAAGGCTGTGACGCTTCACTCTGAAGC	3056
OY	3612	CACTAAGACAGAGCCACCGGAGAGAAATGAACACTCGCGCGGCTGCTTAAGAGC	3671
Db	3057	CACTAAGACAGAGCCACCGGAGAGAAATGAACACTCGCGCGGCTGCTTAAGAGC	3116
OY	3672	TATTAACACTCACCGGAGAGTCTCAGCTTCACTCTCAGCAGCAGAGACCAAGCCA	3731
Db	3117	TATTAACACTCACCGGAGAGTCTCAGCTTCACTCTCAGCAGCAGAGACCAAGCCA	3176
OY	3732	CCAGAAAGAAATCTCGAATCATCTGAACATCAGAAAGAACAAACTCCAGATGCACC	3791
Db	3177	CCAGAAAGAAATCTCGAATCATCTGAACATCAGAAAGAACAAACTCCAGATGCACC	3236
OY	3792	ACCTTAAGAGCTGTAAACACTCAGCAGAGGCTCGCGGCTTCTCTTGAAGTACAGTGA	3851
Db	3237	ACCTTAAGAGCTGTAAACACTCAGCAGAGGCTCGCGGCTTCTCTTGAAGTACAGTGA	3296
OY	3852	ACCAAGCACTCACAGTTTGGGACACAAGCCAGAGTTTGAATCAGCCTGGGCAACAT	3911
Db	3297	ACCAAGCACTCACAGTTTGGGACACAAGCCAGAGTTTGAATCAGCCTGGGCAACAT	3356
OY	3912	GATGAATGGCCCTCTCGCAAAAAAATTAACAAAAATTTGGGGGAGCATGTGGT	3971
Db	3357	GATGAATGGCCCTCTCTCGCAAAAAAATTAACAAAAATTTGGGGGAGCATGTGGT	3416
OY	3972	CCGTGCTGTGTGCCAGCTACCGGGGAGGCTAAAGTGGAGAGTCCCTTGAGCGCTGGA	4031
Db	3417	CCGTGCTGTGTGCCAGCTACCGGGGAGGCTAAAGTGGAGAGTCCCTTGAGCGCTGGA	3476
OY	4032	GGTGAAGCTTCAGTACGCTGTGTATGTACACAGCCCTTATAGCTGGGGAGACAGCTGA	4091
Db	3477	GGTGAAGCTTCAGTACGCTGTGTATGTACACAGCCCTTATAGCTGGGGAGACAGCTGA	3536
OY	4092	GACCTGTTCCTCCCTCCGCAAAAAATTTGACAAAAAGTGAATTAAGAGTCCCTGATATGG	4151

|||||
Db 3537 GACCTGTTCCCTCCGCCAAAAATTGACAAAAAGTATAGAGGTGCTATATNG 3596
Qy 4152 CTAGGCCAGTGGCTCATGCTGTAAATCCAGCACTTTGGAGACCGGAGCGGGTGC 4211
Db 3597 CTAGGCCAGTGGCTCATGCTGTAAATCCAGCACTTTGGAGACCGGAGCGGGTGC 3656
Qy 4212 ACCTAAGGTGAGAGTGAAGCAGCTGGCCAAACATGGAGAAAGCCATCTCTTCAA 4271
Db 3657 ACCTAAGGTGAGAGTGAAGCAGCTGGCCAAACATGGAGAAAGCCATCTCTTCAA 3716
Qy 4272 AAATACAAATTAACCCGCTGTGGGGCAGTGTGTGAGCATGCTGTAAATCCAGCTACT 4331
Db 3717 AAATACAAATTAACCCGCTGTGGGGCAGTGTGTGAGCATGCTGTAAATCCAGCTACT 3776
Qy 4332 CAGAGGCTGAGGAGAGAGATCACTTGAACCCAGAGAGCGCGGCTTGCACTGAGCGAG 4391
Db 3777 CAGAGGCTGAGGAGAGAGATCACTTGAACCCAGAGAGCGCGGCTTGCACTGAGCGAG 3836
Qy 4392 ATCGTGCATTTGCACTCCACCCACTCCAGCTGGGCAACAGAGCCAAACTCTGTAA 4451
Db 3837 ATCGTGCATTTGCACTCCACCCACTCCAGCTGGGCAACAGAGCCAAACTCTGTAA -A 3895
Qy 4452 AAAAAAAAAAAAAAGTGCCTGACATATAGAGGTGTGCAATGCAATAGTTCAGAGCAA 4511
Db 3896 AAAAAAAAAAAAAAGTGCCTGACATATAGAGGTGTGCAATGCAATAGTTCAGAGCAA 3955
Qy 4512 CATGTTAAAGAAATGAGAGTCCCTGCTCCATGCTGCTGTAAATCCACCTCAAGG 4571
Db 3956 CATGTTAAAGAAATGAGAGTCCCTGCTCCATGCTGCTGTAAATCCACCTCAAGG 4015
Qy 4572 CAGAGTCAAGTGCATGCTCATATATCCAGCACTTTGGAGGCGGAGGGGTGATC 4631
Db 4016 CAGAGTCAAGTGCATGCTCATATATCCAGCACTTTGGAGGCGGAGGGGTGATC 4075
Qy 4632 ACCTGAGGTGAGAGTTCGAGACCAAGCTGACCAACATGTAATCCACCTTAC 4691
Db 4076 ACCTGAGGTGAGAGTTCGAGACCAAGCTGACCAACATGTAATCCACCTTAC 4135
Qy 4692 TAAAAATACAAATTAATAGATGATGTTGTTGTCATGCTGTAAATCCACCTTGGAG 4751
Db 4136 TAAAAATACAAATTAATAGATGATGTTGTTGTCATGCTGTAAATCCACCTTGGAG 4195
Qy 4752 GCTGAGGAGAGAAATCACTAGAACAGAGGAGGAGTGTAGTGGCCGAGATCGTG 4811
Db 4196 GCTGAGGAGAGAAATCACTAGAACAGAGGAGGAGTGTAGTGGCCGAGATCGTG 4255
Qy 4812 CCATTCGATTCAGACCTGAGCAATGAGCGAAATCTCTCAAAAAACAAACAAAA 4871
Db 4256 CCATTCGATTCAGACCTGAGCAATGAGCGAAATCTCTCAAAAAACAAACAAAA 4315
Qy 4872 CCCACCTCTACACCCGAGGAGCTGGGTACAGAGCTGGGCCACATCACTGAGTGTG 4931
Db 4316 CCCACCTCTACACCCGAGGAGCTGGGTACAGAGCTGGGCCACATCACTGAGTGTG 4375
Qy 4932 AGCCACAGAGCTAAGGCGAGAGCTCAGAGACCGGAGACAGATAACAGTGTGATCAG 4991
Db 4376 AGCCACAGAGCTAAGGCGAGAGCTCAGAGACCGGAGACAGATAACAGTGTGATCAG 4435
Qy 4992 TGTGTGAGATCAGACGTCCTGCTGCAATGTGTGACCAAGGAGGCGCCCAAGCAGAGA 5051
Db 4436 TGTGTGAGATCAGACGTCCTGCTGCAATGTGTGACCAAGGAGGCGCCCAAGCAGAGA 4455
Qy 5052 TGGCCCATCCAGTACACACATCCACTTCTCATCCAGAGATGTCTGTTTCTTGGCAGCT 5111
Db 4496 TGGCCCATCCAGTACACACATCCACTTCTCATCCAGAGATGTCTGTTTCTTGGCAGCT 4555
Qy 5112 GGGGTAAATTAGGACAGAAGGTGACGTTGGGTGTGTGTCAGTCAACTGTCCCAAGCA 5171
Db 4556 GGGGTAAATTAGGACAGAAGGTGACGTTGGGTGTGTGTCAGTCAACTGTCCCAAGCA 4615
Qy 5172 GGCTTGTGGCTGTAGAAAAAGTTACAGGCTAGGCGGGGACGCTGACGCTGTA 5231
|||||

Db 4616 GGCTTGTGGCTGTAGAAAAAGTTACAGGCTAGGCGGGACAGGTGCTGACGCTGTA 4675
Qy 5232 ATCCAGACACTTTGGGAGGCGGAGCGGGTGGATACAGAGTCAAGAGATGTCATC 5291
Db 4676 ATCCAGACACTTTGGGAGGCGGAGCGGGTGGATACAGAGTCAAGAGATGTCATC 4735
Qy 5292 CTGGCTAACAGGTGAAAAACCCGCTCTACTTAAATACAAAAATTTGGCGGGATGCT 5351
Db 4736 CTGGCTAACAGGTGAAAAACCCGCTCTACTTAAATACAAAAATTTGGCGGGATGCT 4795
Qy 5352 GCGGCGCACTGTACTTCACTACTCGGAGAGCTGAGGACAGAGAAATGGCTGAAACCG 5411
Db 4796 GCGGCGCACTGTACTTCACTACTCGGAGAGCTGAGGACAGAGAAATGGCTGAAACCG 4855
Qy 5412 AGAGGCAAGTTTGCAGTGAAGCCGAGATCGGCGCACTGCACTCCAGCTGGCGCAGAG 5471
Db 4856 AGAGGCAAGTTTGCAGTGAAGCCGAGATCGGCGCACTGCACTCCAGCTGGCGCAGAG 4915
Qy 5472 CAAGACTCCATCTGAAAAAGAAAAAGAAACCTTCAGGCTGAGCCAGAGGCGCAGGCTG 5531
Db 4916 CAAGACTCCATCTGAAAAAGAAAAAGAAACCTTCAGGCTGAGCCAGAGGCGCAGGCTG 4975
Qy 5532 TAATTCGTCACTTACATGACCTTGGCAAGGCACTTCCTGCTGGCCAGTTACAGG 5591
Db 4976 TAATTCGTCACTTACATGACCTTGGCAAGGCACTTCCTGCTGGCCAGTTACAGG 5035
Qy 5592 GGTGGATTCGACTCCAGTCCCTTCCAGCATTAACCTGATGCTTAAAGATGAGAA 5651
Db 5036 GGTGGATTCGACTCCAGTCCCTTCCAGCATTAACCTGATGCTTAAAGATGAGAA 5095
Qy 5652 GATGGGAGAGTTTCCCTCTCTCACCCAGCCGCTGCTCAAGTGAATGACACAGG 5711
Db 5096 GATGGGAGAGTTTCCCTCTCTCACCCAGCCGCTGCTCAAGTGAATGACACAGG 5155
Qy 5712 GAAGTCAAGTTCCTCAATCCGCACTTCCAAAGCCCTTGGGAGCCCTACTGTCAAGGTCG 5771
Db 5156 GAAGTCAAGTTCCTCAATCCGCACTTCCAAAGCCCTTGGGAGCCCTACTGTCAAGGTCG 5215
Qy 5772 TGACAGAGAGGTGAAGTCAAGTGAAGTCAAGTCCGCTGGAAGGTCCTGCTCATTCGGG 5831
Db 5216 TGACAGAGAGGTGAAGTCAAGTGAAGTCAAGTCCGCTGGAAGGTCCTGCTCATTCGGG 5275
Qy 5832 ACAGCATCCGTTTCTCTGCTTACCGGATCTAGGGCTTTAGCCGAATGATCA 5891
Db 5276 ACAGCATCCGTTTCTCTGCTTACCGGATCTAGGGCTTTAGCCGAATGATCA 5335
Qy 5892 TGGGGGCGGGGGGTTCTGGGGAGTTCACGCTAATCAACTTGGGACAGAGACCT 5951
Db 5336 TGGGGGCGGGGGGTTCTGGGGAGTTCACGCTAATCAACTTGGGACAGAGACCT 5395
Qy 5952 GGAATCTTCGATGGTGCCTATCCAGTGTGGGGTGGGACAGACCAAGCAATGTC 6011
Db 5396 GGAATCTTCGATGGTGCCTATCCAGTGTGGGGTGGGACAGACCAAGCAATGTC 5455
Qy 6012 CTTATCTCAGGTAAGGGGCTCAGAGAGTTCACAGACAGGACCTCCGAGAGTTTGGGG 6071
Db 5456 CTTATCTCAGGTAAGGGGCTCAGAGAGTTCACAGACAGGACCTCCGAGAGTTTGGGG 5515
Qy 6072 GTAGGAATGGGAGCAACAGAGCTTTTCTTCTCTTGAATTTGGGGGCTTGGGGGA 6131
Db 5516 GTAGGAATGGGAGCAACGA -GCTTCTTTTCTCTCTTGAATTTGGGGGCTTGGGGGA 5574
Qy 6132 CAGGCTTGAATTCACAAAGAGAGGAGGCAAAAGCACT -CCGCCACAAGTCTGCCAGAG 6190
Db 5575 CAGGCTTGAATTCACAAAGAGAGGAGGCAAAAGCACTGCCGCCCAAGTCTGCCAGAG 5634
Qy 6191 CGAAGAGGAGACCCGACATCAGTGCCTTCCCAAGAGC 6233
Db 5635 C-AGAGAGGAGACCCGACATCAGTGCCTTCCCAAGAGC 5676
|||||

RESULT 7
US-09-845-020a-6


```

Sequence 6 Application US/09845020A
GENERAL INFORMATION:
APPLICANT: Tteco, Douglas A.
APPLICANT: Heartlein, Michel W.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: Genomic Sequences for Protein Production
TITLE OF INVENTION: and Delivery
FILE REFERENCE: 50010/017003
CURRENT APPLICATION NUMBER: US/09/845,020A
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 09/305,384
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: US 60/084,649
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 2834
TYPE: DNA
ORGANISM: Homo sapiens
US-09-845-020A-6

```

Query Match	45.5%;	Score 2834;	DB 35;	Length 2834;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2834;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1890	CCGGCAATCCCTACAGCCCTGTCCTGCTCTGGGGCCCTCTCTGCTCTGGCTCCACTTC	1943
Db	1	CCGGCAATCCCTACAGCCCTGTCCTGCTCTGGGGCCCTCTCTGCTCTGGCTCCACTTC	60
QY	1950	GGTGGCAATTGAGGAGCCCTTCACGCCACCGCTCAGTGTGGAGAGCCCTTCTTGGGCTG	2005
Db	61	GGTGGCAATTGAGGAGCCCTTCACGCCACCGCTCAGTGTGGAGAGCCCTTCTTGGGCTG	120
QY	2010	GCCAAAGCCAGAGCCCGGCTCCCTCAGCTTGCAGGAGGTGTGAGAGGAGGCTTCAGCA	2065
Db	121	GCCAAAGCCAGAGCCCGGCTCCCTCAGCTTGCAGGAGGTGTGAGAGGAGGAGGCTTCAGCA	180
QY	2070	GGAACCGGGGTGGGACAGGGCGTTGGCGGGGAGGTGGAGTTCCGGGTGGGGCTTGGGCT	2125
Db	181	GGAACCGGGGTGGGACAGGGCGCTTGGCGGGGAGGTGGAGTTCCGGGTGGGGCTTGGGCT	240
QY	2130	GGCGGGCCCGCCAGCTCGGAGCAGCGGGCCAGCCCTGCCAGGCCCGCGGCAATGAGAGCT	2185
Db	241	GGCGGGCCCGCCAGCTCGGAGCAGCGGGCCAGCCCTGCCAGGCCCGCGGCAATGAGAGCT	300
QY	2190	TAGAACCCGGGGCCAGGGGTGGGAGGGTGTACTGGGTGGCCCGAGAGTGGCAGCCGCC	2249
Db	301	TAGAACCCGGGGCCAGGGGTGGGAGGGTGTACTGGGTGGCCCGAGAGTGGCAGCCGCC	360
QY	2250	GGCGCTGTGCTGCGCTCGATTTCTACTGGGGCTTAGCAGCCCTCCCGGGGGAGGGCTC	2309
Db	361	GGCGCTGTGCTGCGCTCGATTTCTACTGGGGCTTAGCAGCCCTCCCGGGGGAGGGCTC	420
QY	2310	GGGACCTGAGAGCCCGGCAATGCTCAGTCCCTCCATAGGGCTCTGTGGCGCCGAGGC	2365
Db	421	GGGACCTGAGAGCCCGGCAATGCTCAGTCCCTCCATAGGGCTCTGTGGCGCCGAGGC	480
QY	2370	TCCCGCAGAGCAGCACACCCCTGCTCCACAGCGGCCAGTCCCATTCGACAGCAGCAAGGCT	2425
Db	481	TCCCGCAGAGCAGCACACCCCTGCTCCACAGCGGCCAGTCCCATTCGACAGCAGCAAGGCT	540
QY	2430	GAGAAGTGGGGGCCAGAGGCACCGGGACTGGGCAAGGCACTACCCCTGCAGCCCTGTGGCG	2488
Db	541	GAGAAGTGGGGGCCAGAGGCACCGGGACTGGGCAAGGCACTACCCCTGCAGCCCTGTGGCG	600
QY	2490	GAATCCACTGGGTGAAGCCAGCTGGGCTCCGATCTGTGTGGAGACTTGGAGAACCTTTA	2549
Db	601	GAATCCACTGGGTGAAGCCAGCTGGGCTCCGATCTGTGTGGAGACTTGGAGAACCTTTA	660
QY	2550	TGCTTACCTCAGGGATGTAAATACACCAATCAGACACCTGTGCTTACCTCAGGGCTCTGT	2609
Db	661	TGCTTACCTCAGGGATGTAAATACACCAATCAGACACCTGTGCTTACCTCAGGGCTCTGT	720

QY	2610	GAATGACCAATCCACACTCTGTATCTAGCTACTCTGATGGGGCCCTTGGAAACCTTTAT	2665
Db	721	GAATGACCAATCCACACTCTGTATCTAGCTACTCTGATGGGGCCCTTGGAAACCTTTAT	780
QY	2670	GTTTAGCTCAGAGGATTGTAAATTAACCAACATGGGCACTGTGATCTCAAGGTTTTGTA	2729
Db	781	GTTTAGCTCAGAGGATTGTAAATTAACCAACATGGGCACTGTGATCTCAAGGTTTTGTA	840
QY	2730	AACACCAATCAGACACCTGTGTTCTAGCTCAGGGATATGTAATGCACCAATGCAGACTC	2789
Db	841	AACACCAATCAGACACCTGTGTTCTAGCTCAGGGATATGTAATGCACCAATGCAGACTC	900
QY	2790	TGTAATCTGGCACTTTTCAATGGGCATCCGTGGAAGAGACCAACAGCGTTTGTGTGA	2849
Db	901	TGTAATCTGGCACTTTTCAATGGGCATCCGTGGAAGAGACCAACAGCGTTTGTGTGA	960
QY	2850	GCAATAAAGCTTTCATCACTCGGGGTGCAGGTGGGCTGAGTCCGAAAAGAGATCAGCGAA	2909
Db	961	GCAATAAAGCTTTCATCACTCGGGGTGCAGGTGGGCTGAGTCCGAAAAGAGATCAGCGAA	1020
QY	2910	GGAGATTAAGGTGGGGCCGTTTATAGGATTTGGGTAGTTAAAGAAAATTACAGTCAA	2965
Db	1021	GGAGATTAAGGTGGGGCCGTTTATAGGATTTGGGTAGTTAAAGAAAATTACAGTCAA	1080
QY	2970	AGGGGCTTGTTCCTGCGGGGCGAGGATGGGGGGTCCAGAGGTCAAGTGGGGGTCT	3029
Db	1081	AGGGGCTTGTTCCTGCGGGGCGAGGATGGGGGGTCCAGAGGTCTCAAGTGGGGGTCT	1140
QY	3030	TTTTGAGCCAGATGAGCCAGAAAAGGACTTTCAACAAGTAAATGTCACTAATTAAAGCA	3089
Db	1141	TTTTGAGCCAGATGAGCCAGAAAAGGACTTTCAACAAGTAAATGTCACTAATTAAAGCA	1200
QY	3090	AGGACCCGCCATTACACCTCTTTTGTGTGGAAATGTATCAGTTAAATTTGGGCAAGGC	3149
Db	1201	AGGACCCGCCATTACACCTCTTTTGTGTGGAAATGTATCAGTTAAATTTGGGCAAGGC	1260
QY	3150	ATATTCACCTTTTGTGTGATTCTTCAGTTACTTACAGGCATCTGGGCTATATGTCAAG	3209
Db	1261	ATATTCACCTTTTGTGTGATTCTTCAGTTACTTACAGGCATCTGGGCTATATGTCAAG	1320
QY	3210	TTTACAGGGGATGCGATGGCTTGGGTGGGCTCAAGGCTTGACAGCTACCTGCTGGGGC	3265
Db	1321	TTTACAGGGGATGCGATGGCTTGGGTGGGCTCAAGGCTTGACAGCTACCTGCTGGGGC	1380
QY	3270	CTTGAGAGAAATTTGTGTGCGACACTCTGTATCTAGTTAAATCTAGGGGAGCTGGAGAC	3329
Db	1381	CTTGAGAGAAATTTGTGTGCGACACTCTGTATCTAGTTAAATCTAGGGGAGCTGGAGAC	1440
QY	3330	CTTTGTGTAGCTCAGGGATTGTAAACGACCAATCAGCGCCCTGTCAAAAACAGACAC	3389
Db	1441	CTTTGTGTAGCTCAGGGATTGTAAACGACCAATCAGCGCCCTGTCAAAAACAGACAC	1500
QY	3390	TCGGCTCTACCAATCAGAGAGATTTGGTGGGGCAGATTAAGAAATTTAAAGCAGCGTCG	3449
Db	1501	TCGGCTCTACCAATCAGAGAGATTTGGTGGGGCAGATTAAGAAATTTAAAGCAGCGTCG	1560
QY	3450	CCGAGCCAGCATGTGGCAACGCGCACAGGTCCCTTATCCACATATAGGACGCTTTTCTTT	3509
Db	1561	CCGAGCCAGCATGTGGCAACGCGCACAGGTCCCTTATCCACATATAGGACGCTTTTCTTT	1620
QY	3510	TGCTGTTTGGCATTTAAATCTTCTACTGCTGCTTTTGGGTCCACACTGCTTTTATAGC	3569
Db	1621	TGCTGTTTGGCATTTAAATCTTCTACTGCTGCTTTTGGGTCCACACTGCTTTTATAGC	1680
QY	3570	TGTAAACACTCACCAGAAAGTCTCAGATTACTCTGAAAGCCACTAAAGACACAGACCC	3629
Db	1681	TGTAAACACTCACCAGAAAGTCTCAGATTACTCTCTGAAAGCCACTAAAGACACAGACCC	1740
QY	3630	ACCGGAGGAATGAAACACTTCGCGCGCGCTGCTTAAAGCTAATTAACACTCAGCGGAA	3689
Db	1741	ACCGGAGGAATGAAACACTTCGCGCGCGCTGCTTAAAGCTAATTAACACTCAGCGGAA	1800

3690 GGTCTGACGCTTCACTCTCAGCCAGAGACCAAGACCCAGAGAGAAACTGC 3749
1801 GGTCTGACGCTTCACTCTCAGCCAGAGACCAAGACCCAGAGAGAAACTGC 1860
3750 GAACACATCTGACATCAGAAAGAAACAACTCCAGATCCACACCTTAAAGCTGTACA 3809
1861 GAACACATCTGACATCAGAAAGAAACAACTCCAGATCCACACCTTAAAGCTGTACA 1920
3810 CTCACCTGGAGAGTCCGCGCTCTCTTGAAGTCATGAGACCAACACTCAGCAATT 3869
1921 CTCACCTGGAGAGTCCGCGCTCTCTTGAAGTCATGAGACCAACACTCAGCAATT 1980
3870 TCGGACACACAGCCAGAGATTGAGATCAGCTGGGCAACATGATGAATGCCCTCTGTG 3929
1981 TCGGACACACAGCCAGAGATTGAGATCAGCTGGGCAACATGATGAATGCCCTCTGTG 2040
3930 CAAAAAATTTACAAAAATTTGCGGAGCATGTGTCCTGCTGTGTCAG 3989
2041 CAAAAAATTTACAAAAATTTGCGGAGCATGTGTCCTGCTGTGTCAG 2100
3990 CTACGCGGAGGCTTAAAGTGGAGATGCTTGAAGCTGGAGGAGTGAAGACTGAGTGA 4049
2101 CTACGCGGAGGCTTAAAGTGGAGATGCTTGAAGCTGGAGGAGTGAAGACTGAGTGA 2160
4050 CTGTGATTGTACACAGCCCTCTAGGCTGGGGGACAGACTGAGACCTGTTCCCTCG 4109
2161 CTGTGATTGTACACAGCCCTCTAGGCTGGGGGACAGACTGAGACCTGTTCCCTCG 2220
4110 CAAAAAATTTACAAAAATTTGATTAAGAGTGTGCTGATGCTAGGCGCAGTGTGCTAT 4169
2221 CAAAAAATTTACAAAAATTTGATTAAGAGTGTGCTGATGCTAGGCGCAGTGTGCTAT 2280
4170 GCGTGTATCCAGACTTTGGGAAAGCGGCGGCGGCTACCTAAGTCAGAGAGT 4229
2281 GCGTGTATCCAGACTTTGGGAAAGCGGCGGCGGCTACCTAAGTCAGAGAGT 2340
4230 GAGACACAGCTTGCCCAACATGGAGAAAGCCATCTCTTAAAAATTAAGATTTAGCCGG 4289
2341 GAGACACAGCTTGCCCAACATGGAGAAAGCCATCTCTTAAAAATTAAGATTTAGCCGG 2400
4290 CTGTGGGGGAGTGTGAGCATGCTTAAATCCAGTACTCAGAGGCTGAGGACAGA 4349
2401 CTGTGGGGGAGTGTGAGCATGCTTAAATCCAGTACTCAGAGGCTGAGGACAGA 2460
4350 GAATCAGCTTGAACCCAGAGGCGGCGGCTTGAAGTGAAGGCGGAGATGCTGACATCC 4409
2461 GAATCAGCTTGAACCCAGAGGCGGCGGCTTGAAGTGAAGGCGGAGATGCTGACATCC 2520
4410 ACCCACTCCAGCTTGCCCAACATGGAGAAAGCCATCTCTTAAAAATTAAGATTTAG 4469
2521 ACCCACTCCAGCTTGCCCAACATGGAGAAAGCCATCTCTTAAAAATTAAGATTTAG 2580
4470 CCTGACATTAAGAGTGTGCAATGATGCTGAGGCAACATGTTTAAAGATGTGA 4529
2581 CCTGACATTAAGAGTGTGCAATGATGCTGAGGCAACATGTTTAAAGATGTGA 2640
4530 GCTCTGCTTCATGCTGCTTAAAAAACCCATCCAAAGCCAGGCGGCTGCTAT 4589
2641 GCTCTGCTTCATGCTGCTTAAAAAACCCATCCAAAGCCAGGCGGCTGCTAT 2700
4590 GCTTATATCCAGCACTTTGGAGGCGGAGGCTGGATCACCCTGAGAGTTC 4649
2701 GCTTATATCCAGCACTTTGGAGGCGGAGGCTGGATCACCCTGAGAGTTC 2760
4650 GAGACACAGCTTGACCAACATGTTGAATCCACCTCTACTAAAAATTAAGATTTAGA 4709
2761 GAGACACAGCTTGACCAACATGTTGAATCCACCTCTACTAAAAATTAAGATTTAGA 2820
4710 TGAGCATGTGTGTG 4723
2821 TGAGCATGTGTGTG 2834

RESULT 8
US-09-760-457-490
; Sequence 490, Application US/09760457
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1215
; CURRENT APPLICATION NUMBER: US/09/760,457
; PRIORITY APPLICATION: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 601
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 490
; LENGTH: 2409
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (189)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1465)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1478)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1548)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1602)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1603)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1818)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1819)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1824)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1828)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1836)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1841)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1875)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2145)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2298)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-457-490

Query Match	35.7%	Score 2225.8	DB 33	Length 2409
Best Local Similarity	98.7%	Pred. No. 1.6e-257		
Matches 2367	Conservative 0	Mismatches 14	Indels 17	Gaps 12
QY	3371	CCCTGTCAAAACAGACACCTGGCTCTACCAATCAGCAGATG-TGGGTGGGGCCAGATA	3429	
DB	13	CCNMTCAAAACAGACACCTGGCTCTACCAATCAGCAGATGNTGGGTGGGGCCAGATA	72	
QY	3430	AGAGATTAAGAGCGGCTCCCGAGCCAGCAGTGGCAACGGCACAGTCCCTATCCACA	3489	
DB	73	AGAGATTAAGAGCGGCTCCCGAGCCAGCAGTGGCAACGGCACAGTCCCTATCCACA	132	
QY	3490	ATATGGCAGCTTTGTCTTTGTCTGTGTGCGATAAATCTGTACTGCTGCTTTT-TGG	3548	
DB	133	ATATGGCAGCTTTGTCTTTGTCTGTGTGCGATAAATCTGTACTGCTGCTTTTNTGG	192	
QY	3549	GTCACACTGCTTTTATGAGCTGTAAACATCAGCAGAAAGGTGTGACCTTCACTCTGA	3608	
DB	193	GTCACACTGCTTTTATGAGCTGTAAACATCAGCAGAAAGGTGTGACCTTCACTCTGA	252	
QY	3609	AGCCACTAAGACGAGCCGAGCCGAGGAGATGAACACTCCGGCCGCTGCTTAAG	3668	
DB	253	AGCCACTAAGACGAGCCGAGCCGAGGAGATGAACACTCCGGCCGCTGCTTAAG	312	
QY	3669	AGCTATAACTCAACCGGAGAGTCTGACAGCTTCACTCAGCCAGGAGACACGAAAC	3728	
DB	313	AGCTATAACTCAACCGGAGAGTCTGACAGCTTCACTCAGCCAGGAGACACGAAAC	372	
QY	3729	CCACCAAGAGAGAACTCGGAACACATCTGAACATCAGAAAGAACAACTCCAGATGC	3788	
DB	373	CCACCAAGAGAGAACTCGGAACACATCTGAACATCAGAAAGAACAACTCCAGATGC	432	
QY	3789	ACCACCTTAAGAGCTGTAACTCACTGCCGAGGCTCCGGGCTTCTTGAAGTCACT	3848	
DB	433	ACCACCTTAAGAGCTGTAACTCACTGCCGAGGCTCCGGGCTTCTTGAAGTCACT	492	
QY	3849	GAGACCAAGCAGCTCAGAGTTCGGACACAGCCAGAGTTTGAATCAGCTGGGCAA	3908	
DB	493	GAGACCAAGCAGCTCAGAGTTCGGACACAGCCAGAGTTTGAATCAGCTGGGCAA	552	
QY	3909	CATATGAAATGCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCGGACATGCT	3968	
DB	553	CATATGAAATGCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCGGACATGCT	612	
QY	3969	GGTCGCTGCTGTGGTCCGAGCTACGCGGAGGCTTAAAGTGGAGATCGTTAGCCTG	4028	
DB	613	GGTCGCTGCTGTGGTCCGAGCTACGCGGAGGCTTAAAGTGGAGATCGTTAGCCTG	672	
QY	4029	GGAGTGAAGACTCAGTGAAGCTGTGATTGACCAAGCCCTTAAGCTGGGGAGACAGAC	4088	
DB	673	GGAGTGAAGACTCAGTGAAGCTGTGATTGACCAAGCCCTTAAGCTGGGGAGACAGAC	732	
QY	4089	TGAGACCCCTGTTCCCTCCGCAAAAAATTTGACAAAAATGTAATAAGAGTGCCTGATA	4148	
DB	733	TGAGACCCCTGTTCCCTCCGCAAAAAATTTGACAAAAATGTAATAAGAGTGCCTGATA	792	
QY	4149	TGGCTAGAGCCAGTGGCTCATGCTGTAAATCCAGCACTTTGGAGCCAGGCGGCGG	4208	
DB	793	TGGCTAGAGCCAGTGGCTCATGCTGTAAATCCAGCACTTTGGAGAACCCAGGCGGCGG	852	
QY	4209	GTCACCTAAGAGTGAAGTGTGAGACCAAGCCTGGCCAAATGAGAAAGGCCATCTCTTC	4268	
DB	853	GTCACCTAAGAGTGAAGTGTGAGACCAAGCCTGGCCAAATGAGAAAGGCCATCTCTTC	912	
QY	4269	TAAAAATACAAAAATTAGCCGCTGTGGGGCAGTGTGAGCATGCTGTAAATCCAGCT	4328	
DB	913	TAAAAATACAAAAATTAGCCGCTGTGGGGCAGTGTGAGCATGCTGTAAATCCAGCT	972	
QY	4329	ACTCAGAGAGCTGAGGAGAGATCACTTGAACCCAGAGGCGGCGGTTGCACTGAGCC	4388	
DB	973	ACTCAGAGAGCTGAGGAGAGATCACTTGAACCCAGAGGCGGCGGTTGCACTGAGCC	1032	
QY	4389	GAGATGTCATTTGCACCTCACCACCTCAGCTGGGCAACAAGGCCAAACTCTCTCT	4448	

DB	1033	GAGATCGGCACTTGCACCTCCACCTCCAGCCTGGGCAACAAGAGCCAACTCTGCTCT	1092	
QY	4449	TAAAAAAGAGAGAGTCCCTGACATATTAAGAGGTGCAATGCAATGATGGCCAGG	4508	
DB	1093	T-TAAAAAAGAGAGAGTCCCTGACATATTAAGAGGTGCAATGCAATGATGGCCAGG	1151	
QY	4509	CAACATGTTTAAAGATGTGAGCTCTGCTTCCATGCTGCTTTAAAAACCACTCA	4568	
DB	1152	CAACATGTTTAAAGATGTGAGCTCTGCTTCCATGCTGCTTTAAAAACCACTCA	1211	
QY	4569	AGGCAAGGTGAGGAGGCTCATGCTATTAATCCAGCACTTTGGAGAGCCGAGGGGGTGG	4628	
DB	1212	AGGCAAGGTGAGGAGGCTCATGCTATTAATCCAGCACTTTGGAGAGCCGAGGGGGTGG	1271	
QY	4629	ATCACTGAGGTGAGGAGGCTGAGACACAGCCTGACCAACAATGTTAAATCCACCTC	4688	
DB	1272	ATCACTGAGGTGAGGAGGCTGAGACACAGCCTGACCAACAATGTTAAATCCACCTC	1331	
QY	4689	TACTTAAATATCAAAATTTAGATGAGCATGTGTGTCATGCTGTAAATCCACCTTGG	4748	
DB	1332	TACTTAAATATCAAAATTTAGATGAGCATGTGTGTCATGCTGTAAATCCACCTTGG	1391	
QY	4749	GAGGCTGAGGAGGAGAAATCACTAGAACCAAGGAGCGGAGAGTTGTAGTGGCGAATC	4808	
DB	1392	GAGGCTGAGGAGGAGGAGAAATCACTAGAACCAAGGAGCGGAGAGTTGTAGTGGCGAATC	1451	
QY	4809	GTGCCATTGCACT-CCAGCCTGAGCA-ATGAGCCAAATCTCATCTCAAAAAACAAAC	4866	
DB	1452	GTGCCATTGCACTTCCAGCCTGAGCAGCAATGAGGAGAAATCTCATCTCAAAAAACAAAC	1511	
QY	4867	AAAAACCACTCTTACTCCAGGAGAGTGGGTCA-GAGCTGGGCAATCACTGCAAG	4925	
DB	1512	AAAAACCACTCTTACTCCAGGAGAGTGGGTCAAGAGCTGGGCAATCACTGCAAG	1571	
QY	4926	GTGCTGAGCCAGAGCTAAGGAGGAGCTG--CAGGACCGGGGACAGATTAACGTGTGT	4983	
DB	1572	GTGCTGAGCCAGAGCTAAGGAGGAGCTG--CAGGACCGGGGACAGATTAACGTGTGT	1631	
QY	4984	GAGATCAGTGTGTGAGATCAGACCTCCCTGCTTGGTGAACACAGGGGGCCGCCAAGC	5043	
DB	1632	GAGATCAGTGTGTGAGATCAGACCTCCCTGCTTGGTGAACACAGGGGGCCGCCAAGC	1691	
QY	5044	ACCAAGATGCCCCATCCAGTCAACCAATCCACTTCTCATCCAGAGATGTCTGTTCTT	5103	
DB	1692	ACCAAGATGCCCCATCCAGTCAACCAATCCACTTCTCATCCAGAGATGTCTGTTCTT	1751	
QY	5104	GGCACGCTGGGTTAAATTAGACGAAGGTGACAGTCTTGGGTGTGTCACTGACACTGC	5163	
DB	1752	GGCACGCTGGGTTAAATTAGACGAAGGTGACAGTCTTGGGTGTGTCACTGACACTGC	1811	
QY	5164	CCGAGGCA---GGCTTGTGGCCTGT--AGAAAACTTCAAGGCTTGGGCGGCGGACGGT	5217	
DB	1812	CCGAGGCA---GGCTTGTGGCCTGT--AGAAAACTTCAAGGCTTGGGCGGCGGACGGT	1871	
QY	5218	GGC-TCAAGCCTGTAAATCCAGCACTTTGGAGAGCCGAGCGGGGTGATCAGAGGTCAAG	5276	
DB	1872	GGC-TCAAGCCTGTAAATCCAGCACTTTGGAGAGCCGAGCGGGGTGATCAGAGGTCAAG	1931	
QY	5277	GAGATGTGACATCTGCTGCTTAACAGCGGTAAACCCCGTCTGTACTTAAAAATACAAAAA	5336	
DB	1932	GAGATGTGACATCTGCTGCTTAACAGCGGTAAACCCCGTCTGTACTTAAAAATACAAAAA	1991	
QY	5337	TTGGCGGAGATGTTGGCGGAGCCTGTAGTTGACGCTACTGGGAGGCTGAGGCGAGGAG	5396	
DB	1992	TTGGCGGAGATGTTGGCGGAGCCTGTAGTTGACGCTACTGGGAGGCTGAGGCGAGGAG	2051	
QY	5397	AATGCGGTGAACCCGAGAGGACAGATTGTCAGTGAACCCGAGATCGGCCACTGCTCCA	5456	
DB	2052	AATGCGGTGAACCCGAGAGGACAGATTGTCAGTGAACCCGAGATCGGCCACTGCTCCA	2111	
QY	5457	GCCTGGGCGACAGCAAGACTCATCTGGAAA-AGAAAAAAGAAAGTTCAAGTCTGAG	5515	

Db 733 TGGAGCCCTGTTCCCTCGCGCAAAAATTTGACAAAAGTGTATTAAGAGCTCCGTGATA 792
QY 4149 TGGCTAGGGCGACATGGCTCATGCTGTAAATCCAGCAGCTTTGGGAAGCCGAGCGGGCG 4208
Db 793 TGGCTAGGGCGACATGGCTCATGCTGTAAATCCAGCAGCTTTGGGAAGCCGAGCGGGCG 852
QY 4209 GTCACTTAAGGTAGAGAGTGTGAGACAGCTTGGCCAAACATGGAAGAAAGCCCATCTCTTC 4268
Db 853 GTCACTTAAGGTAGAGAGTGTGAGACAGCTTGGCCAAACATGGAAGAAAGCCCATCTCTTC 912
QY 4269 TAAATAATACAAATTAAGCCGCTGTGGGGCAGTGGTGAAGCATGCTGTAAATCCAGCT 4328
Db 913 TAAATAATACAAATTAAGCCGCTGTGGGGCAGTGGTGAAGCATGCTGTAAATCCAGCT 972
QY 4329 ACTCAGAGGCTGAGGACAGAGAAATCATTTGAACCCAGAGAGCGGGCTTGACAGTGAAGC 4388
Db 973 ACTCAGAGGCTGAGGACAGAGAAATCATTTGAACCCAGAGAGCGGGCTTGACAGTGAAGC 1032
QY 4389 GAGATGTGTCATGTGACATCCAGCATCCAGCTGGGCAACAAGAGCCAACTGTCTCT 4448
Db 1033 GAGATGTGTCATGTGACATCCAGCATCCAGCTGGGCAACAAGAGCCAACTGTCTCT 1092
QY 4449 TAAAAAAG 4508
Db 1093 T-AAAAAAG 1151
QY 4509 CAACATGTTTAAAGATGTGAGAGCTCTGCTCCATGAGTCTGTAAATCCAGCTCTCA 4568
Db 1152 CAACATGTTTAAAGATGTGAGAGCTCTGCTCCATGAGTCTGTAAATCCAGCTCTCA 1211
QY 4569 AGGCGAGGTGCAATGGCTCATGCTTAATCCAGCAGCTTTGGGAGCGGAGCGGGTGG 4628
Db 1212 AGGCGAGGTGCAATGGCTCATGCTTAATCCAGCAGCTTTGGGAGCGGAGCGGGTGG 1271
QY 4629 ATCACTGAGGTGAGAGAGTTCGAGACAGAGCTGACACCAACATGTTGAATCCAGCTC 4688
Db 1272 ATCACTGAGGTGAGAGAGTTCGAGACAGAGCTGACACCAACATGTTGAATCCAGCTC 1331
QY 4689 TACTAAATATCAAAATTAAGATGAGATGAGTGTGATGCTGTAAATCCAGCTACTTGG 4748
Db 1332 TACTAAATATCAAAATTAAGATGAGATGAGTGTGATGCTGTAAATCCAGCTACTTGG 1391
QY 4749 GAGGCTGAGGACAGAAATCATAGAAACAGGAGCGGAGGTTGTAAAGTGAAGCGGAGATC 4808
Db 1392 GAGGCTGAGGACAGAAATCATAGAAACAGGAGCGGAGGTTGTAAAGTGAAGCGGAGATC 1451
QY 4809 GTGCGATTGCACT-CCAGCTTGAGCA-ATGAGCGAAATCTCATCTAAAAAACAACAC 4866
Db 1452 GTGCGATTGCACTNCCAGCTTGAGCAATGAGGAAATCTCATCTAAAAAACAACAC 1511
QY 4867 AAAAAACCACTCTCTACTCCAGGAGCTGGGTACA-GAGCTGGGCGACATCAGTGCAG 4925
Db 1512 AAAAAACCACTCTCTACTCCAGGAGCTGGGTACANAGCTGGGCGACATCAGTGCAG 1571
QY 4926 GTGCTGAGGACAGACTTAAGGGGAGCG- -CAGAGCGCGGACCAAGATGAAGTGTGT 4983
Db 1572 GTGCTGAGGACAGACTTAAGGGGAGCGCTGNNCAGAGACCGGACCAAGATGAAGTGTGT 1631
QY 4984 GAGATCAGTGTGATGATCAGAGCTCCCTGCAATTTGGTGAACACAGAGGGGGCCCCAAGC 5043
Db 1632 GAGATCAGTGTGATGATCAGAGCTCCCTGCAATTTGGTGAACACAGAGGGGGCCCCAAGC 1691
QY 5044 ACCAGAGATGGCCCATTCACATCACCACATTCATCTCATCCAGAGATGTCTTCTT 5103
Db 1692 ACCAGAGATGGCCCATTCACATCACCACATTCATCTCATCCAGAGATGTCTTCTT 1751
QY 5104 GGCACGCTGGGTAAATTAAGACAGAAAGTGAAGTGTGGTGTGCTAGTGAAGTGC 5163
Db 1752 GGCACGCTGGGTAAATTAAGACAGAAAGTGAAGTGTGGTGTGCTAGTGAAGTGC 1811
QY 5164 CCCAGGCA- - -GGCTTGGGCTGT- -AGAAAGATTCAGGCGTAAGGCGGGGCGAG 5217
Db 1812 CCCAGGNNCAGGNCCTNTGTGGCTGTNTANGAANAACGTTCAAGGCTTGAAGCGGGCAG 1871

QY 5218 GGC-TCACGCTGTAAATCCAGCAGCTTTGGGAGCGGAGCGGGTGTGATCAGAGTGCAG 5276
Db 1872 GGCNTCAGCGCTGTAAATCCAGCAGCTTTGGGAGCGGAGCGGGTGTGATCAGAGTGCAG 1931
QY 5277 GAGATGTGACCATCTCTGGGTAAACAGAGTGAAGAAAGCCCGTCTACTTAAATTAAGAAAA 5336
Db 1932 GAGATGTGACCATCTCTGGGTAAACAGAGTGAAGAAAGCCCGTCTACTTAAATTAAGAAAA 1991
QY 5337 TTGGCGGCGATGTGGCGGCGACCTGTAGTTCACGTAATCTGCGGAGGCTGAGGAGAG 5396
Db 1992 TTGGCGGCGATGTGGCGGCGACCTGTAGTTCACGTAATCTGCGGAGGCTGAGGAGAG 2051
QY 5397 AATGCGTGAACCCGAGAGGACAGATTTGCAATGAGCGGAGATCGGCCACTGCTCCA 5456
Db 2052 AATGCGTGAACCCGAGAGGACAGATTTGCAATGAGCGGAGATCGGCCACTGCTCCA 2111
QY 5457 GCCTGGGCGACAGAGCAAGCTCATCTGGAAT-AGAAAAAGAAAGTTCAGTGTGAG 5515
Db 2112 GCCTGGGCGACAGAGCAAGCTCATCTGGAATTAAGAAAGAAAGAAAGTTCAGTGTGAG 2171
QY 5516 CCAGAGGCGCAGGCTGTAAATTCATGTCATTCACATGACCTTTGGGCAAGGACCTTCC 5575
Db 2172 CCAGAGGCGCAGGCTGTAAATTCATGTCATTCACATGACCTTTGGGCAAGGACCTTCC 2231
QY 5576 CTGGCCAGTTTCACGGGCTTGAATGACTCCAGAGTCCCTTCAGCATTTAACGCTGCAT 5635
Db 2232 CTGGCCAGTTTCACGGGCTTGAATGACTCCAGAGTCCCTTCAGCATTTAACGCTGCAT 2291
QY 5636 GGTCT- AAGATGAGAAGATGGGCAAGTTCCCTCTCAGCCAGCGCCGTGTCCACTT 5694
Db 2292 GGTCTTAAGATGAGAAGATGGGCAAGTTCCCTCTCAGCCAGCGCCGTGTCCACTT 2351
QY 5695 CAAGGTGAATGACAGGGAATGACGTGTGCCAATCCGAGTTCCAAAGCCCTTGGG 5752
Db 2352 CAAGGTGAATGACAGGGAATGACGTGTGCCAATCCGAGTTCCAAAGCCCTTGGG 2409

RESULT 10
US-09-760-485-1047
? Sequence 1047, Application US/09760485
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: P217
? CURRENT APPLICATION NUMBER: US/09/760,485
? CURRENT FILING DATE: 2001-01-16
? Prior application data removed - consult PALM or file wrapper
? NUMBER OF SEQ ID NOS: 1477
? SOFTWARE: Patentln Ver. 2.0
? SEQ ID NO 1047
? LENGTH: 2409
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (3)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: SITE
? LOCATION: (15)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: SITE
? LOCATION: (56)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: SITE
? LOCATION: (189)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: SITE
? LOCATION: (1465)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: SITE
? LOCATION: (1478)
? OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE
LOCATION: (1548)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1602)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1603)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1818)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1824)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1828)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1838)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1841)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1875)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (2145)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (2298)
OTHER INFORMATION: n equals a,t,g, or c
US-09-760-485-1047

Query Match 35.7%; Score 2225.8; DB 33; Length 2409;
Best Local Similarity 98.7%; Pred. No. 1.6e-257;
Matches 2367; Conservative 0; Mismatches 14; Indels 17; Gaps 12;

3371 CCCTGTCAAAACAGACACTGGCTCTACCAATCAGCAGAGATG-TGGGTGGGGCCAGATA 3429
13 CCNTGTCAAAACAGACACTGGCTCTACCAATCAGCAGAGATG-TGGGTGGGGCCAGATA 72
3430 AGAGATAAAGCAGAGCTGCCGCCAGCCAGCAGTGGCAACGCCGACAGGTCCCTATCCACA 3489
73 AGAGATAAAGCAGAGCTGCCGCCAGCCAGCAGTGGCAACGCCGACAGGTCCCTATCCACA 132
3430 ATATGGCAGCTTGTCTTTTGTCTTTCCTTTCGATTAATCTTGTCTACTGCTCGCTTTT-7GG 3548
133 ATATGGCAGCTTGTCTTTTGTCTTTCCTTTCGATTAATCTTGTCTACTGCTCGCTTTTNTGG 192
3549 GTCCACACTGCTTTTATGAGCTGTAAACACTCAGCAGAAAGTCTGAGAGTTCACTCCCTGA 3608
193 GTCCACACTGCTTTTATGAGCTGTAAACACTCAGCAGAAAGTCTGAGAGTTCACTCCCTGA 252
3609 AGCCACTAAGACCAAGCCACCGCGGAGGAATGAACAATCCGCGCGCGCTGTAAAG 3668
253 AGCCACTAAGACCAAGCCACCGCGGAGGAATGAACAATCCGCGCGCGCTGTAAAG 312
3669 AGCTTAACACTCAGCCGGAAGTGTGAGCTTTCACCTCTCTCAGCCAGCAGACCAAGAAC 3728
313 AGCTTAACACTCAGCCGGAAGTGTGAGCTTTCACCTCTCTCAGCCAGCAGACCAAGAAC 372
3729 CCACCAAGAGAAAGTGTGAGCAACATCTGAACATCTGAAGAAACAATCTCAGATGC 3788
373 CCACCAAGAGAAAGTGTGAGCAACATCTGAACATCTGAAGAAACAATCTCAGATGC 432
3789 ACCACCTTAAGAGCTGTAACTCACTGCGAGGGTCCGGGCTCTCTTCTTGAAGTCACT 3848
433 ACCACCTTAAGAGCTGTAACTCACTGCGAGGGTCCGGGCTCTCTTCTTGAAGTCACT 492

3849 GAGACCAACCACTCAACAGTTTTCGACACCAAGCCAGAGTTTGATCAGCTGGGCAA 3908
493 GAGACCAACCACTCAACAGTTTTCGACACCAAGCCAGAGTTTGATCAGCTGGGCAA 552
3909 CATGATGAAGTCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCGGAGCATGT 3968
553 CATGATGAAGTCCCTCTCTGCAAAAAAATTTACAAAAATTTGGCGGAGCATGT 612
3969 GGTCCGCTGTGTGTCCAGCTACGCGGAGGCTAAAGTGGAGAGTCCCTTGAAGCTG 4028
613 GGTCCGCTGTGTGTCCAGCTACGCGGAGGCTAAAGTGGAGAGTCCCTTGAAGCTG 672
4029 GGAGGTGAAGACTCAGATGAGTGTATGTAACCAAGCCCTGAGGCTGGGGGACAGAC 4088
673 GGAGGTGAAGACTCAGATGAGTGTATGTAACCAAGCCCTGAGGCTGGGGGACAGAC 732
4089 TGAGACCCCTGTTCCTCCGCAAAAAAATTTACAAAAATTTAGAGAGTGCCTGATA 4148
733 TGAGACCCCTGTTCCTCCGCAAAAAAATTTACAAAAATTTAGAGAGTGCCTGATA 792
4149 TGGCTAGGCGCAGTGTCTATGCTTAATCCAGCACTTTGGGAAGCCGAGCGGGCG 4208
793 TGGCTAGGCGCAGTGTCTATGCTTAATCCAGCACTTTGGGAAGCCGAGCGGGCGG 852
4209 GTACCTTAAGTCAAGAGTGTGTAACCAAGCCCTGAGCAATGAGAAAGCCCATGCTTC 4268
853 GTACCTTAAGTCAAGAGTGTGTAACCAAGCCCTGAGCAATGAGAAAGCCCATGCTTC 912
4269 TAAAAATACAAATTTAGCCGCTGTGGGGGAGTGTGAGCATGCTTAATCCAGCT 4328
913 TAAAAATACAAATTTAGCCGCTGTGGGGGAGTGTGAGCATGCTTAATCCAGCT 972
4329 ACTCAGAGAGCTGAGGCGAGAGATCATCTTGAACCCAGAGCGCGGTTGCAATGAGCC 4388
973 ACTCAGAGAGCTGAGGCGAGAGATCATCTTGAACCCAGAGCGCGGTTGCAATGAGCC 1032
4389 GAGATCGTCCCAATGCACTCCACCACTCCAGCTGGGGCAAGAGCCCAATCTGCT 4448
1033 GAGATCGTCCCAATGCACTCCACCACTCCAGCTGGGGCAAGAGCCCAATCTGCT 1092
4449 TAAAAAAGTGTGCTGCTGATTAAGAGTGTGCAATGCAATGTTGGCAG 4508
1093 T-AAAAAAGTGTGCTGCTGATTAAGAGTGTGCAATGCAATGTTGGCAG 1151
4509 CAACATGTTTAAGATGTGAGCTCTGCTTCATGCTGCTTTAAAAACCACTCTCA 4568
1152 CAACATGTTTAAGATGTGAGCTCTGCTTCATGCTGCTTTAAAAACCACTCTCA 1211
4569 AGGCCAGTGCAGTGTGCTATGCTTAATCCAGCACTTTGGGAGGCCGAGCGGGTGG 4628
1212 AGGCCAGTGCAGTGTGCTATGCTTAATCCAGCACTTTGGGAGGCCGAGCGGGTGG 1271
4629 ATACCTGAGGTCAGAGGTTTCAGACCACTGACCAACATGTTGAATCCACCTC 4688
1272 ATACCTGAGGTCAGAGGTTTCAGACCACTGACCAACATGTTGAATCCACCTC 1331
4689 TACTAAAAATPACAAATTTAGATGAGCTGTGTGATCTCTGTAATCCACCTACTTGG 4748
1332 TACTAAAAATPACAAATTTAGATGAGCTGTGTGATCTCTGTAATCCACCTACTTGG 1391
4749 GAGGCTGAGGCAAGAAATCACTAGAACCAAGGAGCGGAGGTTGAGAGCCGAGTAC 4808
1392 GAGGCTGAGGCAAGAAATCACTAGAACCAAGGAGCGGAGGTTGAGAGCCGAGTAC 1451
4809 GTGCATTTGCACT-CCAGCCTGAGCA-ATGAGCGAAATCTCAATCTCAAAAAACAACAC 4866
1452 GTGCATTTGCACTNCCAGCCTGAGCAATGAGGAGAAATCTCAATCTCAAAAAACAACAC 1511
4867 AAAAACCACTCTTACTCTCCAGAGGAGTGTGATCA-GAGCTGGGCAATCATGATCAAG 4925
1512 AAAAACCACTCTTACTCTCCAGAGGAGTGTGATCAAGGAGTGTGGGCAATCATGATCAAG 1571

QY	3549	GTCCACACTGCTTTTATGAGCTGTGAACCTCACACGAGGTCGTGACCTTCACTCTGA	3608
Db	193	GTCCACACTGCTTTTATGAGCTGTGAACCTCACACGAGGTCGTGACCTTCACTCTGA	252
QY	3609	AGCCACTGAAGCAACGAGCCCAACGGGGGGAATGAACAATCCGGCCGCTGCTTAA	3668
Db	253	AGCCACTGAAGCAACGAGCCCAACGGGGGGAATGAACAATCCGGCCGCTGCTTAA	312
QY	3669	AGCTATAACATCAACCGGAGGTCGTGAGCTTCACTCTCAGCAGGAGACCAACGAA	3728
Db	313	AGCTATAACATCAACCGGAGGTCGTGAGCTTCACTCTCAGCAGGAGACCAACGAA	372
QY	3729	CCACCAGAAGAAACTGCGAAACATCTGAAATATGAAAGAAACAAATCCAGATGC	3788
Db	373	CCACCAGAAGAAACTGCGAAACATCTGAAATATGAAAGAAACAAATCCAGATGC	432
QY	3789	ACCACTTAAAGCTGTAACTACATCTACGAGGGTCGCGGCTTCTTTGAAGTCA	3848
Db	433	ACCACTTAAAGCTGTAACTACATCTACGAGGGTCGCGGCTTCTTTGAAGTCA	492
QY	3849	GAGACCAAGCACTACCACTGTTGGAGACAAGCCAGAGGTTAGATACACCTGGGCAA	3908
Db	493	GAGACCAAGCACTACCACTGTTGGAGACAAGCCAGAGGTTAGATACACCTGGGCAA	552
QY	3909	CATGATGAATAGCCCTCTGTGCAAAAAAAAAAAAAAAAAATTGACAAATTTGGCGAGCAT	3968
Db	553	CATGATGAATAGCCCTCTGTGCAAAAAAAAAAAAAAAAAATTGACAAATTTGGCGAGCAT	612
QY	3969	GGTCCGTCCTGTGTGTGTCACGCTACGCGGGAGGCTAAAGTGGAGATCGCTTGA	4028
Db	613	GGTCCGTCCTGTGTGTGTCACGCTACGCGGGAGGCTAAAGTGGAGATCGCTTGA	672
QY	4029	GGAGGTGAAGCTCAGTGAAGCTGTGATGTGACACAGCCCTGACGCTGGGGGACAG	4088
Db	673	GGAGGTGAAGCTCAGTGAAGCTGTGATGTGACACAGCCCTGACGCTGGGGGACAG	732
QY	4089	TGAGACCCCTGTTCCCTCCGCAAAAAAAAAATTGACAAAGTGTAAATAGAGTGCCTGATA	4148
Db	733	TGAGACCCCTGTTCCCTCCGCAAAAAAAAAATTGACAAAGTGTAAATAGAGTGCCTGATA	792
QY	4149	TGCGTAGCGGAGTGGCTCATGCTGTAAATCCACAGCACTTTGGGAAAGCCAGCGGGCG	4208
Db	793	TGCGTAGCGGAGTGGCTCATGCTGTAAATCCACAGCACTTTGGGAAAGCCAGCGGGCG	852
QY	4209	GTCACCTTAAGGTCAGAGTGTGAGACCAAGCTGGGCAACATGGAAGAAAGCCATCTCTC	4268
Db	853	GTCACCTTAAGGTCAGAGTGTGAGACCAAGCTGGGCAACATGGAAGAAAGCCATCTCTC	912
QY	4269	TAAAAAATCAAAAATTAGCGCGGCTGTGGGGGAGTGGTGGAGCATGCTGTAAATCCAGCT	4328
Db	913	TAAAAAATCAAAAATTAGCGCGGCTGTGGGGGAGTGGTGGAGCATGCTGTAAATCCAGCT	972
QY	4329	ACTCAGAGAGGCTGAGGCGAGAGAAATCACTTGAACCCAGAGAGCGGCTTGCAGTGA	4388
Db	973	ACTCAGAGAGGCTGAGGCGAGAGAAATCACTTGAACCCAGAGAGCGGCTTGCAGTGA	1032
QY	4389	GAGATCGTGCATTTGCACTCCACCCACTCCAGCTGGGGCAACAGAGGCAAACTGTGCT	4448
Db	1033	GAGATCGTGCATTTGCACTCCACCCACTCCAGCTGGGGCAACAGAGGCAAACTGTGCT	1092
QY	4449	TAAAAAATAAAAAAAAAAAGTGCCTGACATATTAAGAGTGTGCAATGCAATAGTTGCCAG	4508
Db	1093	T - AAAAAAAAAAAAAAAAAAAGTGCCTGACATATTAAGAGTGTGCAATGCAATAGTTGCCAG	1151
QY	4509	CAAAATGTTTAAAGATGTGAGGCTCTGCTTCCATGGTCTGTTAAAAAACCAACCTCA	4568
Db	1152	CAAAATGTTTAAAGATGTGAGGCTCTGCTTCCATGGTCTGTTAAAAAACCAACCTCA	1211
QY	4569	AGGCGAGGTGAGAGGCTCATGCTTAAATCCACAGCACTTTGGGAGGCGAGGCGGGGG	4628
Db	1212	AGGCGAGGTGAGAGGCTCATGCTTAAATCCACAGCACTTTGGGAGGCGAGGCGGGGG	1271
QY	4629	ATCACCTGAGGTGAGAGGTTGAGACCAAGCTGACCAACCAATGAGTGAATCCCACTC	4688

Db	1272	ATCAGCTAGGTCAGAGAGTCTGAGACCGCCTGACCAACATGTTGAAATCCACCTC	1331
OY	4689	TACTAAAAATCAAAAATTAGATGAGCAAGGAGGAGCATGGCTGTAACTCCACTCTGG	4748
Db	1332	TACTAAAAATCAAAAATTAGATGAGCAAGGAGGAGCATGGCTGTAACTCCACTCTGG	1391
OY	4749	GAGCGTAGAGCAGAAAAATCTACTAGAACACAGGAGGCGAGGTTGTAGTGAACGAGATC	4808
Db	1392	GAGCGTAGAGCAGAAAAATCTACTAGAACACAGGAGGCGAGGTTGTAGTGAACGAGATC	1451
OY	4809	GTGCCATTGCACT-CCAGCCTGAGCA-ATGAGCGAACTGCATCTCAAAAAACAACAC	4866
Db	1452	GTGCCATTGCACTNCCAGCCTGAGCANATGAGCGAACTGCATCTCAAAAAACAACAC	1511
OY	4867	AAAAAACCACATCTCTACTCTCCAGGAGAGTGGGTACA-GAGCTGGGCCAATCATGTGCAG	4925
Db	1512	AAAAAACCACCCCTCTACTCTCCAGGAGAGTGGGTACANAGCTGGGCCAATCATGTGCAG	1571
OY	4926	GTGCTGAGCCACAGAGCTAAGGCGGAGCTG--CAGGACCGGGGACACATTAACAGTGTGT	4983
Db	1572	GTGCTGAGCCACAGAGCTAAGGCGGAGCTGNNCAGGACCGGAGCAATTAACAGTGTGT	1631
OY	4984	GAGATCAGTGTGTGAGATCAAGCAGTCCCTGCATGTGTGACACACGAGGGGCCCCCAAGC	5043
Db	1632	GAGATCAGTGTGTGAGATCAGACGTCCTGCATGTGTGACACACGAGGGGCCCCCAAGC	1691
OY	5044	ACCAGAGATGGCCCATCATCAGTACACACATCTTCTCATCCAGAGATGTCTGTTTCTT	5103
Db	1692	ACCAGAGATGGCCCATCATCAGTACACACATCTTCTCATCCAGAGATGTCTGTTTCTT	1751
OY	5104	GGCAGCGTGGGGTAAATTAGGACAGAAAGTGCAGTCTTGGGTGGTCAGTCAAGACTGC	5163
Db	1752	GGCAGCGTGGGGTAAATTAGGACAGAAAGTGCAGTCTTGGGTGGTCAGTCAAGACTGC	1811
OY	5164	CCCAAGCA- ---GGCCTTGTGGCCTGT--AGAAAAAGTTTCAGGCCCTAGGCCGGGACGCT	5217
Db	1812	CCCAAGNNCAGANNCTTGTGTGGCCTGTANTANAAAAAGTTTCAGGCCCTAGGCCGGGACGCT	1871
OY	5218	GGC-TCAGCCTGTAAATCCAGCACTTTGGGAGGCGGAGGGGGGTGATCAGAGGTAG	5276
Db	1872	GGCMTCAAGCCTGTAAATCCAGCACTTTGGGAGGCGGAGGGGGGTGATCAGAGGTAG	1931
OY	5277	GAGATCGTGCACATCTCGGTAAACAAGGTGAACCCCGCTCTACTAAAAATACAAAAA	5338
Db	1932	GAGATCGTGCACATCTCGGTAAACAAGGTGAACCCCGCTCTACTAAAAATACAAAAA	1991
OY	5337	TTGGCCGGGCGATGTGTGGCGGCGACCTGTAGTTCCAGTACTTCGGGAGGCTGAGCGAGAG	5396
Db	1992	TTGGCCGGGCGATGTGTGGCGGCGACCTGTAGTTCCAGTACTTCGGGAGGCTGAGCGAGAG	2051
OY	5397	AATGGCGTGAACCCGAGAGGCGAGATTTGCACTGAGCCGGAATGCGCCACTGCATCTCA	5456
Db	2052	AATGGCGTGAACCCGAGAGGCGAGATTTGCACTGAGCCGGAATGCGCCACTGCATCTCA	2111
OY	5457	GCTGGGGGAGAGAGCAAGACTCCATCTGGAAAA-AGAAAAAGAAAAAGTTTAAAGGCTGAG	5515
Db	2112	GCTGGGGGAGAGAGCAAGACTCCATCTGGAAAAAGAAAAAGTTTAAAGGCTGAG	2171
OY	5516	CCAGAGGCCAGGCTGTAAATCTGTCACTTACATGACCTTGGGCAAGGCAAGCTTCCTTCC	5579
Db	2172	CCAGAGGCCAGGCGTAAATCTGTCACTTACATGACCTTGGGCAAGGCAAGCTTCCTTCC	2231
OY	5576	CTGGCCCACTTACAGGGGTTTGAATTCGACTCCAAAGTCCCTTCCAGCATTTAAAGCTGCAT	5635
Db	2232	CTGGCCCACTTACAGGGGTTTGAATTCGACTCCAAAGTCCCTTCCAGCATTTAAAGCTGCAT	2291
OY	5636	GGTTCCT-AGATGGAAGATGGGCGAGTTCCCTCTCAACCCAGCCGCTGTCAACTT	5694
Db	2292	GGTTCCTAAGATGGAAGATGGGCGAGTTCCCTCTCAACCCAGCCGCTGTCAACTT	2351
OY	5695	CAAGGTGAATACCAAGGAAATCTCAAGTTCCTCAATCCCGAGTTCCAAAGCCTTGGG	5752

Db 2352 CAAGTGATGACGAGGGAATACAGTGTCCCAATCCCGCATTCACAAAGCCCTTGGG 2409

RESULT 13
US-10-217-527-490
; Sequence 490, Application US/10217527
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P215CIN
; CURRENT APPLICATION NUMBER: US/10/217,527
; CURRENT FILING DATE: 2002-08-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 601
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 490
; LENGTH: 2409
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (189)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1465)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1548)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1603)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1818)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1819)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1824)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1828)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1838)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1841)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1875)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2145)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2298)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-217-527-490

Query Match 35.7%; Score 2225.8; DB 48; Length 2409;
Best Local Similarity 98.7%; Pred. No. 1.6e-257;
Matches 2367; Conservative 0; Mismatches 14; Indels 17; Gaps 12;

QY 3371 CCCTGTAAACAGACGACCTGCGCTACCAATCAGCAGATG-TGGGTGGGCGCAGATA 3429
Db 13 CCNTGTAAACAGACGACCTGCGCTACCAATCAGCAGATGTTGGTGGGCGCAGATA 72

QY 3430 AGAGAATAAACAGAGCTGCGCCAGCAGCAGATGCGCAACGCGCAGAGTCCCTATCCACA 3489
Db 73 AGAGAATAAACAGAGCTGCGCCAGCAGCAGATGCGCAACGCGCAGAGTCCCTATCCACA 132

QY 3490 ATATGCGAGCTTGTCTTCTTGTGCTTGGATTAATCTTGCTACTGCTGCTTGT-TGG 3548
Db 133 ATATGCGAGCTTGTCTTCTTGTGCTTGGATTAATCTTGCTACTGCTGCTTGTG 192

QY 3549 GTCCACACGCTTTTATGACCTGTAAACACACACAGAGTGTGAGCTTCACTCTGA 3608
Db 193 GTCCACACGCTTTTATGACCTGTAAACACACAGAGTGTGAGCTTCACTCTGA 252

QY 3609 AGCCACTAAGACACGAGCCACCGGAGGAGTAACAACTCCGCGCGCTCCCTTAAG 3668
Db 253 AGCCACTAAGACACGAGCCACCGGAGGAGTAACAACTCCGCGCGCTCCCTTAAG 312

QY 3669 AGCTATTAACACTACCGCGAAGGCTGACGCTTCACTCTGACCCAGCAGACAGCAAC 3728
Db 313 AGCTATTAACACTACCGCGAAGGCTGACGCTTCACTCTGACCCAGCAGACAGCAAC 372

QY 3729 CCAACGAAGGAAGAACTCGGAACATGTGAACATCAAGAAACAACTCCAGATGC 3788
Db 373 CCAACGAAGGAAGAACTCGGAACATGTGAACATCAAGAAACAACTCCAGATGC 432

QY 3789 ACCACCTTAAGACCTGTAAACACTGACGAGGTCGCGGCTTCTCTTGAAGTCAGT 3848
Db 433 ACCACCTTAAGACCTGTAAACACTGACGAGGTCGCGGCTTCTCTTGAAGTCAGT 492

QY 3849 GAGACCAAGCACTACCAAGTTTCGGACACAAAGCCAGAGTTTGAGATCAGCTGGGCAA 3908
Db 493 GAGACCAAGCACTACCAAGTTTCGGACACAAAGCCAGAGTTTGAGATCAGCTGGGCAA 552

QY 3909 CATGATGAATGCGCCCTCTGCAAAAAAAATTAACAAAAATTTGGCGGAGCAGTGT 3968
Db 553 CATGATGAATGCGCCCTCTGCAAAAAAAATTAACAAAAATTTGGCGGAGCAGTGT 612

QY 3969 GGTCCGCTGCTGTGTCCTCAGCTACGCGGAGGCTAAAGTGGAGAGTCCCTGAGCCTG 4028
Db 613 GGTCCGCTGCTGTGTCCTCAGCTACGCGGAGGCTAAAGTGGAGAGTCCCTGAGCCTG 672

QY 4029 GGAGGTGAAGCTGCAAGTGAAGTGTGATTTACACAGCCCTTAAGCTGGGGAGACAGC 4088
Db 673 GGAGGTGAAGCTGCAAGTGAAGTGTGATTTACACAGCCCTTAAGCTGGGGAGACAGC 732

QY 4089 TGAAGACCCCTGTTCCCTCGCAAAAAATTTGCAAAAAAGTGAATGAAGAGTCCCTGATA 4148

|||||
Db 733 TGAGACCCCTGTTCCCTCCGCAAAAAATTGACAAAAAGTGAATAGAGGTGCTGTATA 792
4149 TGGGTAGCCGAGAGGCGCTCATGCTGTATATCCAGCACTTTGGGAAGCGGAGCGGGG 4208
793 TGGGTAGCCGAGAGGCGCTCATGCTGTATATCCAGCACTTTGGGAAGCGGAGCGGGG 852
4209 GTCACTTAAGGTCAAGAGTGTAGAACCGAGCTGGCCCAATGAGAGAACCCATCTTTC 4268
853 GTCACTTAAGGTCAAGAGTGTAGAACCGAGCTGGCCCAATGAGAGAACCCATCTTTC 912
4269 TAAAAATACAAATTTAGCCGCTGTGGGGGCAAGTGTGAGCAATGCTGTATCCAGCT 4328
913 TAAAAATACAAATTTAGCCGCTGTGGGGGCAAGTGTGAGCAATGCTGTATCCAGCT 972
4329 ACTGAGGAGGCTGAGGCGCAGAGAAATCACTTGAACCCAGAGAGCGCGGTGTCAGTAC 4388
973 ACTGAGGAGGCTGAGGCGCAGAGAAATCACTTGAACCCAGAGAGCGCGGTGTCAGTAC 1032
4389 GAGATCGTGCATTGCACTCCACCACCTCCAGCCCTGGGCAACAAGAGCCAACTCTCT 4448
1033 GAGATCGTGCATTGCACTCCACCACCTCCAGCCCTGGGCAACAAGAGCCAACTCTCT 1092
4449 TAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4508
1093 T-AAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1151
4509 CAATATGTTAAGATGTGAGAGTCTGCTTCCATGCTGTAAAAACCCACCTCA 4568
1152 CAATATGTTAAGATGTGAGAGTCTGCTTCCATGCTGTAAAAACCCACCTCA 1211
4569 AGGCGAGGTGCAAGTGGCTCATGCTATATCCAGCACTTTGGGAGCGGAGGAGGAGG 4628
1212 AGGCGAGGTGCAAGTGGCTCATGCTATATATCCAGCACTTTGGGAGCGGAGGAGGAG 1271
4629 ATCACTGAGGTGCAAGTGGCTGAGACCAAGCTGACCAACATGTTGAAATCCACCTC 4688
1272 ATCACTGAGGTGCAAGTGGCTGAGACCAAGCTGACCAACATGTTGAAATCCACCTC 1331
4689 TACTAAAAATACAAATTTAGATGAGCATGTTGTCATGCTGTATCCCACTACTTGG 4748
1332 TACTAAAAATACAAATTTAGATGAGCATGTTGTCATGCTGTATCCCACTACTTGG 1391
4749 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4808
1392 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1451
4809 GTGCAATTGCACT-CCAGGCTGAGCA-ATGAGCGAATCTCATCTCAAAAAAACAACAC 4866
1452 GTGCAATTGCACTNCCAGGCTGAGCANAATGAGCGAATCTCATCTCAAAAAAACAACAC 1511
4867 AAAAAACCACTCTTACTCCAGGAGAGTGGGTACA-GAGTGGGCGCATCAGTGCAG 4925
1512 AAAAAACCACTCTTACTCCAGGAGAGTGGGTACA-GAGTGGGCGCATCAGTGCAG 1571
4926 GTGCTGAGGCGCAGAGGCTAAGGCGGAGGCT--CAGGACCGGGGACAGATTAAGTGTG 4983
1572 GTGCTGAGGCGCAGAGGCTAAGGCGGAGGCTGNNCAGAGCGGGGACAGATTAAGTGTG 1631
4984 GAGATCAGTGTGTAGATCAGACGCTCCCTGCAATTTGTGACACACAGGGGGCCCCAAGC 5043
1632 GAGATCAGTGTGTAGATCAGACGCTCCCTGCAATTTGTGACACACAGGGGGCCCCAAGC 1691
5044 ACCAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5103
1692 ACCAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1751
5104 GGCAGCTGGGGTAAATTTAGAGCAGAGGTGACAGTCTGGGTGGGTCATCGAGCTGC 5163
1752 GGCAGCTGGGGTAAATTTAGAGCAGAGGTGACAGTCTGGGTGGGTCATCGAGCTGC 1811
5164 CCCAGGCA---GGCCTTGTGGCCTGT--AGAAAAAGTTACAGGCTTACGCGGCGGCGGCT 5217
|||||

Db 1812 CCCAGGNNCAGGNCCTNTGTGGCTGNTANGAAAAAGTTACAGGCTTAGCGGCGACGGT 1871
Qy 5218 GGC-TCAGGCTGTATATCCAGCACTTTGGGAGGCGGAGGCGGAGTATCAGAGGTGAG 5276
Db 1872 GGCNTACGCGCTGTATATCCAGCACTTTGGGAGGCGGAGGCGGAGTATCAGAGGTGAG 1931
Qy 5277 GAGATCGTACCATCTGCTTAACAGGAGTGAACCCGCTCTCTACTTAAAAATACAAAAA 5336
Db 1932 GAGATCGTACCATCTGCTTAACAGGAGTGAACCCGCTCTCTACTTAAAAATACAAAAA 1991
Qy 5337 TTGGCGGCGCATGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5396
Db 1992 TTGGCGGCGCATGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2051
Qy 5397 AATGCGGTGAACCCAGAGGCGAGTATTGCAATGAGCCGAGATTCGCGGCGGCGGCGGCGG 5456
Db 2052 AATGCGGTGAACCCAGAGGCGAGTATTGCAATGAGCCGAGATTCGCGGCGGCGGCGGCGG 2111
Qy 5457 GCCTGGGCGACAGAGCAAGACTCCATCTGGAAG-AGAAAAAGAAAAAGTTACAGTCTGAG 5515
Db 2112 GCCTGGGCGACAGAGCAAGACTCCATCTGGAAGAAAGAAAAAGTTACAGTCTGAG 2171
Qy 5516 CCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5575
Db 2172 CCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2231
Qy 5576 CTGGCCGAGTTACAGGCGGTTGGAATGCACTCCAGAGTCCCTTCCAGCATTAACGTCAT 5635
Db 2232 CTGGCCGAGTTACAGGCGGTTGGAATGCACTCCAGAGTCCCTTCCAGCATTAACGTCAT 2291
Qy 5636 GGTCT-AAGATGAGAAAGTGGGCGAGTTTCCCTCTCCAGCCGCGGCGGCGGCGGCGG 5694
Db 2292 GGTCTAAGATGAGAAAGTGGGCGAGTTTCCCTCTCCAGCCGCGGCGGCGGCGGCGGCGG 2351
Qy 5695 CAAGGTGATGACAGGAGAGTCAAGTCCCAATCCCGAGTTCCAAAGGCGGCGGCGGCGG 5752
Db 2352 CAAGGTGATGACAGGAGAGTCAAGTCCCAATCCCGAGTTCCAAAGGCGGCGGCGGCGG 2409

RESULT 14
US-10-217-651-592
; Sequence 592, Application US/10217651
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P21LICIN
; CURRENT APPLICATION NUMBER: US/10/217,651
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 09/760,491
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647

PRIOR FILING DATE:	2000-07-07
PRIOR APPLICATION NUMBER:	60/225, 267
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/216, 880
PRIOR FILING DATE:	2000-07-07
PRIOR APPLICATION NUMBER:	60/225, 270
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/251, 869
PRIOR FILING DATE:	2000-12-08
PRIOR APPLICATION NUMBER:	60/235, 834
PRIOR FILING DATE:	2000-09-27
PRIOR APPLICATION NUMBER:	60/234, 274
PRIOR FILING DATE:	2000-09-21
PRIOR APPLICATION NUMBER:	60/234, 223
PRIOR FILING DATE:	2000-09-21
PRIOR APPLICATION NUMBER:	60/228, 924
PRIOR FILING DATE:	2000-08-30
PRIOR APPLICATION NUMBER:	60/224, 518
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/236, 369
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/224, 519
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/220, 964
PRIOR FILING DATE:	2000-07-26
PRIOR APPLICATION NUMBER:	60/241, 809
PRIOR FILING DATE:	2000-10-20
PRIOR APPLICATION NUMBER:	60/249, 299
PRIOR FILING DATE:	2000-11-17
PRIOR APPLICATION NUMBER:	60/236, 327
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/241, 785
PRIOR FILING DATE:	2000-10-20
PRIOR APPLICATION NUMBER:	60/244, 617
PRIOR FILING DATE:	2000-11-01
PRIOR APPLICATION NUMBER:	60/225, 268
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/236, 368
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/251, 856
PRIOR FILING DATE:	2000-12-08
PRIOR APPLICATION NUMBER:	60/251, 868
PRIOR FILING DATE:	2000-12-08
PRIOR APPLICATION NUMBER:	60/229, 344
PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/234, 997
PRIOR FILING DATE:	2000-09-25
PRIOR APPLICATION NUMBER:	60/229, 343
PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/229, 345
PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/229, 287
PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/229, 513
PRIOR FILING DATE:	2000-09-05
PRIOR APPLICATION NUMBER:	60/231, 413
PRIOR FILING DATE:	2000-09-08
PRIOR APPLICATION NUMBER:	60/229, 509
PRIOR FILING DATE:	2000-09-05
PRIOR APPLICATION NUMBER:	60/236, 367
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/237, 039
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/237, 038
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/236, 370
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/236, 802
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/237, 037
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/237, 040
PRIOR FILING DATE:	2000-10-02

PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/233,063
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/232,397
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/232,399
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/232,401
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/241,808
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/241,826
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/241,786
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/241,221
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/246,475
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/231,243
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/233,065

Query Match	35.7%	Score	2225.8	DB	48	Length	2409
Best Local Similarity	98.7%	Pred. No.	1.6e-257				
Matches 2367; Conservative	0	Mismatches	14	Indels	17	Gaps	12

QY	3371	CCCTGTCAAAACAGACCACACGCGGCTCACCACATGAGAGATG-TGGGTGGGGCCACATA	3423
Db	13	CCATGTCAAAACAGACCACTGGCTGTACCAATTCAGAGAGATGATGATGGTGGGGCCACATA	72
QY	3430	AGAGAAATAAAAGCAGGCTGCCCGAGCCAGCAGCAGTGGCAACGCGCACAGTCCCTATCCACA	3489
Db	73	AGAGAAATAAAAGCAGGCTGCCCGAGCCAGCAGCAGTGGCAACGCGCACAGTCCCTATCCACA	132
QY	3490	ATTATGGCAGCTTGTGTTCTTTTGGCTGTTTGGATTAATCTTGCTACTGCTGCTTTT-TGG	3548
Db	133	ATTATGGCAGCTTGTGTTCTTTTGGCTGTTTGGATTAATCTTGCTACTGCTGCTTTTWWG	192
QY	3549	GTCACACATGCTTTTATGACCTGTAAACACACACACAGCAGTGTGACAGCTTCACTCTGA	3608
Db	193	GTCACACATGCTTTTATGACCTGTAAACACACACAGCAGTGTGACAGCTTCACTCTGA	252
QY	3609	AGGCACATTAAGACCAACGAGCCACCGGAGGATTAATGAACACTCCGCGCGCTGCTTAAG	3668
Db	253	AGGCACATTAAGACCAACGAGCCACCGGAGGATTAATGAACACTCCGCGCGCTGCTTAAG	312
QY	3669	AGCTATTAACTACACGCGGAGGCTTGACACTTCACTCTCAAGCAGCAGACACGAC	3728
Db	313	AGCTATTAACTACACGCGGAGGATTTGACACTTCACTCTCAAGCAGCAGACACGAC	372
QY	3729	CCACCCAGAAAGAAAACTCGCAACACATCTGAACATCAGAAAGAACAACTCCAGATGC	3788
Db	373	CCACCCAGAAAGAAAACTCGCAACACATCTGAACATCAGAAAGAACAACTCCAGATGC	432
QY	3789	ACCACCTTAAGACCTGTAAACATCACTACGAGGCTCGCGGCTCTCTCTTGAAGTACGT	3848
Db	433	ACCACCTTAAGACCTGTAAACATCACTACGAGGCTCGCGGCTCTCTCTTGAAGTACGT	492
QY	3849	GAGACCAAGCAGCTACACAGTTTGGACACAAAGCCAGAGTTTGAATCAGCCGCGCAA	3908
Db	493	GAGACCAAGCAGCTACACAGTTTGGACACAAAGCCAGAGTTTGAATCAGCCGCGCAA	552
QY	3909	CATGATGAAGAAATGCCCTCTCTGCAAAAAAATAAATAAATAATTTGGGCGAGCATGCT	3968
Db	553	CATGATGAAGAAATGCCCTCTCTGCAAAAAAATAAATAAATAATTTGGGCGAGCATGCT	612
QY	3969	GGTCGCTGCTGTGGTCCAGCTACGCGGGAGGCTAAATGGGAGATTCCTTAAGCCTG	4028
Db	613	GGTCGCTGCTGTGGTCCAGCTACGCGGGAGGCTAAATGGGAGATTCCTTAAGCCTG	672
QY	4029	GGAGGTGAAGATTCGACGTAGCTGTGATTTTACACAGCCCTTAAGCTGGGGACAGAC	4088

Db	673	GGAGGTGAAGAC	TGCAGTGTGAC	TGTGATTGTAC	CACAGCCCTCTA	AGCTGGGGGAC	AGAC	732
OY	4089	TGAGACCCCTGTTCCCTCCGCAAAAAATTGACAAAAAGTGTAA	TAAAGGTGCTGTATA	4148				
Db	733	TGAGACCCCTGTTCCCTCCGCAAAAAATTGACAAAAAGTGTAA	TAAAGGTGCTGTATA	792				
OY	4149	TGGCTAGGCGCAGATGCTCATGCTGTATATCCACAGACTTTGGGAAGCCGAGCGGGCGG	4208					
Db	793	TGGCTAGGCGCAGATGCTCATGCTGTATATCCACAGACTTTGGGAAGCCGAGCGGGCGG	852					
OY	4209	GTCACTTAAGGTCAGAGAGTGTGAGACCGAGCCGGGCAACATGGAAAAAGCCATCTCTTC	4268					
Db	853	GTCACTTAAGGTCAGAGAGTGTGAGACCGAGCCGGGCAACATGGAAAAAGCCATCTCTTC	912					
OY	4269	TAAAAATACAAAAATTAGCCGGCTGTGGGGGAGTGTGGAGCATGCTGTAA	TCCAGCT	4328				
Db	913	TAAAAATACAAAAATTAGCCGGCTGTGGGGGAGTGTGGAGCATGCTGTAA	TCCAGCT	972				
OY	4339	ACTCAGAGAGCTGAGGCGAGAGAAATCACTTAAACCCAGAGGCGGGCTTGCA	GTGAGCC	4388				
Db	973	ACTCAGAGAGCTGAGGCGAGAGAAATCACTTAAACCCAGAGGCGGGCTTGCA	GTGAGCC	1032				
OY	4389	GAGATCGGTCATTGCTCACTCCACCCACATCCAGCCGCGGCAACAGAGCAAACTGTCT	4448					
Db	1033	GAGATCGGTCATTGCTCACTCCACCCACATCCAGCCGCGGCAACAGAGCAAACTGTCT	1092					
OY	4449	TAAAAAAAAAAAAAAAAAGTCCCTGTACATTAAGAGGTGTCAATGTCA	TATAGTGTCCAGG	4508				
Db	1093	T-AAAAAAAAAAAAAAAAAGTCCCTGTACATTAAGAGGTGTCAATGTCA	TATAGTGTCCAGG	1151				
OY	4509	CAACATGTTTAAAGATGTGAGATCTCCCTTCATGTCTGTTAAAAAACCCACCTCA	1152					
Db	1152	CAACATGTTTAAAGATGTGAGATCTCCCTTCATGTCTGTTAAAAAACCCACCTCA	1211					
OY	4559	AGGCCAGGTGCAATGTGCTCATATCTATATATCCACAGACTTTGGAGCGCCAGGGGGGTGG	4628					
Db	1212	AGGCCAGGTGCAATGTGCTCATATCTATATATCCACAGACTTTGGAGCGCCAGGGGGGTGG	1271					
OY	4629	ATCACTTAGGTCAGAGAGTTGTGAGACCGCCGACCAACATGTGTAAATCCACCTC	4688					
Db	1272	ATCACTTAGGTCAGAGAGTTGTGAGACCGCCGACCAACATGTGTAAATCCACCTC	1331					
OY	4689	TACTAAAAATACAAAAATTAGATGAGCATGTGTGTGCATGCTGTAA	TCCACTACTTTGG	4748				
Db	1332	TACTAAAAATACAAAAATTAGATGAGCATGTGTGTGCATGCTGTAA	TCCACTACTTTGG	1391				
OY	4749	GAGCGTGAAGCGAGGAAAAATCACTGTAGAACAGAGGAGGGAGGTGTAGTGA	CGCAGATC	4808				
Db	1392	GAGCGTGAAGCGAGGAAAAATCACTGTAGAACAGAGGAGGGAGGTGTAGTGA	CGCAGATC	1451				
OY	4809	GTGCGATTTGCACT-CCAGCCGTGACA-ATGAGCCAAACTCCATCTCA	AAAAAACCAACAC	4866				
Db	1452	GTGCGATTTGCACTCCACCTGTAGACCAANATGAGCCAAACTCCATCTCA	AAAAAACCAACAC	1511				
OY	4867	AAAAAACCCACATCTCTACTCCAGGAGGAGTGGGTACA-GAGTGTGGGCCATCA	GTGCAAG	4925				
Db	1512	AAAAAACCCACCTCTACTCCAGGAGGAGTGGGTACANAGAGTGGGCCATCA	GTGCAAG	1571				
OY	4926	GTGCTGAAGCCACAGAGCTTAAGCGGAGCTG--GAGACCGCGGACACAGATTA	ACAGTGTGT	4983				
Db	1572	GTGCTGAAGCCACAGAGCTTAAGCGGAGCTG--GAGACCGCGGACACAGATTA	ACAGTGTGT	1631				
OY	4984	GAGATTCAGTGTGTAGATTCAGAGCTCCCTGTGCATTTGGTGAACACAGAGGGGCCCCCAAGC	5043					
Db	1632	GAGATTCAGTGTGTAGATTCAGAGCTCCCTGTGCATTTGGTGAACACAGAGGGGCCCCCAAGC	1691					
OY	5044	ACCAGAGATGTGCCCATATCCAGTACACACATCTTCATCCAGAGATGTCTTTCTT	5103					
Db	1692	ACCAGAGATGTGCCCATATCCAGTACACACATCTTCATCCAGAGATGTCTTTCTT	1751					
OY	5104	GGCAGCGCTGGGTAATTAAGACAGAAAGTGACAGTCTTGGGTGTGCTCA	GTCAAGATCCG	5163				
Db	1752	GGCAGCGCTGGGTAATTAAGACAGAAAGTGACAGTCTTGGGTGTGCTCA	GTCAAGATCCG	1811				

```

OY 5164 CCGAGGCA-----GGCCTTGTGGCCTGT-AGAAAAGCTTCAGGCTTAGGCCGGGACGGT 5217
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 1812 CCGAGGNNCAGGNNCTNTGTGGCTGTGNANGAAAAAGTTTCAGGCGCTTAGGCCGGGACGGT 1871
OY 5218 GGC-TCAGAGCCGTAAATCCAGACACTTTGGGGGCGAGGGGGGGGGGATCAGAGGTCAG 5276
    |||      |||||      |||||      |||||      |||||      |||||      |||||
Db 1872 GGCNTACGCCCTGTATATCCAGACACTTTGGGGGCGAGGGGGGATCAGAGGTCAG 1931
OY 5277 GAGATCTGACCATCTGAGCTAACACGGGTGAACCCCGCTCTCTACTTAAATAATACAAAAA 5336
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 1932 GAGATCGTAGCATCTCTGGCTTAACAGGGGAACCCCGCTCTACTTAAATAATACAAAAA 1991
OY 5337 TTGGCCGGGGCATGGTGGCGGGGACCTGTAGTTCACAGTACTTCGGAGGCTGAGGACGAG 5396
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 1992 TTGGCGGGGGCATGTGTGGCGGGGCACCTGTAGTTCAGTACTCTGGAGGCTGAGGACGAG 2051
OY 5397 AATGGCGTGAACCCGAGAGGGACAGATTTGTCATGAGCCGAGATTCGGGCACCTGCACCTCA 5456
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 2052 AATGGCGTGAACCCGAGAGGGACAGATTTGTCATGAGCCGAGATTCGGGCACCTGCACCTCA 2111
OY 5457 GCCTGGCGGACAGAGACACTCATCTGGAAA-AGAAAAAAGAAAGCTTCAGGTCGTAG 5515
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 2112 GCCTGGGGGACAGAGACAGACTCCATCTGGAANAAGAAAAAGAAACGTTCAAGGTCGTAG 2171
OY 5516 CCAGAGGCCACAGGCTGTAAATCTGTCACTTACCATGACCTTGGGGAAGGCACTTCCTCC 5575
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 2172 CCAGAGGCCACAGGCTGTAAATCTGTCACTTACCATGACCTTGGGGAAGGCACTTCCTCC 2231
OY 5576 CTGGGCCAGTTACGGGGTTGGAATCGACTCCAAAGTCCCTTCAGACATTAACGCTGCAT 5635
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 2232 CTGGGCCAGTTACGGGGTTGGAATCGACTCCAAAGTCCCTTCAGACATTAACGCTGCAT 2291
OY 5636 GGTTCCT-AAGATGAGAAGATGGGGCAGTTTCCCTCTCTACACCCAGCCCGTGTCACTT 5694
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 2292 GGTTCNAAGATGAGAAGATGGGGCAGTTTCCCTCTCTACACCCAGCCCGTGTCACTT 2351
OY 5695 CAGGTGAATGACACAGGGAGATCAGGTGCCCAATCCGCAATTCGCAAAAGCCCTGGG 5752
    |||||      |||||      |||||      |||||      |||||      |||||      |||||
Db 2352 CAGGTGAATGACACAGGGAGATCAGGTGCCCAATCCGCAATTCGCAAAAGCCCTGGG 2409

RESULT 15
US-60-466-412-86428/c
; Sequence 86428, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86428
; LENGTH: 46997
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(46997)
; OTHER INFORMATION: n = A,T,C or G
US-60-466-412-86428

```

Query Match	31.4%;	Score 1959.4;	DB 101;	Length 46997;
Best Local Similarity	99.8%;	Pred. No. 6.5e-226;		
Matches 2004: Conservative	0;	Mismatches 1;	Indels 4;	Gaps 4;

QY	4226	GFTGAGACCAAGCCTGGCCACATGGAGAAAGCCCATCTCTTCTAAAAATACAAAATTAG	4285
Db	46997	TTTTTTTCTGAGTCCACACCTGGCCACATGGAGAAAGCCCATCTCTCTTAAAAATACAAAATTAG	46938

OY	4286	CCGGCTCTGGGGGCGAGTGTGGAGCATGCTGTAAATCCAGACTACTCAGAGAGGCTGAGGC	4345
Dd	46937	CCGGCTCTGGGGGCGAGTGTGGAGCATGCTGTAAATCCAGACTACTCAGAGAGGCTGAGGC	46878
OY	4346	AGGAGATTCATTGAACCCAGAGAGGGGGGTGGTCAGTAGAGCCGAGATCGTGCCATTGCA	4405
Dd	46877	AGGAGATTCATTGAACCCAGAGAGGGGGGTGGTCAGTAGAGCCGAGATCGTGCCATTGCA	46818
OY	4406	CTCCACCACATCGAGGCTGGGGCAACAAGAGCCAAACTGTGTCTTAAAAAAAAAAAAAAAA	4465
Dd	46817	CTCCACCACATCGAGGCTGGGGCAACAAGAGCCAAACTGTGTCTT -AAAAAAAAAAAAA	46759
OY	4466	AGTGTCCAGACATATAAAGGTGTGCATATGTTGGCAGGCAACATGTTTAAAGATG	4535
Dd	46758	AGTGTCCAGACATATAAAGGTGTGCATATGTTGGCAGGCAACATGTTTAAAGATG	46699
OY	4526	TGGAGCTCGAGCTTCATGGTCTGTCTTTAAAAACCAACCTCAGCCAGGGGCGAGTGGC	4585
Dd	46698	TGGAGCTCGAGCTTCATGGTCTGTCTTTAAAAACCAACCTCAGCCAGGGGCGAGTGGC	46639
OY	4586	TCATGCTTAAATCCAGACATTTGGGAGGCGGAGCGGGGTGGATCACCCTGAGGTCAAGA	4645
Dd	46638	TCATGCTTAAATCCAGACATTTGGGAGGCGGAGCGGGGTGGATCACCCTGAGGTCAAGA	46579
OY	4646	GTTTCGAGACCAAGCTTGACCAACAATGTTGAATCCACCTCTACTATAAAATACAAAT	4705
Dd	46578	GTTTCGAGACCAAGCTTGACCAACAATGTTGAATCCACCTCTACTATAAAATACAAAT	46519
OY	4706	TAGATGAGCATGGTGGGAGATGCTGTATATCCACCTACTTGGGAGGCTGAGGCGAGAA	4785
Dd	46518	TAGATGAGCATGGTGGGAGATGCTGTATATCCACCTACTTGGGAGGCTGAGGCGAGAA	46459
OY	4766	ATCACTAGAACCAAGGAGGCGGAGGTGTAGTAGCCGAGATCGAGCATTCAGACTCCAG	4835
Dd	46458	ATCACTAGAACCAAGGAGGCGGAGGTGTAGTAGCCGAGATCGAGCATTCAGACTCCAG	46399
OY	4826	CCTGAGCATGAGCGAAACTCCATCTCAAAAAACACAACAAAACCACCTCTCTACTC	4885
Dd	46398	CCTGAGCATGAGCGAAACTCCATCTCAAAAAACACAACAAAACCACCTCTCTACTC	46339
OY	4886	CCAGGGAGCTGGGTACAGAGCTGGGCGCATAGTGAAGGTGGAGCCACAGAGCTAA	4945
Dd	46338	CCAGGGAGCTGGGTACAGAGCTGGGCGCATAGTGAAGGTGGAGCCACAGAGCTAA	46279
OY	4946	GCGGAGACTCAGAGACCGGCGSACCAATAAAGTGTGAGATCAGTGTGTAGATCAGA	5005
Dd	46278	GCGGAGACTCAGAGACCGGCGSACCAATAAAGTGTGAGATCAGTGTGTAGATCAGA	46219
OY	5006	CGTCCCTGCAATTGTGACACCAGGCGGCCCCCAAGACACAGAGATGGCCCATCCAGT	5065
Dd	46218	CGTCCCTGCAATTGTGACACCAGGCGGCCCCCAAGACACAGAGATGGCCCATCCAGT	46159
OY	5066	CACCACTATCCACTTTCATCCAGAGATGTCTTTCTTGGCACGCTGGGGTAAATTAAGA	5125
Dd	46158	CACCACTATCCACTTTCATCCAGAGATGTCTTTCTTGGCACGCTGGGGTAAATTAAGA	46099
OY	5126	CAGAGGTGACAGTCTTGGGTGTGTGACATCAGACTGCCCCAGGAGCCTTGTGGCCTG	5185
Dd	46098	CAGAGGTGACAGTCTTGGGTGTGTGACATCAGACTGCCCCAGGAGCCTTGTGGCCTG	46039
OY	5186	TAGAAAACTTTCAGGCTAGGCCGGGCGACAGGTGGCTACAGCCTGTAAATCCAGACATTTG	5245
Dd	46038	TAGAAAACTTTCAGGCTAGGCCGGGCGACAGGTGGCTACAGCCTGTAAATCCAGACATTTG	45979
OY	5246	GGAGGCCGAGGCGGGTGTGATCAGAGAGTCAAGAGATCGTAGCATCTGTGGTTAACAGGT	5305
Dd	45978	GGAGGCCGAGGCGGGTGTGATCAGAGAGTCAAGAGATCGTAGCATCTGTGGTTAACAGGT	45919
OY	5306	GAACCCCGCTCTACTATAAAATATCAAAAAATTTGGCGCGGCGATGGTGGCGGGGACCTGTA	5365
Dd	45918	GAACCCCGCTCTACTATAAAATATCAAAAAATTTGGCGCGGCGATGGTGGCGGGGACCTGTA	45859
OY	5366	GTTTCAGACTACTCTGGGAGGCTGAGCGAGAGATGGCTGGAACCCGAGAGGCAAGATTG	5425

Db 45858 GTTCAGCTACTCGGAGGCTGAGGACAGAGAAATGGCTGAACCGAGAGGACAGATTG 45799
QY 5426 CAGTGACCCGAGATCGGCGCCACTGCATCCAGCCTGGGGGACAGAGCAAGACTCCATCTG 5485
Db 45798 CAGTGAGCCGAGATCGGCGCCACTGCATCCAGCCTGGGGGACAGAGCAAGACTCCATCTG 45739
QY 5486 GAAAGAGAAAGAAACGTTAGTCTGAGCCAGAGGCCAGGCTGTAATCTGTCACTT 5545
Db 45738 GAAAGAGAAAGAAACGTTAGTCTGAGCCAGAGGCCAGGCTGTAATCTGTCACTT 45679
QY 5546 ACCATGACCTTGGGCAAGGCACTTCCTCCCTGGGCCAGTTCACGGGGTTGGAATCGACT 5605
Db 45678 ACCATGACCTTGGGCAAGGCACTTCCTCCCTGGGCCAGTTCACGGGGTTGGAATCGACT 45619
QY 5606 CCAAGTCCCTTCCAGCATTAACCTGCATGCTCTAAGATGAGAAATGGGGCAGTTTC 5665
Db 45618 CCAAGTCCCTTCCAGCATTAACCTGCATGCTCTAAGATGAGAAATGGGGCAGTTTC 45559
QY 5666 CCGTCTGCACCCAGCCCGCTGTCCACTTCAAGGTGAATGACCAAGGAAGTCACTGTCC 5725
Db 45558 CCGTCTGCACCCAGCCCGCTGTCCACTTCAAGGTGAATGACCAAGGAAGTCACTGTCC 45499
QY 5726 CAATCCGCACTTCCAAAGCCCTTGGGGACCCTAAGTGTGAGGGTGTGCACGAGAGGTG 5785
Db 45498 CAATCCGCACTTCCAAAGCCCTTGGGGACCCTAAGTGTGAGGGTGTGCACGAGAGGTG 45439
QY 5786 AAGGTCAAGTGAAGCCATCGGCGGAGGCTTGGCTTCATTCGGGACAGACATCCGGTT 5845
Db 45438 AAGGTCAAGTGAAGCCATCGGCGGAGGCTTGGCTTCATTCGGGACAGACATCCGGTT 45379
QY 5846 TCCTCTGCTTACCGGATTCAGGGCTTTAGCCGAATGATCATGGGGGCGGGGG 5905
Db 45378 TCCTCTGCTTACCGGATTCAGGGCTTTAGCCGAATGATCATGGGGGCGGGGG 45319
QY 5906 GTTCTGGGGAGTTCCAGCTAATCAACTTGGGACAGAGACCCCTGGAACCTTGCATGG 5965
Db 45318 GTTCTGGGGAGTTCCAGCTAATCAACTTGGGACAGAGACCCCTGGAACCTTGCATGG 45259
QY 5966 TGCTATCCAGTGTGGGGTGGGACAGCAGCAAGCAAGCAATGCTTATCTCAGGTAG 6025
Db 45258 TGCTATCCAGTGTGGGGTGGGACAGCAGCAAGCAAGCAATGCTTATCTCAGGTAG 45199
QY 6026 GGGCTCAGAGGCTCCAGACAGAGCACTCCGAGAGTTTGGGGGTAGGATGGAGC 6085
Db 45198 GGGCTCAGAGGCTCCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGC 45139
QY 6086 AACGAGGCTTCTTTTCTCTTGAATTTGGGGCTTGGGGACAGGCTTGAATTC 6145
Db 45138 AACCA-GCTTCTTTTCTCTTGAATTTGGGGCTTGGGGACAGGCTTGAATTC 45080
QY 6146 CCAAGAGAGAGGGGCAAGGCACT-CCCCCAAGTGTCCAGAGCGAGAGAGGAGAC 6204
Db 45079 CCAAGAGAGAGGGGCAAGGCACTGCCCCGCAAGTGTCCAGAGC-AGAGAGGAGAGC 45021
QY 6205 CCGAGCTCAGCTGCACCTTCCCAAGGC 6233
Db 45020 CCGAGCTCAGCTGCACCTTCCCAAGGC 44992

Search completed: August 17, 2003, 01:29:01
Job time : 11330 secs

THIS PAGE BLANK (USPTO)

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	5532.6	88.7	14381	7	US-60-487-610-19745	Sequence 19745, A
	2	942	15.1	190672	7	US-60-487-610-19215	Sequence 19215, A
	3	860	13.8	1748349	5	US-09-947-914-48	Sequence 48, Appl
	4	767	12.3	30105	7	US-60-487-610-19434	Sequence 19434, A
	5	767	12.3	30105	7	US-60-485-450-11978	Sequence 11978, A
c	6	752	12.1	108815	7	US-60-487-610-19424	Sequence 19424, A
c	7	752	12.1	108815	7	US-60-485-450-11975	Sequence 11975, A
8	751.2	12.0	13831263	5	US-09-947-914-41	Sequence 41, Appl	
9	733.2	11.8	121724	6	US-10-450-826-50	Sequence 50, Appl	
c	10	720.6	11.6	29405	7	US-60-487-610-19466	Sequence 19466, A
c	11	710.4	11.4	13040	7	US-60-485-450-11933	Sequence 11933, A
c	12	710.4	11.4	48853	7	US-60-485-450-11934	Sequence 11934, A
13	693	11.1	40207	7	US-60-487-610-20017	Sequence 20017, A	
14	677.2	10.9	70556	7	US-60-487-610-19299	Sequence 19299, A	
15	668	10.7	185371	6	US-10-470-050-852	Sequence 852, App	
c	16	636.8	10.2	71087	7	US-60-487-610-20097	Sequence 20097, A
c	17	633.4	10.2	60717	7	US-60-487-610-20086	Sequence 20086, A
c	18	633.4	10.2	60717	7	US-60-485-450-12341	Sequence 12341, A
c	19	631	10.1	113231	7	US-60-485-450-12302	Sequence 12302, A
20	626.2	10.0	27027	7	US-60-485-450-12084	Sequence 12084, A	
c	21	607.6	9.7	13831263	5	US-09-947-914-41	Sequence 41, Appl
c	22	602.6	9.7	362800	7	US-60-487-610-19447	Sequence 19447, A
c	23	598.2	9.6	544420	7	US-60-487-610-19233	Sequence 19233, A
24	584.2	9.4	882901	6	US-10-292-798-1393	Sequence 1393, Appl	
c	25	578.2	9.3	8059021	5	US-09-947-914-53	Sequence 53, Appl
26	574.8	9.2	21329	7	US-60-487-610-19363	Sequence 19363, A	

27	573.8	9.2	12333.1	US-60-487-610-19335	A	Sequence 13358, A
28	573.8	9.2	17933.0	US-09-947-914-46	A	Sequence 46, App
29	564.4	9.1	41578.7	US-60-487-610-19754	A	Sequence 19754, A
30	559	9.0	80590.21	US-09-947-914-45	A	Sequence 53, App
31	557.2	8.9	194614.1	US-09-947-914-42	A	Sequence 42, App
32	554	8.8	34944.3	US-09-947-914-47	App	Sequence 47, App
33	547.8	8.8	22083.5	US-60-487-610-19793	A	Sequence 19793, A
34	533.6	8.6	16973.9	US-10-450-826-93	App	Sequence 93, App
35	530	8.5	13253.7	US-60-485-450-12194	A	Sequence 12194, A
36	520.4	8.3	15688.7	US-60-485-450-11874	A	Sequence 11874, A
37	515	8.3	34287.4	US-60-485-450-11986	A	Sequence 11974, A
38	502.8	8.1	32015	US-60-487-610-19671	A	Sequence 19671, A
39	502.8	8.1	32015	US-60-485-450-12118	A	Sequence 12118, A
40	499.6	8.0	74079.7	US-60-487-610-19261	A	Sequence 19261, A
41	498.4	8.0	37715.7	US-60-487-610-19429	A	Sequence 19429, A
42	490	7.8	37637.7	US-60-485-450-11859	A	Sequence 11859, A
43	487.2	7.8	127261.7	US-60-485-450-11857	A	Sequence 11857, A
44	469.4	7.5	47689.7	US-60-485-450-12330	A	Sequence 12330, A
45	465	7.5	94564.7	US-60-487-610-19683	A	Sequence 19683, A

ALIGNMENTS

```

RESULT 1
US-60-487-610-19745
: Sequence 19745, Application us/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19745
: LENGTH: 14381
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-60-487-610-19745

```

Query Match	88.78;	Score 5532.6;	DB 7;	Length 14381;
-------------	--------	---------------	-------	---------------

Matches 5655; Conservative 0; Mismatches 14; Indels 14; Gaps 10;

QY	558	AAAAACAGCTCGTTTATGTCTCCGGGCAATCATATCACTATAGTATATATAGTTGGAA	61
Db	1	AAAAACAGCTCTGTTTATGTCTCCTGGTACATCA---TACTATATATATAGTTGCAA	57
QY	618	ACTCAAGAATCCAGATAGTCAATTTTTTATAGGCTTGTGGGCGGTATAGTCTGTACAAAT	677
Db	58	ACTCAAGAATCCAGATAGTCAATTTTTTATAGGCTTGTGGGCGGTATAGTCTGTACAAAT	11
QY	678	CACCTGCCCCGTCTTTTACAGACAAAAGCAGCTATAAACAATATACATGAATTTTTTT	73
Db	118	CACCTGCCCCGTCTTTTACAGACAAAAGCAGCTATAAACAATATACATGAATTTTTTT	177
QY	738	ATAGACATGAGACATTTGAATTTTCATATGATTTTTTACATTTATATAAATAATCTTTTAA	79
Db	178	ATAGACATGAGACATTTGAATTTTCATATGATTTTTTACATTTATATAAATAATCTTTTAA	23
QY	798	AATTTTCCCCATACCAATTTAAAGTATAAAGCCGGCCA---GGCGGCATCGTACAGCC	85
Db	238	AATTTTCCCCATACCAATTTAAAGTATAAAGCCGGCGCCGCCATGCGTACAGCC	29
QY	855	TGTAAATTCAGACACTTTGGAGGCTGAGAGTGGGCGAGATCACTTGAGATCAACAGTTTCAG	91
Db	298	TGTAAATTCAGACACTTTGGAGGCTGAGAGTGGGCGAGATCACTTGAGATCAACAGTTTCAG	35
QY	915	ACCAGCTGGCCACATAGCAAAACCCCAATTTCTACTATAAATAAATAAATAATGCTGGCC	97

D	b	358	ACGACGCTGGCCAACTATGACAAACCCTTTCTCTATAAAATTAATTAAGTGGGC	417
O	y	975	ATAAGTGTGCACACCTGTGTATCCAGCTACTTGGGAGGCTGAGCGAGAAATCCGCTTGA	103
D	b	418	ATAGTGTGTACACCTGTGTATCCAGCTACTTGGGAGGCTGAGCGAGAAATCCGCTTGA	477
O	y	1035	ACCTGGGAAGCGGAGGTGGCACTGAGCCAACTCATGCCACTGTCCAGCTCCGGGTGA	109
D	b	478	ACCTGGGAAGCGGAGGTGGCACTGAGCCAACTCATGCCACTGTCCAGCTCCGGGTGA	537
O	y	1095	CAGAGTGAAGACTTGCCTCAACGAAAAAAGTGAATACCCTATTCCTAATTAGTGT	115
D	b	538	CAGAATGAGACTTGCCTCAACGAAAAAAGTGAATACCCTATTCCTAATTAGTGT	597
O	y	1155	ACATCAGTGTACATCTAGAGTCTGCGCTACTCTGCTGTGAGGCACTTGGAGTGTAGA	121
D	b	598	ACATCAGTGTACATCTAGAGTCTGCGCTACTCTGCTGTGAGGCACTTGGAGTGTAGA	657
O	y	1215	GTTGCTTGGTCAAGGACATACATTTCCACATTAACTAGACACTACCAAGTTCGCTC	127
D	b	658	GTTGCTTGGTCAAGGACATACATTTCCACATTAACTAGACACTACCAAGTTCGCTC	717
O	y	1275	CAAGGAGG-TTTTTTTTTTACAACTCATACCTCCCCCAGCAAAATGAGTTCCTCA	133
D	b	718	CAAGGAGGTTTTTTTTTTTACAACTCATACCTCCCCCAGCAAAATGAGTTCCTCA	777
O	y	1334	GATCCTTTACAAAGATGCTCTAAGCCAGTACCATATGAAACAGAAAGTGGAGGGGA	139
D	b	778	GATCCTTTACAAAGATGCTCTAAGCCAGTACCATATGAAACAGAAAGTGGAGGGGA	837
O	y	1394	GCTGCGACGCCCTTCTTAAACATGAAAGAAATACCTGTAGAGCCTTCTGGATCTGGAAG	145
D	b	838	GCTGCGACGCCCTTCTTAAACATGAAAGAAATACCTGTAGAGCCTTCTGGATCTGGAAG	897
O	y	1454	ATGAATTAACGGGGGCTCTGAGAGCTGCCCTGTCAATCACTGTACTTGTGAGCCTC	151
D	b	898	ATGAATTAACGGGGGCTCTGAGAGCTGCCCTGTCAATCACTGTACTTGTGAGCCTC	957
O	y	1514	CAGTCCAGCTTCAGGCCCATGTGATGGCCAGTAAATGAGCCCTGACCTCTGTTTG	157
D	b	958	CAGTCCAGCTTCAGGCCCATGTGATGGCCAGTAAATGAGCCCTGACCTCTGTTTG	101
O	y	1574	GTCCTTATTCCT-CCCCATGTGGGGCTGAAGTCTGGATTGAGCCGCTTATTCAAGATGTACA	163
D	b	1017	GTCCTTATTCCTCCCCCATGTGGGGCTGAAGTCTGGATTGAGCCGCTTATTCAAGATGTACA	107
O	y	1633	GCTTCTTGAAGGAAGTACTGTGTACAGAAACAGCAGGGCTTGGCAAGTATCTAAC	169
D	b	1077	GCTTCTTGAAGGAAGTACTGTGTACAGAAACAGCAGGGCTTGGCAAGTATCTAAC	113
O	y	1693	TGCAAAATCTCACTGGGCTCAGCCACACACACTAGTCTGTGATCTTGAACAGTTTTTTAC	173
D	b	1137	TGCAAAATCTCACTGGGCTCAGCCACACACACTAGTCTGTGATCTTGAACAGTTTTTTAC	119
O	y	1753	TTCTCTGAGGCCATCCTTGGCTACCAACACACAGTGTGGTGAAGATGGAATGACG-A	181
D	b	1197	TTCTCTGAGGCCATCCTTGGCTACCAACACACAGTGTGGTGAAGATGGAATGACGAA	125
O	y	1812	AGTCCCTTACACCTGTATATCCACAGACTTTTGGGAGGCCAAGCGGGTGTGATGAGC	187
D	b	1257	AGTCCCTTACACCTGTATATCCACAGACTTTTGGGAGGCCAAGCGGGTGTGATGAGC	131
O	y	1872	CTGAGAGGTGACACATCCGCGCAGTCTCAGAGCCGCTGTTGCTCTCGCGGCTCCTC	193
D	b	1317	CTGAGAGGTGACACATCCGCGCAGTCTCAGAGCCGCTGTTGCTCTCGCGGCTCCTC	137
O	y	1932	TGCTTGGGCTCCACTTCGGTGGCACTTGAAGAGCCCTTCAAGCCACCGCTGCACGTGG	199
D	b	1377	TGCTTGGGCTCCACTTCGGTGGCACTTGAAGAGCCCTTCAAGCCACCGCTGCACGTGG	143
O	y	1992	GAGCCCTTCTGGGCTGGCCAAAGCCAGAGCCGGCTCCCTCAGCTTTCAGAGAGTGTG	205

Db	1437	GAGCCCCCTTCTTGGGCTGGCCAAAGGCCAAGACCAGGCTCCCTCAGCTTGCAAGGAGGTGTG	1496
QY	2052	GAGGAGAGAGGCTCAAGACAGAAACCGGGGCTGGCCAGCGGCTTGGGGGCCAGCTGAGT	2111
Db	1497	GAGGAGAGAGGCTCAAGACAGAAACCGGGGCTGGGGCCAGCTTGAGT	1555
QY	2112	CCGGGTGGGCGTGGGCTTGGCGGGCCCGCACTCGGAGACAGCGGGCCAGCCCTGCCAGGC	2177
Db	1557	CCGGGTGGGCGTGGGCTTGGCGGGCCCGCACTCGGAGACAGCGGGCCAGCCCTGCCAGGC	1611
QY	2172	CCCCGGGCAATGAGAGGCTTAGACACCCGGGGCCAGCGGCTGGGAGGCTGACTGGGTGCC	2233
Db	1617	CCCCGGGCAATGAGAGGCTTAGACACCCGGGGCCAGCGGCTGGGAGGCTGACTGGGTGCC	1676
QY	2232	CAGCAGTGCACAGCCCGCGGGCCTGTGGTCCGCTGCATTTCTACATGGGGCTTAGAGAGCCT	2299
Db	1677	CAGCAGTGCACAGCCCGCGGGCCTGTGGTCCGCTGCATTTCTACATGGGGCTTAGAGAGCCT	1738
QY	2292	TCCCGCGGGGCGAGGGCTGGGGACCTGCAGCCCGCATCTGAGCCTCCCTCCATATGGGC	2355
Db	1737	TCCCGCGGGGCGAGGGCTGGGGACCTGCAGCCCGCATCTGAGCCTCCCTCCATATGGGC	1796
QY	2352	TCCTGTGGGGCCCGAGCCCTCCCGCAGAGCACACACCCCTGCTCCACAGCCCGCAGTCCC	2411
Db	1797	TCCTGTGGGGCCCGAGCCCTCCCGCAGAGCACACACCCCTGCTCCACAGCCCGCAGTCCC	1856
QY	2412	ATCGACCAAGCAAGGGGCTGAGAGAGGGGGGCGACGGGACCGGGGACTGGCAGAGAGCTAC	2477
Db	1857	ATCGACCAAGCAAGGGGCTGAGAGAGGGGGGCGACGGGACCGGGGACTGGGAGAGAGCTAC	1916
QY	2472	CCCTGACAGCCCTGGTGGCGGAATCCACTGGGTGAGAACCACTGGGGCTGCTGATCTGGTGG	2533
Db	1917	CCCTGACAGCCCTGGTGGCGGAATCCACTGGGTGAGAACCACTGGGGCTGCTGATCTGGTGG	1976
QY	2532	AGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCTGAATACACCAATCAGACACCCCTGT	2599
Db	1977	AGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCTGAATACACCAATCAGACACCCCTGT	2038
QY	2592	GTCATAGCTCAGAGGCTGTGAAATGCAACCAATCCACACTGTGATCTAGCTACTCTGATGGG	2655
Db	2037	GTCATAGCTCAGAGGCTGTGAAATGCAACCAATCCACACTGTGATCTAGCTACTCTGATGGG	2096
QY	2652	GCCTTGGAGAACCTTTATGTCTAGCTCAGGGATCTGAATACACCAATCCGCGACCTCTGTA	2711
Db	2097	GCCTTGGAGAACCTTTATGTCTAGCTCAGGGATCTGAATACACCAATCCGCGACCTCTGTA	2156
QY	2712	TCCTAGCTCAGGTTTGTAAACACACACCAATCAGACCCCTGTCTAGCTCAGGGATGTGA	2779
Db	2157	TCCTAGCTCAGGTTTGTAAACACACCAATCAGACCCCTGTCTAGCTCAGGGATGTGA	2218
QY	2772	ATGACACCAATGACAGTCTGTATATCGGTACTTTCAATGGGGATCCGTGTGAAGAGACCAAC	2833
Db	2217	ATGACACCAATGACAGTCTGTATATCGGTACTTTCAATGGGGATCCGTGTGAAGAGACCAAC	2276
QY	2832	CAAAACAGGCTTTGTGTAGACAATAAAGCTTCTACACCTGGGTCCAGGTGGCGTAGAGTCC	2893
Db	2277	CAAAACAGGCTTTGTGTAGACAATAAAGCTTCTACACCTGGGTCCAGGTGGCGTAGAGTCC	2336
QY	2892	GAAAAAGAGCTCAGCCGAAGGGAGATAAAGGTGGGGCCGTTTATAGATTTGGGTAGGTA	2953
Db	2337	GAAAAAGAGCTCAGCCGAAGGGAGATAAAGGTGGGGCCGTTTATAGATTTGGGTAGGTA	2396
QY	2952	AAGGAAAAATTAACATCAAAAGGGGTTTGTCTCTGGGGGGAGAGATGGGGGCTCCAGAG	3011
Db	2397	AAGGAAAAATTAACATCAAAAGGGGTTTGTCTCTGGGGGGAGAGATGGGGGCTCCAGAG	2456
QY	3012	GTGCTCAGTGGGGGTGCTTTTGTAGCCAGATGTAGCCAGAAAAAGCATTTTACAAAGSTA	3071
Db	2457	GTGCTCAGTGGGGGTGCTTTTGTAGCCAGATGTAGCCAGAAAAAGCATTTTACAAAGSTA	2516
QY	3072	ATGTTCATCAATTAAGGCAAGGACCCGGCATTTTACACCTCTTTTGTGTGATGTCTATCA	3131
Db	2517	ATGTTCATCAATTAAGGCAAGGACCCGGCATTTTACACCTCTTTTGTGTGATGTCTATCA	2576

QY	3132	GTAAAGTTGGGGCAGGGCATATTCACCTCTTTGTGATTCCTCAGTTACTTCAGGCCATC	3191	QY	4212	ACCTAAGGTCAGAGGTGTGAGACCAGCCTGGCCAAACATGAGAAAGCCCATCTCTTTAA	4271
Db	2577	GTTAAGTTGGGGCAGGGCATATTCACCTCTTTGTGATTCCTCAGTTACTTCAGGCCATC	2636	Db	3657	ACCTAAGGTCAGAGGTGTGAGACCAGCCTGGCCAAACATGAGAAAGCCCATCTCTTTAA	3716
QY	3192	TGGCGCTATATGTGCAAGTTACAGAGGGATGCGATGGCTTGCGCTCAGAGGCTTGA	3251	QY	4272	AAATACAAATTTAGCGGCTGTGGGGGCACTGTGTGAGACATGCTGTAAATCCAGCTACT	4331
Db	2637	TGGCGCTATATGTGCAAGTTACAGAGGGATGCGATGGCTTGCGCTCAGAGGCTTGA	2636	Db	3717	AAATACAAATTTAGCGGCTGTGGGGGCACTGTGTGAGACATGCTGTAAATCCAGCTACT	3776
QY	3252	CAGCTACTGTGTGGGCGCTTGGAGAAATGTTGTGTGCACACTGTATCTAGTTAATCT	3311	QY	4332	CAGAGGCTGAGGCAGAGAAATCACTTGTGACCCAGAGAGCGCGGCTTGCAGTGAAGCAG	4391
Db	2697	CAGCTACTGTGTGGGCGCTTGGAGAAATGTTGTGTGTGACACTGTATCTAGTTAATCT	2756	Db	3777	CAGAGGCTGAGGCAGAGAAATCACTTGTGACCCAGAGAGCGCGGCTTGCAGTGAAGCAG	3836
QY	3312	AGTGGGACGTGGAGAACCTTGTGTAGCTCAGGGATGTGTAACGCACCAATCAGAGGC	3371	QY	4392	ATCGGCATGTGCATCCACCACTCCAGCCTGGGCAACAAGAGCCAAACCTGTCTAA	4451
Db	2757	AGTGGGACGTGGAGAACCTTGTGTGTAGCTCAGGGATGTGTAACGCACCAATCAGAGGC	2816	Db	3837	ATCGGCATGTGCATCCACCACTCCAGCCTGGGCAACAAGAGCCAAACCTGTCTAA	3895
QY	3372	CTGTCAAAAACAGACACACCTCGGCTCTACCAATCAGCAGGATGTGGTGGGCCAGATPAG	3431	QY	4452	AAAAAAGTGCCTGACATATPAGAGGTGTGCAATGCAATAGTTGCCAGGCA	4511
Db	2817	CTGTCAAAAACAGACACACCTCGGCTCTACCAATCAGCAGGATGTGGTGGGCCAGATPAG	2876	Db	3896	AAAAAAGTGCCTGACATATPAGAGGTGTGCAATGCAATAGTTGCCAGGCA	3955
QY	3432	AGAAATAAAGCAGGCTGCGGAGCCAGCAGTGGCAAGCCGACAGGTCCATTCACAAAT	3491	QY	4512	CATGTTTAAGAAATGTGAGCTCTGCTTCCATGCTGCTTTAAAAACCCACCTCAAGG	4571
Db	2877	AGAAATAAAGCAGGCTGCGGAGCCAGCAGTGGCAAGCCGACAGGTCCATTCACAAAT	2936	Db	3956	CATGTTTAAGAAATGTGAGCTCTGCTTCCATGCTGCTTTAAAAACCCACCTCAAGG	4015
QY	3492	ATGGCAGCTTGTCTTTTGTGCTGTTGCGATAAATCTTGTACGTCGCTGTTTGGGTC	3551	QY	4572	CCAGGTGCAAGTGGCTCATGCTTAAATCCAGCACTTGTGGAGGCGGAGGGGTGATC	4631
Db	2937	ATGGCAGCTTGTCTTTTGTGCTGTTTGTGCGATAAATCTTGTGTACTGTGCTGTTTGGGTC	2996	Db	4016	CCAGGTGCAAGTGGCTCATGCTTAAATCCAGCACTTGTGGAGGCGGAGGGGTGATC	4075
QY	3552	CACACTGCTTTTATGAGCTGTAAACACTACACAGAGGTCTGACGTTCACTCTCGTGAAGC	3611	QY	4632	ACCTGAGGTCAGAGATTGAGACAGCCTGACCAACCAATGTGTGTAATCCACCTCTAC	4691
Db	2997	CACACTGCTTTTATGAGCTGTAAACACTACACAGAGGTCTGACGTTCACTCTCGTGAAGC	3056	Db	4076	ACCTGAGGTCAGAGATTGAGACAGCCTGACCAACCAATGTGTGTAATCCACCTCTAC	4135
QY	3612	CACTAACACACAGAGCCACCGGAGAGAAATGAACACTCCGGCGCGCTGCTTAAAGC	3671	QY	4692	TAAAAATCAAAATTAATGATGACATGTGTGTGATGCTGTATATCCACCTACTTTGGAG	4751
Db	3057	CACTAACACACAGAGCCACCGGAGAGAAATGAACACTCCGGCGCGCTGCTTAAAGC	3116	Db	4136	TAAAAATCAAAATTAATGATGACATGTGTGTGATGCTGTATATCCACCTACTTTGGAG	4195
QY	3672	TATTAACACTACCGGAGAGTCTGACCTTCACTCACTCAGCAGCAGAGACAGCAACCA	3731	QY	4752	GCTGAGGAGAGAAATCACTGAACCAAGAGGCGGAGGTTGTATGTAGCCGAGATGCTG	4811
Db	3117	TATTAACACTACCGGAGAGTCTGACCTTCACTCACTCAGCAGCAGAGACAGCAACCA	3176	Db	4196	GCTGAGGAGAGAAATCACTGAACCAAGAGGCGGAGGTTGTATGTAGCCGAGATGCTG	4255
QY	3732	CCAGAGAGAAAGAACTCGGAACACATCTGAACATCAGAGAGAACAACTCCAGATGCACC	3791	QY	4812	CCATTGCACTCAGCCTGAGCAATGAGCGAAACTTCATCTCAAAAAACAACAAACAAA	4871
Db	3177	CCAGAGAGAAAGAACTCGGAACACATCTGAACATCAGAGAGAACAACTCCAGATGCACC	3236	Db	4256	CCATTGCACTCAGCCTGAGCAATGAGCGAAACTTCATCTCAAAAAACAACAAACAAA	4315
QY	3792	ACCTTAAGAGCTGTAAACACTACAGAGGTCCGCGGCTTCTTGAAGTCAATGAG	3851	QY	4872	CCCACTCTACTCCCAAGGAGCTGGGTGATGACAGACTGGGCCACATCAATGCAAGTGTG	4931
Db	3237	ACCTTAAGAGCTGTAAACACTACAGAGGTCCGCGGCTTCTTGAAGTCAATGAG	3296	Db	4316	CCCACTCTACTCCCAAGGAGCTGGGTGATGACAGACTGGGCCACATCAATGCAAGTGTG	4375
QY	3852	ACCAAGCACTACAGAGTTTGGACACAGCCAGAGAGTTTGAATCAGGCTGGGCAACAT	3911	QY	4932	AGCCACAGAGCTTAAGGCGGAGCTGAGAGACCGGAGACAGATTAACAGTGTGAGATCAG	4991
Db	3297	ACCAAGCACTACAGAGTTTGGACACAGCCAGAGAGTTTGAATCAGGCTGGGCAACAT	3356	Db	4376	AGCCACAGAGCTTAAGGCGGAGCTGAGAGACCGGAGACAGATTAACAGTGTGAGATCAG	4435
QY	3912	GATGAATATGCCCTCTCTGCAAAAAAAATTTACAAAAATTTGGCGGAGCATGTGTGT	3971	QY	4992	TGTGTGATGATGAGAGTCCCTGCAATGTGTGATGACCAACAGGGGGGCCCAACACACAGAG	5051
Db	3357	GATGAATATGCCCTCTCTGCAAAAAAAATTTACAAAAATTTGGCGGAGCATGTGTGT	3416	Db	4436	TGTGTGATGATGAGAGTCCCTGCAATGTGTGATGACCAACAGGGGGGCCCAACACAGAG	4495
QY	3972	CCGTGCTGTGTGTGCTGCAAGCTACGCGGAGGTTAAAGTGGAGATTCGCTTGAGCTGGGA	4031	QY	5052	TGGCGCCATTCAGATCACCACATTCATCTCATCAGAGATGTCTGTTTCTTGGCAGCT	5111
Db	3417	CCGTGCTGTGTGTGCTGCAAGCTACGCGGAGGTTAAAGTGGAGATTCGCTTGAGCTGGGA	3476	Db	4496	TGGCGCCATTCAGATCACCACATTCATCTCATCAGAGATGTCTGTTTCTTGGCAGCT	4555
QY	4032	GGTGAAGACTGAGTGTGATGTATACACAGCCCTCAGGCTGGGGGACAGACTGA	4091	QY	5112	GGGGTAAATTTAGCAGAGAGTGAAGCTTGGGTGTGTGTGATGATCAGACTGCCAGGCA	5171
Db	3477	GGTGAAGACTGAGTGTGATGTATACACAGCCCTCAGGCTGGGGGACAGACTGA	3536	Db	4556	GGGGTAAATTTAGCAGAGAGTGAAGCTTGGGTGTGTGTGATGATCAGACTGCCAGGCA	4615
QY	4092	GACCTGTTTCCCTCGCAAAAAAATTTGACAAAAATGTATATAAGAGTGTGCTATATGG	4151	QY	5172	GGCCTGTGCTGTAGAAAAAGCTTACAGGCTTACGCGGAGCAGCGGTGCTACGCTGTA	5231
Db	3537	GACCTGTTTCCCTCGCAAAAAAATTTGACAAAAATGTATATAAGAGTGTGCTATATGG	3596	Db	4616	GGCCTGTGCTGTAGAAAAAGCTTACAGGCTTACGCGGAGCAGCGGTGCTACGCTGTA	4675
QY	4152	CTAGGCGCAGTGGCTCATGCTGTATATCCAGCACTTGGAGACCGAGCGCGGCTC	4211	QY	5232	ATCCAGCAGCTTTTGGAGGCGGAGCGGCTGTGATCAGAGTGCAGAGATGTGACATC	5291
Db	3597	CTAGGCGCAGTGGCTCATGCTGTATATCCAGCACTTGGAGACCGAGCGCGGCTC	3656	Db	4676	ATCCAGCAGCTTTTGGAGGCGGAGCGGCTGTGATCAGAGTGCAGAGATGTGACATC	4735
				QY	5292	CTGGCTTAACACGGTGAAGAACCCCGTCTCTACTTAAAAATTAACAAAAATTTGGCGGCGATGCT	5351

```
Db 4736 CTGGCTAACACGCTGTAACCCCTCTCTACTTAAATAATACAAAATTTGGCGGCAATGCT 4795
OY 5352 GGGGGGACACTGTAGTTCAGCTACTCGGAGGCTGAGGAGAGAGATGGCTGAACCCG 5411
Db 4796 GGGGGGACACTGTAGTTCAGCTACTCGGAGGCTGAGGAGAGATGGCTGAACCCG 4855
OY 5412 AGAGGAGAGATTGGCAGTGAAGCCAGATGCGCCACTGCACCTCCAGCTTGGGAGACAG 5471
Db 4856 AGAGGAGAGATTGGCAGTGAAGCCAGATGCGCCACTGCACCTCCAGCTTGGGAGACAG 4915
OY 5472 CAAGACTCATCTGGAAAAAGAAAAAGAAAAAGTTGAGTGTGAGCCAGAGGCCAGGCTG 5531
Db 4916 CAAGACTCATCTGGAAAAAGAAAAAGAAAAAGTTGAGTGTGAGCCAGAGGCCAGGCTG 4975
OY 5532 TAATCTGTCACTTACCATGACCTTGGGCAAGGCACTTCCCTCCCTGGCCAGTTGACGG 5591
Db 4976 TAATCTGTCACTTACCATGACCTTGGGCAAGGCACTTCCCTCCCTGGCCAGTTGACGG 5035
OY 5592 GGTGGCAATCGACTCCAGAGTCCCTTCAGACATTAACGCTGCACTGGTTCTAAGATGAA 5651
Db 5036 GGTGGCAATCGACTCCAGAGTCCCTTCAGACATTAACGCTGCACTGGTTCTAAGATGAA 5095
OY 5652 GATGGGGCAATTCCTCCCTCTCTCAGCCAGCCGCTGTCACCTTCAAGGTGAATGACACAG 5711
Db 5096 GATGGGGCAATTCCTCCCTCTCTCAGCCAGCCGCTGTCACCTTCAAGGTGAATGACACAG 5155
OY 5712 GAAATGACGTGTCCCAATCCCGAGTTCCAAAAGCCCTTGGGGAACCTTACTGTCAAGGTCG 5771
Db 5156 GAAATGACGTGTCCCAATCCCGAGTTCCAAAAGCCCTTGGGGAACCTTACTGTCAAGGTCG 5215
OY 5772 TGCACAGAGAGTGAAGGTGACAGTGAAGCAATGCTCCAGAGGCTTGGCTTATTCGGG 5831
Db 5216 TGCACAGAGAGTGAAGGTGACAGTGAAGCAATGCTCCAGAGGCTTGGCTTATTCGGG 5275
OY 5832 ACAGACATCGGCTTCTCTGAGCTTACCGGGATTCAGGGGCTTACGGCAATGAGTCA 5891
Db 5276 ACAGACATCGGCTTCTCTGAGCTTACCGGGATTCAGGGGCTTACGGCAATGAGTCA 5335
OY 5892 TGGGGGGCGGGGGGTTTCTGGGGGAGTTCACAGCTAATCACTTGGGAGAGACAGCT 5951
Db 5336 TGGGGGGCGGGGGGTTTCTGGGGGAGTTCACAGCTAATCACTTGGGAGAGACAGCT 5395
OY 5952 GGAACCTTGGAGTGTGCTCATCAAGTGTGGGTGGGACAGACAGCAATGTC 6011
Db 5396 GGAACCTTGGAGTGTGCTCATCAAGTGTGGGTGGGACAGACAGCAATGTC 5455
OY 6012 CTATCTCAGGTAGGGGCTCAGAGAGTCTCCAGACAGGCAAGCTCCGGAGATTGGGG 6071
Db 5456 CTATCTCAGGTAGGGGCTCAGAGAGTCTCCAGACAGGCAAGCTCCGGAGATTGGGG 5515
OY 6072 GTAGGAATGGGACAACAGGCTTCTTTTCTCTTGAATTTGGGGGCTTGGGGGA 6131
Db 5516 GTAGGAATGGGACAACAGGCTTCTTTTCTCTTGAATTTGGGGGCTTGGGGGA 5574
OY 6132 CAGGCTTGAAGATCCCAAGAGAGAGGAGGCAAGAGACAT-CCCCCAAGTCTGCCAGAG 6190
Db 5575 CAGGCTTGAAGATCCCAAGAGAGAGGAGGCAAGAGACATGCCCCCAAGTCTGCCAGAG 5634
OY 6191 CGAGAGAGGAGAGACCCGACTGAGTCCACTCCCAAGGC 6233
Db 5635 C-AGAGAGGAGAGACCCGACTGAGTCCACTCCCAAGGC 5676
```

RESULT 2
US-60-487-610-19215
: Sequence 19215, Application us/60487610

: GENERAL INFORMATION:
: APPLICANT: CARBIL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LAYER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF

```
: FILE REFERENCE: CU001469  
: CURRENT APPLICATION NUMBER: US/60/487, 610  
: CURRENT FILING DATE: 2003-07-17  
: NUMBER OF SEQ ID NOS: 97101  
: SOFTWARE: FASTSEQ for Windows Version 4.0  
: SEQ ID NO 19215  
: LENGTH: 190672  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: misc.feature  
: LOCATION: (1)..(190672)  
: OTHER INFORMATION: n - A,T,C or G, or insertion/deletion polymorphism (see Table  
US-60-487-610-19215  
  
Query Match 15.1%; Score 942; DB 7; Length 190672;  
Best Local Similarity 73.2%; Pred. No. 9,4e-144;  
Matches 1473; Conservative 1; Mismatches 341; Indels 197; Gaps 13;  
  
OY 1873 TGAAGGTGACAGCATGCGGCGAGTCTCAGACGCTCGTTCGCTCGGCGCTCTCT 1932  
Db 178820 TGAAGGTGAGAGCGCTGCGAGTCTCAGAGCCCTCGCTCGGCGACTGCGCT 178879  
OY 1933 GCGTGGGCTCCCACTTCGCGGACCTTGAAGAGCCCTTCAGCCACCGCTGAGTGGG 1992  
Db 178880 GCGTGGGCTCTACTTGGCGGCAATTTGAGAGACCTTTCAGCCGCCACTGACTGGG 178939  
OY 1993 AGCCCTTCTTGGGCTGCGCCAGAGCCAGCCGCTCCCTCAGCTTGCAGAGAGTGTGG 2052  
Db 178940 AGCCCTTCTTGGGCTGCGCCAGAGCCAGCCAGCTCCCTCAGCTTGCAGAGAGTGTGG 178999  
OY 2053 AGGAGAGGCTCAAGCAGAGAACCGGGGCTGCGACCGGCGCTTGGCGGCAAGTGA 2112  
Db 179000 AGGAGAGGCTCAAGCAGAGAACCGGGGCTGCGACCGGCGCTTGGCGGCAAGTGA 179059  
OY 2113 CGGTTGGGCGTGGGCTTGGGGG-CCCGGACTCGAGAGCGGGGCGAGCGCTGCGAGG 2171  
Db 179060 CAGGTAGGCTGAGGCTTGGGGGCGGGGCGCGGACTGCGGAGAGCCAGGCGCTG-CTGGC 179118  
OY 2172 CCCGGCAATAGAGCTTGAACCCGCGGAGCGGCTGCGGAGGCTGACTGAGTGGCC 2231  
Db 179119 CCCGGCAATAGAGCTTGAACCCGCGGAGCGGCTGCGGAGGCTGACTGAGTGGCC 179178  
OY 2232 CAGCAGTGCAGCCCGCGGCGCTGCTGCTGATTTCTACCTGGGCTTGAAGACCT 2291  
Db 179179 CAGCAGTGCAGCCCGCGGCGCTGCTGCTGATTTCTACCTGGGCTTGAAGACCT 179234  
OY 2292 TCCCGGGGCGAGGCGTGGGAGCTGAGCGCGCAATGCTGAGCGCTGCC-CTGCCA 2346  
Db 179235 TCCCGGGGCGAGGCGTGGGAGCTGAGCGCGCAATGCTGAGCGCTGCC-CTGCCA 179294  
OY 2347 TGGGCTCTGTGTGGGCGCGAGCTCCCGAGAGCAACACCCCTGCTCCAGACGCGCA 2406  
Db 179295 TGGGCTCTGTGTGGGCGCGAGCTCCCGAGAGCAACACCCCTGCTCCAGACGCGCA 179354  
OY 2407 GTCCCATCGACACGCAAGGCTGAGAGTGGCGGCGAGCGCAACCGGCACTGGAGCA 2466  
Db 179355 GTCCCATCGACACGCAAGGCTGAGAGTGGCGGCGAGCGCAACCGGCACTGGAGCA 179413  
OY 2467 GCTACCCCTGACACCCCTGGTGGGGAATCCAGTGGGTGAAGGCAAGCTGGGGTCTGAGTCT 2526  
Db 179414 GCTACCCCTGACACCCCTGGTGGGGAATCCAGTGGGTGAAGGCAAGCTGGGGTCTGAGTCT 179473  
OY 2527 GGTGGAGACTTGGAGAACCTTATGTCTAGCTCAGGAGTGTAAATACAAATACAGCA 2586  
Db 179474 GGTGGAGACTTGGAGAGTGTATGTCTAGCTCAGGAGTGTAAATACAAATACAGCA 179533  
OY 2587 CCTGTGTAGCTCAGGCTGTGAATGCAACCAATCCACTGTGTACTGTACTGTG 2646  
Db 179534 CCTGTGTAGCTCAGGCTGTGAATGCAACCAATCCACTGTGTACTGTACTGTG 179593  
OY 2647 ATGGGGCTTGGAGAACCTTATGTAGTCAAGGATGTAAATACCAATCGGCACT 2706  
Db 179593 ATGGGGCTTGGAGAACCTTATGTAGTCAAGGATGTAAATACCAATCGGCACT 179646
```

```
Db 179594 GTGGGCGCTTGAGAACCTTTATGCTAGCTCAGGATGTAAACATACAGTACGACT 179653
Qy 2707 CTGTATAGCTCAAGTTTGTAAACACCAATCAGACCTGTGTACTACAGGTA 2766
Db 179654 CTGTGTAGCTCAGGGTGTGTAGTGCACCAATGACACTGTGTACTACTGTCTGG 179713
Qy 2767 TGTAAATGACCACTCAGCTGTGTATCTGTACTACTTCAATGGGCACTCGTGAAG 2826
Db 179714 TGGGGCCTTGAAAAACCTTTATGTCTAGCTCAGGATTTAAATATACCAATCCGAC 179773
Qy 2827 ACCACCAAAACAGGCTTTGTGTAGCAATAAAGCTTCAATCCTGGGTGACAGTGGGCTG 2886
Db 179774 TGTATCTAGCTCAAGTTGTAAACAC----- 179800
Qy 2887 AGTCCGAAAAGAGTACGCAAGGAGATTAAGGTGGGCGCTTTTATAGATTTGGCT 2946
Db 179801 -----ACCAATCAGACCCCTGTGTACTCTCAAGGTT 179832
Qy 2947 AGTAAAGAAAATTTACAGTCAAAAGGGGTTGTCTCTGGCGGACAGAGTGGGGGTC 3006
Db 179833 TGTAGTGCACCAATCCACACTCTGTACTAGCTCTCTGGTGG----- 179876
Qy 3007 GCAAGTGTCTCAGTGGGGGCTTTTGTAGCCAGGATGACCAGAAAAGACTTTCACA 3066
Db 179877 -----GGCCTTGGAAAACCTTATGTCT 179899
Qy 3067 AGTAAATGTATCATATTAAGCAAGACCCGCAATTAACCTCTTTGTGTGTGAATGT 3126
Db 179900 AGCTCAGGATTTGAATATATACCAATGGGCACTGTATCTAGCTCAAGGTTTGAACA 179959
Qy 3127 CATCAGTTAAAGTTGGGCGAGGCAATATCACTTCTTGTATCTTCACTTACTTACG 3186
Db 179960 CACCAATCA-----GCACCTGTGTAGTCTCAG 179989
Qy 3187 CCAATCTGGGCTATATGTCTCAGTTACAGGGATGCGATGGCTGGCTTCAGAG 3246
Db 179990 GTTGTGTAGTCCACCAATCA-----CACCT 180016
Qy 3247 CTGACAGCTACTCTGTGGGGGCTTGAGAAATGTTGTGTGACACTGTATCTATCT 3306
Db 180017 GTATCTAGCTCTCTGGGGGCTTGAGAAACCTTGTGTGTATCTGTATCT-----T 180072
Qy 3307 AATCTAGTGGGAGCTGAGAACTTGTGTCTAGCTCAGGATTTGAAGCAACAATC 3366
Db 180073 AATCTAGTGGGAGCTGAGAACTTGTGTCTAGCTCAGGATTTGAAGCAACAATC 180132
Qy 3367 AGCCGCTGTCAAAACAGACACTGTGGCTTACCAATCAGAGATGGGTGGGCGCAG 3426
Db 180133 AGCACTGTGTCAAAACAGGCGCTGTACCAATCAGAGATGGGTGGGCGCAG 180192
Qy 3427 ATAGAGATTAAGAGCGGCTGGCGGAGCCAGAGTGGCAAGCGCCATCCATCC 3486
Db 180193 ATAGAGATTAAGAGCGGCTGGCGGAGCCAGAGTGGCAAGCGCCATCCATCC 180252
Qy 3487 ACAATATGCGAGCTTGTCTTGTCTGTGTGCGTAATCTGTACTGTCTGCTTTT 3546
Db 180253 ACAATGCGAGCTTGTCTTGTCTGTGTGCGTAATCTGTACTGTCTGCTTCTC--TCT 180309
Qy 3547 GGTGTACACTGTCTTTATGAGCTGTAACTCACTCAACGAAAGTCTGCACTCTCT 3606
Db 180310 GGTGTACACTGTCTTTATGAGCTGTAACTCACTCAACGAAAGTCTGCACTCTCT 180369
Qy 3607 GAAGGCACTAGACAGAGCGCCAGCCGAGAGTAATGAACACTCCGGCGGCTGCTTA 3666
Db 180370 GAAGGCACTAGACAGAGCGCCAGCCGAGAGTAATGAACACTCCGGCGGCTGCTTA 180429
Qy 3667 AGAGCTATTAACACTCAGCGCAAGGTCTGAGCTTCACTCTCAGCGGAGAGACAGCA 3726
Db 180430 AGAGCTATTAACACTCAGCGC--AAGGTCTGAGCTTCACTCTCTGAGTACGCGAGACAGCA 180488
Qy 3727 ACCCAGCAGAGAGAAACTGCAACATCTGAATCAGAGAGAAACAACTCCAGAT 3786
Db 180489 ACCCAGCAGAGAGAAACTGCAACATCTGAATCAGAGAGAGACAGACTCCAGAC 180548
```

```
Qy 3787 GCACCACTTAAGAGCTGTAAACACTGAGAGGTCGGGCTCTCTCTTGAAGTCA 3846
Db 180549 GCGCCACCTTAAGAGCTGTAAACACTGAGAGGTCGGGCTCTCTCTTGAAGTCA 180608
Qy 3847 GTGAGACCAACACTCAGCAGGATTTGAGACACA 3878
Db 180609 GTGAGACCAACACTCAGCAGGATTTGAGACACA 180640

RESULT 3
US-09-947-914-48/c
; Sequence 48, Application us/09947914
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON
; FILE REFERENCE: C1001298
; CURRENT APPLICATION NUMBER: US/09/947,914
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 48
; LENGTH: 1748349
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1748349)
; OTHER INFORMATION: n = A,T,C or G
US-09-947-914-48

Query Match      13.8%  Score 860; DB 5; Length 1748349;
Best Local Similarity 56.6%; Pred. No. 2,1e-130; Inbels 404; Gaps 16;
Matches 2186; Conservative 0; Mismatches 1270;

Qy 71 AAATATGCGCGGCGATGTGCTCAGCTCTGTAAATCCCTGAACTTTGGGACATCAAGC 130
Db 1132483 AGAATGAGACTGGACACAGTGGCTCAGCGCTGTATATCCAGACTTTGGAGCGTGAGGC 1132424
Qy 131 AAGTGATCACTTGAAGTGCAGAGATTCAGAGTACCTTGGCCAACTGTGAACCTTAT 190
Db 1132423 GGGCGGTCACCTTGAAGGCGCAGAGATTTAGACCACTGGGCCCAATGTGTAACCTGT 1132364
Qy 191 CTCACCTA-----AAAAATACAAAATTTAGCCAGGATGGTGGCAGCACTGTATATCCG 246
Db 1132363 CTACTACTTATTAATAATACAGATTTAGCCAGGCGTGTGGCAGCGCTGTACTTCCA 1132304
Qy 247 GCTACTCAGAGAGCTGAGGAGAGAAATCACTTGAATCCAGAGGCGGAGGTTGCAGTGA 306
Db 1132303 GCTACTTGGAGGCTGAGGCGCAAGAACCGCTTGAACCAAGAGGAGGTTGCAGTGA 1132244
Qy 307 GCTGATACACACACTGCACTCAGCTGGGTGACAGAGCAAGACTCTATCTCAAAAA 366
Db 1132243 GCCCGATCTGTCCCTCTCAGCTCAGCTAGTATACAGAGTGAAGCTTTGCCAAAAATA 1132184
Qy 367 AATAAATAATTAATAAATTTAGCCAGGATGGTATGACACCTGTAGCTCAGCTATC 426
Db 1132183 AATAAATAATTAATAAATTTAGCCAGGATGGCTATTTAAAAAATGAGTTTCAATTTAGACG 1132124
Qy 427 AGGAGCTGAGTGGAGAGATCACTTGAACCTGGGCGAGTCAAGGCTACAGTACCAAG 486
Db 1132123 TACTAAAGAAAGATGTAGAGCTTGTCTTTTGGGTGTGAAGAAAGATCACTTTC 1132064
Qy 487 ATCATGCACTTACCTCAGCGCTGGGCAACAGAGACAGACCTGTCTTAATAAATAAT 546
Db 1132063 TCTTTCACTTTAAGTCAAAACAGATATAAAGSATAACAGCAATATGTCTCAACCCA 1132004
Qy 547 AATATATAAGAAAAAAGAGCTGTGTATGTCTCTG---GTCAATCATCTACTATG 603
Db 1132003 GCTGGGCTGGGGAAGCTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTCTAG 1131944
Qy 604 TATATAGTTCAAACTCAAAAGATCAGATAGTCAATTTTATTTTATTTTATTTTATTTT 663
```

Db 1131943 GTGTAAATATCCCAATTAGCCCAATTTCAAGCTACCAAGATTATATGACCAAGCTGAC 1131884
QY 664 GTCTGTGACATCACTGTGCCCTGCTTTTCAGACAAAAGCAGCTATTAACAATAC 723
Db 1131883 AATTCCTGAAAATTTTCATTAATTTGGCTCCCTGGACACACACTGGAGTAGCAAGAG 1131824
QY 724 TACATCAATTTTTTATAGACATCGAGATTTGAATTTTCATATGATTTTACATT---TAT 780
Db 1131823 GTGAGTGGCTTAAGATTTCTTTCATGCCCCGTCTTTATTTTGGTTGTAACCTCATTTGT 1131764
QY 781 AAAATATCTTTTAA-----AATTTTCCCTAACCACTTTTAAAGTGAAGAGCGCG 834
Db 1131763 TAAATTAACCACTAAAAAGTGAATTTTCACTGATATATCACTTTAAACAGCTTTT 1131704
QY 835 CAGCGCGCATGCTGACAGCCTGTAAATTCAGACATTGGGAGGCTGAGGTGGGAGATCA 894
Db 1131703 AAATATGTTTCATCTCTAGTGTATTAACACTCAGGTTATTAATAATATTCGATTA 1131644
QY 895 CTGAGATCAACAGTTTCAGACCAAGCCTGGCCACATAGCAAAACCCCACTTTTACTAAA 954
Db 1131643 TATAGAAATATTTTGAAGAAATATTTTAAAGTGAATATGTTGACAGATGACCCAA 1131584
QY 955 AATTAATAATTAAGCTGGGCAATAGTGTGCACACCTGTGATCCAGCTACTGGAGGCT 1014
Db 1131583 TTTGCAATATRAAAA---TGACTTGAAGGATATACCTCAAAATGTGATATTTA-TAT 1131528
QY 1015 GAGGACGAGAAATCGCTTAACCTGGGAAAGCGGAGGTGCAGTGAAGCAATCATGCCA 1074
Db 1131527 GTAAAGATATATGCTTATTTCTTTCTTTGCTTTTCTATTTTTCAGATTTTGGA 1131468
QY 1075 CTGCACTCCAGCCTGGGTGACAGAGTGAAGACTTCGTCTCAAGCAAAAAAAGTAA 1134
Db 1131467 ATGTTTACAACTGGGAAAAAAATTAAGCCAAATTAATATATATGTTTGAAAAAATATA 1131408
QY 1135 AGCAATCTCAATTCAGTGTACATCAGTGTACATCAAGTGTGCTGCTGCT----- 1185
Db 1131407 TAGCAATTTAGATATATGTATAGCTGCTTACAGAGATGAATCAGATTGACTCTATTTAA 1131348
QY 1186 ----CCTGCTGTGAGGCACTACCTGAAAGTAGAGTGTGCTGTGCACAGGACATACAT 1240
Db 1131347 TAAAGCTAAATCTTTATCCCTTATTTTATGTATGTTTACTGCTTTCAAGTAGTGTCA 1131288
QY 1241 TTCCACATTTACTAGACACTACCAAGTTGCCATCCAAAGAGTTTTTTTTTTTACAATCTA 1300
Db 1131287 ATGCATTTATCTAATTTGATCATCTTGAAGCAGGAAAGACAGGTTTATTAATCTTCATTA 1131228
QY 1301 CACTCCCCCAGCAACAATGAGAGTACTCCAGATCTTTTACAAAGAGCTGTACGCC 1360
Db 1131227 TACAGATGCAAAAACGATGATTAATGATTTGCCCTGATCAGATGGCTAATTAAGCAG 1131168
QY 1361 AGTACCAATGAAAACAGAAAGTGGGAGGGAAGTGCAGGCCCTTCTTAACCATGAAG 1420
Db 1131167 TTAAGCTGGAGCTTTGACCCTGGATTTTGTGTTGTTACCCCAAGACCCCTCTCAAAA 1131108
QY 1421 AATACCTGTAGACCTTCTGATGCTGGAAGGATTAATACGGGGGTCTCTGGAGCCTG 1480
Db 1131107 CAGCTGGGGGAAGCTTCTCTCATGTGCTCTTGTTAAGAGTTCTTACTGAAAACTTA 1131048
QY 1481 CCCCCGTGACATCTGTGACTTCTGAGCCTCCAGCTCCAGTCTCA--GCCCACTGTGTC 1538
Db 1131047 GATCTGATTTCTGCAACGGGTCCCTCTCTGCTCTTGAAGCAATTTAATGTCCTATCTTG 1130988
QY 1539 ATGGCAGTGAATATAGCCCTCACTCTCTGTTTGTCTTATTTCTCCCATGTGGGGCT 1598
Db 1130987 ACTAGAAATCATCGGGTAGACACATGCATTCAGGCAATGCATACACAGATGTGC 1130928
QY 1599 GAAGTGTGATTTGAGCCGTTAATTAAGATGTACAGCTTCTTGACAGAAAGTGTGTCA 1658
Db 1130927 CTTCAGTGGACTTTAGCTTGAATATGATGAGCTGAGAGAACTTGCACAAAGACA 1130868
QY 1659 -----CAGAAACAGCAGGGGCTTGGCAAGATGATCTTAAGTCAAAATCTTA 1703
Db 1130867 GCACCCACACTCTGGGATGAAGAAACAGGACAAATGTTCTTACAAACATTCAGTTACACAA 1130808

QY 1704 CTTGGCTCAAGCCACAGCTAGTTCTGTGATCTTGAACAAAGTTTTTCACTTCTGTAGGC 1763
Db 1130807 TCTTTAAAGGCGCATACACAGGTTTGTGAATCATGTTTCCCTATCTCTCCCTTAAGAACT 1130748
QY 1764 CATCCCTTGGCTTCAAAACACACAGCTTGTGTTGACAGATGAATATGACGAAGTCCCTTAC 1823
Db 1130747 AGGAGTGGCTTTTATAGAAATGCGCAAGAGATTAATCTTGGGAGATCTGTCTAAG 1130688
QY 1824 CTGTAAATCCAGACTTTTGGAGAGCCAGGCGGGTGGATGTGCTTGAAGCTTGAAGGTGAC 1883
Db 1130687 CTGTGCTGGGTCCCGGTGTGTTGGCTTGGGACATCCGCTCTG---CTGAAGGTGAC 1130631
QY 1884 AGCATCCGGCAGTCTCTACAGCCCTTCTGCTGTGCGTGTGCGGCTCTCTGCTGAGCTCC 1943
Db 1130630 AGCCTGCTGCACTCTCAGAGCCCTTCTGCTGTGCGGACCTCCCTGCTGCTGAGCTCC 1130571
QY 1944 CACTTGGGTGGCACTTGAAGAGCCCTTCAAGCCACCGCTGCACTGTGGGAGCCCTTTCT 2003
Db 1130570 CACTTGTGTGCACTGTGAGAGAGCCCTTCAAGCCCTTCAAGCTGTGGGAGCCCTTTCT 1130511
QY 2004 GGGCTGGCCAAAGCCAGAGCCGCTCTCTACGCTTGCAGGAGGTGTGAAGGAGAGCT 2063
Db 1130510 GGGCTGGCCAAAGCTTGAAGCCCTCTCCGACCTTGCAGGAGGTGTGAAGGAGAGCTA 1130451
QY 2064 CAAGCAGAAACCGGGCTGTGCACAGGCGCTTGTGCGGCGCAGCTGGAATCCGGTGGGCT 2123
Db 1130450 CGAGCGGAAACTGGGCTGTGCTGTGCGCTTGTGCGGCGCAGCTGGAATCCGGTGGGCT 1130391
QY 2124 GGGCTGTGGGGGCGCCGCACTGGAGACAGCGGGCCAGCCCTGCGAGGCCCGGGCAATGA 2183
Db 1130390 GGGCTGTAGTGGGCGCCGCACTTGAAGCAGCAACAGCCCTG--CTGGCCCGGGCAATGA 1130332
QY 2184 GAGCTTTAGACCCCGGCGCCAGCGGCTGCGGAGGGTGTACTGGGTGCCCGCAGAGTGCAG 2243
Db 1130331 GGGACTTATGACCTTGGGCGCAGTGGCTTGCAGAGGCTTACTGAGTCCCGCAGCATGCCG 1130272
QY 2244 CCGCGCGGCGTGTGCTGTGCTGATTTCTACTTGGGCTTTAGCAGGCTTCCCGGGGGCA 2303
Db 1130271 CCCAGCGGCGCTGT----GCTGATTTCTCGCCAGGCGCTTACTGCTTCCCGGGGGCA 1130216
QY 2304 GGGCTGGGAGCTGTGACGCCCGCATGCTGTAGGCTCCC-----CTCATAGGGCTCTGTG 2358
Db 1130215 GGGCTGAGGACCTGTGACGCCCGCATGCTGTAGGCTCCCACCCACTCATAGGGCTCTGTG 1130156
QY 2359 CGGCGGAGGCTCCCGAGAGCAGCACCCCGCTGTCTCACAGAGGCCAGTCCCATGAGC 2418
Db 1130155 TGGCCGAGGCTCCCGAGAGCAGCACCCCGCTGTCTCACAGAGGCCAGTCCCATGAGC 1130096
QY 2419 ACGCAAGGCTGAAAGTGGGGGCGACAGGCGACCGGAGCTGGCAGGACAGTACCCCTGCA 2478
Db 1130095 ACCCAAGGCTGTGAAGTGTGAAGCAGAGGCA--CAGAGCGGAGGACAGCTCCAGCTGCA 1130037
QY 2479 GCCCTGTGCGGAGTCACTGGGTGAAGCAGCTGGGCTCTGTAGTGTGTGAGAGCTTG 2538
Db 1130036 GCCCGGTGTGGGATCACTAGGTGAAGCAGCTGGGCTCTGTAGTGTGTGAGAGCTTG 1129977
QY 2539 GAGAACCTTATGTAGCTAGCGAGGATCGAAATTAACCAATAGAGCAACCTGTGTACG 2598
Db 1129976 GAGAGCTTTATATCTAGCTCAAGGATGTAAATTAACCAATAGAGCAACCTGTGTACG 1129917
QY 2599 TCAGGCTGTGAAATGCAACCAATCCAGCTGTATCTAGTACTGTGATGGGCGCTTGG 2658
Db 1129916 TCAGGCTTTGTAGTGCACCAANTCGGCACTGTATCTAGTGTGTGAGAGCATGG 1129857
QY 2659 AGAACCTTATGTCTAGCTGAGGATGTGAATATACCAATGCGACCTGTGTATCTAGT 2718
Db 1129856 AGAGCTTTATATCTAGCTCAGGAGTGTAAATATACCAATAGGACCTGTGTATCTAGT 1129797
QY 2719 CAAGGTTGTAAACACCAATCAGCAACCTGTGTACTGAGGATGTGAATGCACT 2778
Db 1129796 CAAGGTTGTGAGTGCACCAATCAGCACTGTGTATCTAGC----- 1129757

QY 2779 AATGACAGTCTGTATCTGGCTACTTTCATGGGATCCGTTGGAAGACCAACCAAG 2838
Db 1129756 ----- 1129757
QY 2839 GCTTTGTGTGACATAAAGCTTCTATCACCCTGGTGACAGTGCGCTGATCCGAAAAGA 2898
Db 1129756 ----- 1129757
QY 2899 GAGTCAGGGAAGGAGATTAAGGTGGGCGCTTTTATAGATTGGTAGTAAAGAAA 2958
Db 1129756 ----- 1129757
QY 2959 ATTACAGTCAAAAGGGGTTTGTCTCTGGCGGACGAGATGGGGGTGCAAGTGTCA 3018
Db 1129756 ----- 1129757
QY 3019 GTGGGGGTGCTTTTGTGACCAAGATGACCGAAAAGACTTTCACAAGTAAATGTCAAT 3078
Db 1129756 ----- 1129757
QY 3079 CAATTAAAGGCAAGGACCGCCATTACACCTCTTTTGTGGTGAATGTCAATCAGTTAACT 3138
Db 1129710 GTAATATACCAATCCGAGCTCTGTATCTAGCTCAAGGTTTGTAAATACCAATCA-- 1129654
QY 3139 TGGGCGAGGCAATATTCATCTCTTTGTGATTTCTCAGTTACTTCAGGCCAATCTGGCGGT 3198
Db 1129653 ----- 1129654
QY 3199 ATATGTGCAAGTTACAGGGGATGCGATGGCTTGGGCTCAGAGGCTTGACAGCTAC 3258
Db 1129653 --GCACCTGTGTAGCTCAAGGTTTGTGAATGACCAATCAACACTCTATCTAGCTGCG 1129596
QY 3259 TCTGTGGGGGCTTGGGAATAGTTGTGTGCAACCTCTGTATCTAGTTATCTACTAGTGGG 3318
Db 1129585 TCTGTGGGGGCTTGGGAATAGTTGTGTGCAACCTCTGTATCTAGTTATCTACTAGTGGG 1129536
QY 3319 ACGTGGAGAACCTTTGTGTAGCTCAGGGAATTTGAACGCAACATAGCGCCCTGTCA 3378
Db 1129535 ACGTGGAGAACCTTTGTGTAGCTCAGGGAATTTGAACGCAACATAGCGCCCTGTCA 1129476
QY 3379 AAACAGACACTCGGCTTACCAATCAGAGAGATGTGGGTGGGCCAGATAAGAAATPA 3438
Db 1129475 AAACAGGCACTCGGCTTACCAATCAGAGAGATGTGGGTGGGCCAGATAAGAAATPA 1129416
QY 3439 AAGCAGGCTGCGCGAGCAGAGATGGGAAACGCGAGTCCCTATCCAAATATAGGAG 3498
Db 1129415 AAGCAGGCTGCGCGAGCAGAGATGGGAAACGCGAGTCCCTATCCAAATATAGGAG 1129356
QY 3499 CTTTGTCTTTTGTGTGTGGATTAATCTTGTCTACTGCTGCTTTTGGTCCACACTG 3558
Db 1129355 CTTTGTCTTTTGTGTGTGGATTAATCTTGTCTACTGCTGCTTTTGGTCCACACTG 1129296
QY 3559 CTTTGTATGAGCTGTAACTACACGAGAGTGTGACGCTTCACTCTGAAGCCACTAG 3618
Db 1129295 CTTTGTATGAGCTGTAACTACACGAGAGTGTGACGCTTCACTCTGAAGCCACTAG 1129236
QY 3619 ACCGAGACCCGCGGAGGAGATGAACAATCCGCGCGCTGCTTAAAGACTATACA 3678
Db 1129235 ACCGAGACCCGCGGAGGAGATGAACAATCCGCGCGCTGCTTAAAGACTATACA 1129176
QY 3679 CTCACCGGAGGCTGTGAGCTTCACTCTCAGCAGGAGAGACGCAAGCCACAGAG 3738
Db 1129175 CTCACCGGAGGCTGTGAGCTTCACTCTCAGCAGGAGAGACGCAAGCCACAGAG 1129116
QY 3739 GAAGAACTGCGAATCTGAACATGAGAAGAACTCCAGATGCAACACTTAA 3798
Db 1129115 GAAGAACTGCGAATCTGAACATGAGAAGAACTCCAGATGCAACACTTAA 1129056
QY 3799 GAGGTGAACACTCACTGCGAGGCTCCGCGCTCTCTTCTGAAGTCACTGAGCAACG 3858
Db 1129055 GAGGTGAACACTCACTGCGAGGCTCCGCGCTCTCTTCTGAAGTCACTGAGCAACG 1128996
QY 3859 ACTCACCAGTTTGGACACA 3878

Db 1128995 ACCCAACCAATTCGGACACA 1128976
RESULT 4
US-60-487-610-19434
Sequence 19434, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487, 610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19434
LENGTH: 30105
TYPE: DNA
ORGANISM: Homo sapiens
US-60-487-610-19434
Query Match 12.3%; Score 767; DB 7; Length 30105;
Best Local Similarity 68.8%; Pred. No. 1.5e-115;
Matches 1402; Conservative 0; Mismatches 205; Indels 432; Gaps 8;
QY 1866 TTGACCTGAGAGGTGACAGATGCGGCGAGTCTCAGAGCCCTGCTCGTGGCGC 1925
Db 3445 TTGATTAATGACAGGTGACAGCGGTGCGAGTCTCAGAGCCCTGCTTGTGGCAC 3504
QY 1926 CTCCTCTGCTGGCTCCCACTTCTGCTGAGGCACTTGAAGACCTTCAAGCCGCTGCA 1985
Db 3505 CTCCTCTGCTGGCTCCCACTTCTGCTGAGGCACTTGAAGACCTTCAAGCCGCTGCA 3564
QY 1986 CTGTGGAGACCCCTTCTGCTGGCTGGCCAGAGGCAAGCGGCTCCCTCAGTTGAGGGA 2045
Db 3565 CTGTGGAGACCCCTTCTGCTGGCTGGCCAGAGGCAAGCGGCTCCCTCAGTTGAGGGA 3624
QY 2046 GGTGTGAGAGGAGGCTTCAGAGCAAGAACCGGGGCTGCGACGGGCTTGGCGGCACT 2105
Db 3625 GGTGTGAGAGGAGGCTTCAGAGCAAGAACCGGGGCTGCGAGGCTTGGCGGCACT 3684
QY 2106 GGAGTTCGGGGTGGGCGT--GCTTGGCGGGGCGGCACTTGGAGACAGCGGCGACGC 2162
Db 3685 GGAGTTCGGGGTGGGCGT--GCTTGGCGGGGCGGCACTTGGAGACAGCGGCGACGC 3744
QY 2163 CTGCCAGGCGCGGCGCAATGAGAGGCTTGAAGACCGGGGCGAGCGGCTGGAGGGTAC 2222
Db 3745 CTG-CTTGGGCTTGGGCAATGAGAGGCTTGAAGACCGGGGCGAGCGGCTGGAGGGTAC 3803
QY 2223 TGGGTGCCCGACAGTGCAGGCGCGCGGCTGTCTGCTGATTTCTCACTGGGCT 2282
Db 3804 TGGGTGCCCGACAGTGCAGGCGCGCGGCTGTCTGCTGATTTCTCACTGGGCT 3859
QY 2283 TAGCAGCTTCCCGGGGCGAGGCTGGAGACTGACAGCCGCAATGCTGAGCTGCC- 2341
Db 3860 TAGCAGCTTCCCGGGGCGAGGCTGGAGACTGACAGCCGCAATGCTGAGCTGCCA 3919
QY 2342 ---CTCATGGGCTCTGTGGGCGCGAGGCTCCCGAGAGCAACCCCTGCTCA 2397
Db 3920 CCCACTCATGGGCTCTGTGGGCGCGAGGCTCCCGAGAGCAACCCCTGCTCA 3979
QY 2398 CAGCGCCAGTCCATCAGACAGCAAGGCTGAGAGTGGGGGCGACAGCGCGGAG 2457
Db 3980 TGGCGCCAGTCCATCAGACAGCAAGGCTGAGAGTGGGGGCGACAGCGGAG -GGGAGC 4038
QY 2458 TGGCAGGCACTACCTCTGACAGCCCTGTGTGGGAATCCACTGTGGAAAGCCAGTGGCT 2517
Db 4039 TGGCAGGCACTACCTCTGACAGCCCTGTGTGGGAATCCACTGTGGAAAGCCAGTGGCT 4098
QY 2518 CCTGAGTGTGGTGGAGACTTGGAGAACTTATGTAGCTAGGAGATCGTAAATACAC 2577

||||| 4099 TCTGAGCTAGTGGGAGCTGAGAGCTTTATGCTAGCTCAGGAGTTGTAATACACC 4158
||||| 2578 AATCAGACCCCTGTGTCTAGCTCAGGAGTCTGTGATGATCACCATCAGCTCTATCTA 2637
||||| 4159 AATCAGACCCCTGTGTGTAGTCTAAGGTTGTGATGACACCAATGACACGCTATCTA 4218
||||| 2638 GCTACTGTATGGGGCCTTGGAGAACCTTTATGCTAGCTCAGGAGTTGTAATACACA 2697
||||| 4219 GCTGCTGTGGGGCCTTGGAGAACCTTTATGCTAGCTCAGGAGTTGTAATACACA 4278
||||| 2698 ATCGCAGCTGTATCTAGCTCAGGAGTTGTAATACACA - CCAATCAGACCCCTGTGCTA 2756
||||| 4279 ATCGCAGCTGTGTATCTAGCTCAGGAGTTGTAATACACCATCAGGAGTTGTAATGTA 4338
||||| 2757 GCTCAGGAGTTGTAATGACCAATGACAGCTGTATCTGCTACTCTTCACTTGGCAGTCC 2816
||||| 4339 GCTCAGGAGTTGTAATGACCAATGACAGCTGTATCTGCTACTCTTCACTTGGAGTGC 4398
||||| 2817 GCTGAGAGAGCCACCAACAGGCTTGTGTGACCAATTAAGCTTCTATCCTGGGTGC 2876
||||| 4399 ACCAATGACACCTGTGTATC----- 4418
||||| 2877 AGGTGGCTGAGTCCGAAAGAGATCAGCGAAGGAGATTAAGGTGGGCGCTTTTATA 2936
||||| 4419 ----- 4418
||||| 2937 GGAATTTGGTAGGTAAGAAATAATACAGTCAAAAGGGGTTTGTCTCTGGCGGAGGA 2996
||||| 4419 ----- 4418
||||| 2997 GTGGGGGCTCGAAGGTGTCTAGTGGGGGTCTTTTGGAGCAGATGAGCCAGAAAG 3056
||||| 4419 ----- 4418
||||| 3057 GACTTTCACAAGTAATGATCATCAATTAAGGAGGAGCCGCCATTTACACCTCTTGT 3116
||||| 4419 ----- 4418
||||| 3117 GTTGAATGTCATCAGTTAAGTTGGGCGAGGGCATATTCACCTTTGTGATTCCTCAG 3176
||||| 4419 ----- 4418
||||| 3177 TTAATTGAGGCATCTGGGGGTATATGTGCAAGTTACAGGAGATGCTTGGCTTG 3236
||||| 4419 ----- 4418
||||| 3237 GGCTCAGAGCTTGACAGCTACTGTGGGGCTTGGAGAAATGTTGTGCGACACTCT 3296
||||| 4419 -----TAGCTGCTGTGGGGCTTGGAGAACCTGTGTCTCAACTCT 4463
||||| 3297 GTATCTAGTTAATCTAGTGGGAGCTGGAGAACCTTTGTGTAGCTCAGGAGTTGTA 3356
||||| 4464 GTATCTAATTAATGATGATGGGAGGTGGAGAACCTTTGTATCAAGCTCAGGAGTTGTA 4523
||||| 3357 CGACCAATAGGGCCCTGTCAAAACAGACACCTGGCTTACCAATCAGCAGATGTGG 3416
||||| 4524 CGACCAATAGTGCCTGTGAAACAGGCGACCTGGCTTACCAATCAGCAGATGTGG 4583
||||| 3417 GTGGGGGAGATAGAGAAATAAGAGAGCTGCCCGAGCAGAGTGGCAAGCGGAG 3476
||||| 4584 GTGGGGGTAGATAGAGAAATAAGAGAGCGTGTGAGGAGCAGATTTGGCAACCGGCTCG 4663
||||| 3477 GTCCCTATTCACAATATGAGAGCTTTGTCTTTGTGCTTTGGGATTAATCTTGTACTG 3536
||||| 4644 GTCCCTTTCCGAGTGTGGGTGCTTTGTCTTTGTGCTTTGCAATTAATCTTGTACTG 4703
||||| 3537 CTGGCTTTTGGGTCACAGCTTTTATAGCTGTACAGCTCAGCAGAGGTGTGAG 3596
||||| 4704 CTGACTC--TGGGTTCACGCTGCTTTTATAGCTGTAACTCAGCAGAGATCTGAG 4761
||||| 3597 CTTCACCTCGTAGAGCACTAAGACAGAGCCAGCGGAGGAGTAACTCCGCGCG 3656
|||||

Db 4762 TTTCAGCTCTGAGCCACGACAGCAGAGCCACTGTGGAGGAACAATCTCAGATG 4821
Qy 3657 CGCTGCCCTTAAGACTATTAACACTACCGGCGAAGGTGTGACGTTCACCTCTCAGCAGC 3716
Db 4822 CGCGGCTTTAAGACTGTAACTACACCGGCGAAGGTGTGACGTTCACCTCTCAGCAGC 4881
Qy 3717 GAGACAGAGACCCACCAAGAAAGAAATGCGACACATCTGACATCAGAAAGACA 3776
Db 4882 GATACCTACCAACCCACCAAGAAAGAAATCTCAACACATCCAAACATCAGAAAGACA 4941
Qy 3777 AATCAGATGACACCTTTAAGAGCTGTAACTACATCTGAGAGGTCCGGGCTCTCT 3836
Db 4942 GAATTCAGAGCCGCGACCTTTAAGAGCTGTAACTACATCTGAGAGGTCCGGGCTCTAT 5001
Qy 3837 CTGGAAGTCACTGAGACCAAGCAGTCAACAGTTTCGAGACAAAGCCAGAGTTTGAGA 3895
Db 5002 CTGGAAGTCACTGAGACCAAGCAGTCAACAGTTTCGAGACAAATATATGTTTGA 5060

RESULT 5
US-60-485-450-11978
; Sequence 11978, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-xung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CLO01470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 4789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11978
; LENGTH: 30105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-485-450-11978

Query Match 12.3%; Score 767; DB 7; Length 30105;
Best Local Similarity 68.8%; Pred. No. 1,5e-115;
Matches 1402; Conservative 0; Mismatches 205; Indels 432; Gaps 8;

Qy 1866 TTGAGCTGTAGAGGTGACAGCAGTCCGCGAGTCTCAAGCCCTCTCGCTCGGCGC 1925
Db 3445 TTGATATGACAGGTGACAGGCTGCTGCAAGTCTCAGAGCCCTCGCTTGTGGCAC 3504
Qy 1926 CTCTCTGCTGGGCTCCCACTTGTGGTGCATTTGAGAGCCCTTCAAGCCCGCTGCA 1985
Db 3505 CTCTCTGCTGGGCTCCCACTTGTGGTGCATTTGAGAGCCCTTCAAGCCCGCTGCA 3564
Qy 1986 CTGAGGAGCCCTTTCTGGGCTGGCCAGAGCCGAGCTCCCTCAGCTTGCAGAGGA 2045
Db 3565 CTGAGGAGCCCTTTCTAGCTGTGGCCAGAGCCGAGCTCCCTCAGCTTGCAGAGGA 3624
Qy 2046 GTTGTGAGGAGAGGCTCAAGCAGAAAGGAGCTGCGAGCGGCTTGGGCGGAGCT 2105
Db 3625 GTTGTGAGGAGAGGCGCCAGCGGAGAAAGGAGCTGCGAGCGGCTTGGGCGGAGCT 3684
Qy 2106 GGAATTCGGGGTGGGCGT---GGCTTGGGCGGCGGCGAGCTGCGAGAGCGGAGCC 2162
Db 3685 GGAATTCGGGGTGGGCGGCTTGGGCGGCGGCGAGCTGCGAGAGCGGAGCC 3744
Qy 2163 CTGCGAGAGCCCGGAGAAATGAGAGGCTTACACCGGCGGAGGCGGAGAGGTGATC 2222
Db 3745 CTG-TTGGCCCTTGGGCAATGAGGACTTACACCGGCGGAGGCTGCGAGAGGTGATC 3803
Qy 2223 TGGGTGCGGAGAGTGCACAGCCCGCGCTGTGCTCTGATTTTCTCACTGGGCGCT 2282
Db 3804 TGGGTGCGGAGAGTGCACAGCCCGCGGCTG---GCTTATTTTCTCAACGAGGCT 3859
Qy 2283 TACGAGCTTTCGCGGCGGAGGCTTGGGAGCTGACAGCCCGGAGGCTGAGCTGCC- 2341


```

Db      3860 TAGGCGGCTTCCGGAGGCGAGGGCTCCGAGCTGAGCCCGGCATGCTGAGGCTCCCA 3919
QY      2342 ----CTCATGGGCTCTCTGTGGGCCGAGGCTCCCCGACGACACACCCCTGCTCA 2397
Db      3920 CCCACTCTAGGGGCTCTGTGGGCCCGGACCTCCCGACAGCACACCCCTGCTCA 3979
QY      2398 CAGCGGCCAGTCCGACGACGACGAGGCGTGAAGAGTGGCGGCGCAGGACCGGGAC 2457
Db      3980 TGGCGGCCAGTCCGACGACGACGAGGCGTGAAGAGTGGCGGCGCAGGACG-6GGGAC 4038
QY      2458 TGGCAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2517
Db      4039 TGGCAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 4098
QY      2518 CCGTGAAGTGTGAGAGACTTGAAGACCTTTATGTCTAGCTCAGGAGTGTAAATACAC 2577
Db      4099 TCTGAGTCTAGTGGGACCTGGAGAGTCTTTATGTCTAGCTCAGGAGTGTAAATACAC 4158
QY      2578 AATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2637
Db      4159 AATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 4218
QY      2638 GCTACTGTGATGGGCTGTGAGAACCTTTATGTCTAGCTCAGGAGTGTAAATACAC 2697
Db      4219 GCTGCTGTGATGGGCTGTGAGAACCTTTATGTCTAGCTCAGGAGTGTAAATACAC 4278
QY      2698 ATGCGACTCTGTATCTAGCTCAGGAGTGTAAATACAC -CCATACGACGACGACGACG 2756
Db      4279 ATGCGACTCTGTATCTAGCTCAGGAGTGTAAATACAC -CCATACGACGACGACGACG 4338
QY      2757 GCTGAGGATGTGATGACCAATGACAGTGTGTGAGCAATTAAGCTTATCAGCTGGATC 2816
Db      4339 GCTGAGGATGTGATGACCAATGACAGTGTGTGAGCAATTAAGCTTATCAGCTGGATC 4398
QY      2817 GTGTGAGGACCAACCAAGAGCTTGTGTGAGCAATTAAGCTTATCAGCTGGATC 2876
Db      4399 ACCAATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 4418
QY      2877 AGGTGGGCTGAGTCCGAAAAGAGCTCAGGAGGAGATTAAGGGTGGGCGCTTTTATA 2936
Db      4419 ----- 4418
QY      4419 ----- 4418
Db      2937 GGATTTGGGTAGTAAGGAAAATTACATCAAGGGGTTTGTCTGTGGCGGACAGA 2996
QY      4419 ----- 4418
Db      2997 GTGGGGGTCGCAAGGTGCTCAGTGGGGTGTCTTTTGTAGCCAGATGAGCAGAAAAG 3056
QY      4419 ----- 4418
Db      3057 GACTTTCACAGGTAATGTCAATTAAGGCAAGGACCGGCATTTACACTCTTTTGT 3116
QY      4419 ----- 4418
Db      3117 GGTGAATGTATCAATTAGTTGGGGGAGGCAATTCATCTTTTGTGATTTCTCAG 3176
QY      4419 ----- 4418
Db      3177 TTACTTCAGGCACTGTGGCGTATATGTGCAAGTTACAGGGGATGCGATGGGCTTG 3236
QY      4419 ----- 4418
Db      3237 GGCTAGAGGCTTGAACAGCTACTGTGTGGGCTTGGGAATGTTGTGTGACAGCTCT 3296
QY      4419 -----TACTGTCTGTGTGGGCTTGGGAACCTGTGTGTGCAAACTCT 4463
Db      3297 GTATCTAGTAACTAGTGGGAGGAGGAGACCTTTGTGTAGTCTGAGGATTTCTATA 3356
QY      4466 GTATCTAGTAACTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4523
QY      3357 GCGACCAATCAGGCGGCTGTCAAAACAGACGACGCTGCTACCAATCAGCAGAGATGTG 3416

```

```

Db      4524 CCGACCAATCAGTGGCCCTGACAAACAGGCGACGCTGCTTACCAATCAGCAGATGTGG 4583
QY      3417 GTGGGGCCAGATTAAGGAATTAAGCAGGCTGCCAGCAGCAGGAGGAGGAGGAGGAGG 3476
Db      4584 GTGGGGCTAGATTAAGGAATTAAGCAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGG 4643
QY      3477 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3536
Db      4644 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4703
QY      3537 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3596
Db      4704 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4761
QY      3597 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3656
Db      4762 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4821
QY      3657 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3716
Db      4822 GTCCCATCAGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4881
QY      3717 GAGACCAAGACCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3776
Db      4882 GATACCAAGACCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4941
QY      3777 AACTCAGATGACACGCTTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3836
Db      4942 GATACCAAGACCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5001
QY      3837 GTTGAAGTCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3895
Db      5002 GTTGAAGTCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5060

RESULT 6
US-60-487-610-19424/C
: Sequence 19424, Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CANGIL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19424
: LENGTH: 108815
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-487-610-19424

Query Match      12.1%; Score 752; DB 7; Length 108815;
Best Local Similarity 68.8%; Pred. No. 4,6e-113;
Matches 1408; Conservative 1; Mismatches 131; Indels 508; Gaps 7;

```

D 59650 AGGAGAGGTCCAGCCGGGAACCGGCTCGCTCGGCGCTTGGGGCCAGCTGGAATTC 59591
Q 2113 CGGGTGGGCTGGGCTTGGGGGCCCCGCACTCGAGACAGCGGCCAGCCCTGGCAGGCC 2172
D 59590 CGTGTGGGCAATGGGCTTGGTGGCCAGCACTCGAGAGAGAGCGCTGGCCGTG-CTGGCC 59532
Q 2173 CCGGGCAATGAGAGCTTACACCCGGGGCCAGCGGCTCGGAGAGGTGTACTGGTCCCC 2232
D 59531 CCGGGCAATGAGAGCTTACACCGGGCCAGCGGCTCGGAGAGGTGTACTGGTCCCC 59472
Q 2233 AGCAGTCCAGAGCCCGCGGCTGTGCTCGCTGATTTTCTACTGGGCTTACGACCTT 2292
D 59471 AGCAGTCCAGAGCCCGAGCGCTGTG-6CTCATTTCTTCGCGGCGCTTACGTCCTT 59416
Q 2293 CCGCGGGGCAAGGCTGTGGGCACTGCAAGCCCGCCATGCTGAGCT-CCCTCCAT 2347
D 59415 CCGCGGGGCAAGGCTGTGGGCACTGCAAGCTGCTGAGCTGCTCCACCCCTCCAT 59356
Q 2348 GGGCTCGTGGGCGCGGAGCTCCGAGAGCAACACCCCTTCCTCCAGAGGCCAG 2407
D 59355 GGGCTCGTGGGCGCGGAGCTCCGAGAGCAACCCCTTCCTCCAGAGGCCAG 59296
Q 2408 TCCCATGAGACCAACCAAGGGCTGAGAGTGAAGTGAAGGCGAGCG-AGCAGAGCTGCGAGCGAG 59237
D 59295 TCCCATGAGACCAACCAAGGGCTGAGAGTGAAGTGAAGGCGAGCG-AGCAGAGCTGCGAGCGAG 59237
Q 2468 CTACCCCTGCAAGCCCTGTGGGCAATGCACTGCTGTAAGCAGCTGGGCTCTGAGCTG 2527
D 59236 CTACCCCTGCAAGCCCTGTGGGCAATGCACTGCTGTAAGCAGCTGGGCTCTGAGCTG 59177
Q 2528 GTGAGACTTGGAGACCTTATGTATGCTAGCTCAGGAGTGTAAATACCAATGAGCAGCC 2587
D 59176 GTGAGACTTGGAGACCTTATGTATGCTAGCTCAGGAGTGTAAATACCAATGAGCAGCT 59117
Q 2588 CTGTGTAGCTCAGGCTGTGTGAATGCAACCAATGCACTGCTG-2631
D 59116 CTGTGTAGCTCAGGCTGTGTGAATGCAACCAATGCACTGCTGCTAGCTGAGTGT 59057
Q 2632 TATCTAGCTACTGCTGATGGGCTTGGAGACCTTTATG 2670
D 59056 TGTGAATGCAACCAATGCACTGCTGCTGAGTGTGGGCTTGGAGACCTTTATG 58997
Q 2671 TCTAGCTCAGGAGTGTAAATACCAATGCACTGCTGATGCTAGCTCAGGCTTGTAA 2730
D 58996 TCTAGCTCAGGAGTGTAAATACCAATGCACTGCTGATGCTAGCTCAGGCTTGTAA 58937
Q 2731 ACACACCAATCAGCACTGTGTAGCTCAGGCTGTGTGAATGCACTGCTGAGCT 2790
D 58936 ATACACCAATCAGCACTGTGTAGCTCAGGCTGTGTGAATGCACTGCTGAGCT 58877
Q 2791 GTATCTGGCTACTTTCATGGGCAATCCGTGTGAAGAGCAACCAAGGCTTTGTGAG 2850
D 58876 ATCT-58873
Q 2851 CAATAAAGCTTCTATCAGCTGGTGTGAGTGTGGCTGAGTCCGAAAGAGAGTCAAGAG 2910
D 58872 58873
Q 2911 GGAGATTAAGGTGGGCGCTTTTATAGATTTGGGTAGGTAAAGAAATTAAGTCAAA 2970
D 58872 58873
Q 2971 GGGGGTTTGTCTGTGCGGGGAGAGTGGGGGTCCCAAGGTGCTAGTGGGGTGTCT 3030
D 58872 58873
Q 3031 TTGTAGCAGAGATGAGCAGAAAGACTTTTCAAGAGTATGTCATCAATTAAGCAA 3090
D 58872 58873
Q 3091 GGAACCCGCAATTAACCTCTTTTGTGTGAATGTATCATGATTAAAGTTGGGCGAGGCA 3150
D 58872 58873

Q 3151 TATTCATCTTCTTGTGATTCCTAGTTACTTACAGGCCATCTGGCGTATATGTCAAGT 3210
D 58872 58873
Q 3211 TACAGGGATGCGATGGCTTGGCTTGGGCTGAGAGCTTGCACACTACTCTGGTGGGCC 3270
D 58872 58873
Q 3271 TTGAGAGATTTGTGTGACACTCTGATATGATTAATGATGAGGAGCTGAGAGAAC 3330
D 58854 TTGAGAGATTTGTGTGAGAAC--CTGCATTTACTTAATCTGGTGGGAGCTGAGAGAAC 58797
Q 3331 TTGTGTCTAGCTCAGGAGTGTAAAGCAGCAATACAGCGCTGTGTAAGACAGCACT 3390
D 58796 TTGTGTCTAGCTCAGGAGTGTAAAGCAGCAATACAGCGCTGTGTAAGACAGCACT 58737
Q 3391 CCGGCTTACCAATGAGAGATGTGGGGGCGGAGTAAGAGTAAGTAAGCAGGCTGCC 3450
D 58736 CAGCTTACCAATGAGAGATGTGGGGGCGGAGTAAGAGTAAGTAAGCAGGCTGCC 58677
Q 3451 CGAGCAGCACTGAGCAAGCGCAGAGGCTCCATTCACAAATATGAGAGCTTGTCTTTT 3510
D 58676 GGAGCAGCACTGAGCAAGCGCAGAGGCTCCATTCACAAATATGAGAGCTTGTCTTTT 58617
Q 3511 GCTGTTTGCATTAATCTTGTCTACTGCTGCTTTTGGGCTCAGCACTGCTTTATGAGCT 3570
D 58616 GCTGTTTGCATTAATCTTGTCTACTGCTGCTTTTGGGCTCAGCACTGCTTTATGAGCT 58557
Q 3571 GTACACTCAGCAGAGGCTGAGAGTGTGAGCTTCTGAGCTGAGCAGCACTGAGCAGCAGC 3630
D 58556 GTACACTCAGCAGAGGCTGAGAGTGTGAGCTTCTGAGCTGAGCAGCAGCAGCAGCAGC 58497
Q 3631 CCGGAGAGTAAGCAACTCCGCGCGCTGCTTAAAGAGCTATTAAGCACTGAGCAGCAG 3690
D 58496 CCGGAGAGTAAGCAACTCCGCGCGCTTAAAGAGCTATTAAGCACTGAGCAGCAGCAG 58437
Q 3691 GTCTGAGCTTCACTCTGAGCAGCAGGAGCAGCAAGCAACCCAGAGAGAAACTGCG 3750
D 58436 GTCTGAGCTTCACTCTGAGCAGCAGGAGCAGCAAGCAACCCAGAGAGAAACTGCG 58377
Q 3751 AACCACTGTAACATCAAGAGAGCAAACTCAGATGAGCAGCAGCTTAAAGCTGTAACAC 3810
D 58376 AACCACTGTAACATCAAGAGAGCAAACTCAGATGAGCAGCAGCTTAAAGCTGTAACAC 58317
Q 3811 TCAGTGGAGGGTCCGCGGCTTCTTGTGAAGTCAAGTGAAGCAAGCACTCAGCAGTTT 3870
D 58316 TCAGTGGAGGGTCCGCGGCTTCTTGTGAAGTCAAGTGAAGCAAGCACTCAGCAGTTT 58257
Q 3871 CCGACACA 3878
D 58256 CCGACACA 58249

RESULT 7
US-60-485-450-11975/c
; Sequence 11975, Application us/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: C1001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11975
; LENGTH: 108815
; TYPE: DNA
; ORGANISM: Homo sapiens

US-60-485-450-11975

Query Match 12.1%; Score 752; DB 7; Length 108815;
Best Local Similarity 68.8%; Pred. No. 4,6e-113;
Matches 1408; Conservative 1; Mismatches 131; Indels 508; Gaps 7;

QY 1873 TGAGAGGTGACAGATCCCGGACAGCTCCACAGCCCTTCGCTCGGCGCCCTCT 1932
DB 59830 TGAAGGTGACAGCTCCGCTGACATCTCCACAGCCCTTCGCTCGGCGCCCTCT 59771
QY 1933 GCGTGGGCTCCCACTTGGGTGGGACCTTGAGAGCCCTTCAGCCCAACCGCTCAGTGGG 1992
DB 59770 GCGTGGGCTCCCACTTGGGTGGGACCTTGAGAGCCCTTCAGCCCAACCGCTCAGTGGG 59711
QY 1993 AGCCCCCTTTCGGGCTGGCCAGGCGCAGAGCCGCTCCCTCAGCTTGAGAGGAGTGGG 2052
DB 59710 AGCCCCCTTTCGGGCTGGCCAGGCGCAGAGCCGCTCCCTCAGCTTGAGAGGAGTGGG 59651
QY 2053 AGGAGAGGCTCAAGAGAGACCGGGGCTGGCGAGCGGCTTGGGGGCGAGCTGGAGTTC 2112
DB 59650 AGGAGAGGCTCAAGAGAGACCGGGGCTGGCGAGCGGCTTGGGGGCGAGCTGGAGTTC 59591
QY 2113 CGGGTGGGCTGGGCTTGGCGGGGCCCGCACTCGAGAGCGGGCCAGCCCTCGCAGGCC 2172
DB 59590 CGGTGGGCAATGGGCTTGGGTGGGCGCAGCACTCGAGAGCGGGCTGGCGCTG-CTGGCC 59532
QY 2173 CCGGGCAATGAGAGGCTTACAGCCCGGCGCAGCGGCTGGAGGGGTGACTGGGCTCCC 2232
DB 59531 CCGGGCAATGAGAGGCTTACAGCCCGGCGCAGCGGCTGGAGGGGTGACTGGGCTCCC 59472
QY 2233 AGCAGTGCACAGCGCGGGGCTGTGCTCGCTGATTTCTACAGGGGCTTACAGAGCCCTT 2292
DB 59471 AGCAGTGCACAGCGCGGGGCTGTGCTCGCTGATTTCTACAGGGGCTTACAGAGCCCTT 59416
QY 2293 CCGCGGGGCGAGGGCTCGGGAGCTGCAGCCCGCATGCTGAGCT-----CCCTCCAT 2347
DB 59415 CCGCGGGGCGAGGGCTCGGGAGCTGCAGCCCGCATGCTGAGCT-----CCCTCCAT 59336
QY 2348 GGGCTCTGTGCGGGCCCGAGGCTCCCGAGCAGCAGCAGCCCTTCCTCAGAGCGCCAG 2407
DB 59336 GGGCTCTGTGCGGGCCCGAGGCTCCCGAGCAGCAGCAGCCCTTCCTCAGAGCGCCAG 59296
QY 2408 TCCCATGACACAGCAGAGGCTGAGAACTGCGGGCGCAGCGCAGCGGGATGGCAGGAG 2467
DB 59295 TCCCATGACACAGCAGAGGCTGAGAACTGCGGGCGCAGCGCAGCGGGATGGCAGGAG 59237
QY 2468 CTACCCCTGCAGCCCTGGTGGGAGTCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTG 2527
DB 59236 CTACCCCTGCAGCCCTGGTGGGAGTCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTG 59177
QY 2528 GTGAGACTGGAGAACTTATATGTCTAGCTCAGGAGATCGTAATATACCAATACAGCAGC 2587
DB 59176 GTGAGACTGGAGAACTTATATGTCTAGCTCAGGAGATCGTAATATACCAATACAGCAGC 59117
QY 2588 CTGTGTAGCTCAGGCTGTGTGATGATGACCAATCCACTCTG----- 2631
DB 59116 CTGTGTAGCTCAGGCTGTGTGATGATGACCAATCCACTCTG----- 59057
QY 2632 -----TATCTAGCTACTGTGATGGGCTTGGAGAACTTTATG 2670
DB 59056 TGTGAAATGACCAATCGACATATCTAGCTACTGTGATGGGCTTGGAGAACTTTATG 58997
QY 2671 TCTAGCTCAGGAGATTTGTAATATACCAATTCGGCACTGTGTCTATAGCTCAAGGTTTGTAA 2730
DB 58996 TCTAGCTCAGGAGATTTGTAATATACCAATTCGGCACTGTGTCTATAGCTCAAGGTTTGTAA 58937
QY 2731 ACACCAATGACAGCCTGTGTAGCTCAGGATGATGATGATGATGATGATGATGATGATGAT 2790
DB 58936 ATACCAATGACAGCCTGTGTAGCTCAGGATGATGATGATGATGATGATGATGATGATGAT 58877
QY 2791 GTATCTGGCTACTTTCATGGGCAATCCGTGTAAGAGACCAACAGGCTTTGTGTAG 2850
DB 58876 ATCT----- 58873

QY 2851 CAATAAGCTTCTATCACCCTGGGTGAGGTGGGCTGAGTCCGAAAAAGAGTCAAGCAAG 2910
DB 58872 ----- 58873
QY 2911 GCAGATTAAGGTTGGGCGGCTTTTATAGATTTGGTAGTAAGGAAAAATATACAGTCAA 2970
DB 58872 ----- 58873
QY 2971 GGGGTTTGTCTCTGGCGGCGCAGAGATGGGGGGTCCGAAAGGTCTCAGTGGGGTCTT 3030
DB 58872 ----- 58873
QY 3031 TTTGAGCAGGATGAGCCAGGAAAAAGACTTTCAACAGATATGTCATCAATTAAGCAA 3090
DB 58872 ----- 58873
QY 3091 GGACCGGCATTTACACCTTTTGTGGTGAATGTCAATGATTAAAGTTGGGCGAGGCA 3150
DB 58872 ----- 58873
QY 3151 TATTCATCTTTTGTGATTTCTCAGTTACTTCAAGCCATCTGGCGTATATGTCAAAT 3210
DB 58872 ----- 58873
QY 3211 TACAGGAGATGAGATGGCTTGGCTTGGCTCAGAGGCTTGCAGAGCTACTTGTGGGCGC 3270
DB 58872 ----- 58873
QY 3271 TTTGAGATTTTGTGTGACACCTGATATGATGATTAATCTAGTGGGAGCGGAGAAC 3330
DB 58874 TTTGAGATTTTGTGTGACACCTGATATGATGATTAATCTAGTGGGAGCGGAGAAC 58797
QY 3331 TTTGTGTAGTCAAGGATTTGTAACACCAATCAACAGCCCTTCCTCAAAACAGACACT 3390
DB 58796 TTTGTGTAGTCAAGGATTTGTAACACCAATCAACAGCCCTTCCTCAAAACAGACACT 58737
QY 3391 CCGCTCTACCAATCAACAGATGTGGGTGGGCGCAGATTAAGATTAAGACAGGCTGCC 3450
DB 58736 CCGCTCTACCAATCAACAGATGTGGGTGGGCGCAGATTAAGATTAAGACAGGCTGCC 58677
QY 3451 CGAGCAGCAGTGGCAAGCGCGAGTCCCTATCCAAATATGAGCAGCTTGTCTTTT 3510
DB 58676 CGAGCAGCAGTGGCAAGCGCGAGTCCCTATCCAAATATGAGCAGCTTGTCTTTT 58617
QY 3511 GCTGTTGCATTAATCTTGTCTACTGTGCTGCTTTTGGGTCCACACTGCTTTATGAGCT 3570
DB 58616 GCTGTTGCATTAATCTTGTCTACTGTGCTGCTTTTGGGTCCACACTGCTTTATGAGCT 58557
QY 3571 GTAACACTCAGCAGAAAGTCTGAGCTTCACTCTCTGAAAGCCACTTAAGACAGAGCCCA 3630
DB 58556 GTAACACTCAGCAGAAAGTCTGAGCTTCACTCTCTGAAAGCCACTTAAGACAGAGCCCA 58497
QY 3631 CCGGAGGAGATGAACAACTCGGCGCGCTCTTAAGAGTATTAACACTCAGCCGAG 3690
DB 58496 CCGGAGGAGATGAACAACTCGGCGCGCTCTTAAGAGTATTAACACTCAGCCGAG 58437
QY 3691 GTCTGACGCTTCACTCTCAGCCAGGAGACAGACCAACCAACAGAGAAAGAACTGCG 3750
DB 58436 GTCTGACGCTTCACTCTCAGCCAGGAGACAGACCAACCAACAGAGAAAGAACTGCG 58377
QY 3751 AATCACTGTAACATCAAAAGAAACAACTCAATGACCAACCTTAAGAGCTGTAAC 3810
DB 58376 AATCACTGTAACATCAAAAGAAACAACTCAATGACCAACCTTAAGAGCTGTAAC 58317
QY 3811 TCACGCGAGGAGTCCGCGGCTTCTTCTTGAAGTCAAGAGCAACAGCACTCAGGATTT 3870
DB 58316 TCACGCGAGGAGTCCGCGGCTTCTTCTTGAAGTCAAGAGCAACAGCACTCAGGATTT 58257
QY 3871 CGGACACA 3878
DB 58256 CGGACACA 58249

OY	3661	GCCCTTAAGAGCTATTAACACTCACCAGGAGGTTCGGACCTTCACTCCACAGCCAGCGAGA	3720
Db	7883293	ACCTTTAAGAGCGCTTAACAACCTCACCGGAAGGTTCGGACCTTCACTCCACAGCCAGCGAGA	7883352
OY	3721	CCACGAACCCACACGAAAGGAAGAACTGCAGAACACATCTGAACATCAGAAAGAACT	3780
Db	7883353	CCACGAACCCACACGAAAGGAAGAAATTCCGAACATCTCGAAACATCAGAAAGAACT	7883412
OY	3781	CCAGATGCACACCTTAAGAGCTGTAACTCATCTACCTGCGAGGGTCCGGGCTTCTTG	3840
Db	7883413	CCAGATGCACACCTTAAGAGCTGTAACTCATCTACCTGCGAGGGTCCGGGCTTCTTG	7883472
OY	3841	AAGTCAGTGAAGACCAACGACCTCACCAGTTTCGACACA	3878
Db	7883473	AAGTCAGTGAAGACCAACGACCTCACCAGTTTCGACACA	7883510
RESULT 9			
US-10-450-826-50			
Sequence 50, Application US/10450826			
GENERAL INFORMATION:			
APPLICANT: JI, Darren			
APPLICANT: Axelrod, Douglas W.			
APPLICANT: Cook, Jonathan S.			
APPLICANT: Jaiswal, Neelam			
APPLICANT: Eistein, Richard			
APPLICANT: Houghton, Adam			
APPLICANT: Mertz, Lawrence			
TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation			
FILE REFERENCE: 044921-5039-WO			
CURRENT APPLICATION NUMBER: US/10/450,826			
CURRENT FILING DATE: 2003-06-18			
PRIOR APPLICATION NUMBER: US 60/255,882			
PRIOR FILING DATE: 2000-12-18			
PRIOR APPLICATION NUMBER: US 60/285,691			
PRIOR FILING DATE: 2001-04-24			
NUMBER OF SEQ ID NOS: 149			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 50			
LENGTH: 121724			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE: OTHER INFORMATION: Genbank Accession No. AL136139			
US-10-450-826-50			
Query Match 11.8%; Score 733.2; DB 6; Length 121724;			
Best Local Similarity 90.1%; Pred. No. 5.1e-110;			
Matches 856; Conservatively 0; Mismatches 78; Indels 16; Gaps 6;			
OY	1867	TGAGCTGTAGAGAGGAGACGATGCCGCGACGCTCACAGCCCTGTTGCGCTCGGGGCC	1926
Db	4692	TGCGCATGAGAGAGGAGGACGCTGCTGGCAGTCTCAGAGGCCCTGCTGCTGCGCAC	4751
OY	1927	TCTCTGCTGAGGCTGCCACTTTCGCTGACCTTAGAGAGCCCTTACGCCACCGCTGCAC	1986
Db	4752	TCTCTGCTGAGGCTGCCACTTTCGCTGACCTTAGAGAGCCCTTACGCCACCGCTGCAC	4811
OY	1987	TGTGGGAGCCCTTTCGCGGTGGGCGCAAGCGACCGCGCTCCCTCAGCTTGAGGGAG	2046
Db	4812	TGTGGGAGCCCTTTCGCGGTGGGCGCAAGCGACCGCGCTCCCTCAGCTTGAGGGAG	4871
OY	2047	GTTGTGAGAGGAGAGGCTCAAGCAGAGAACCGGGGCTGGCAGCGGGCTTGGCGGCGAC	2106
Db	4872	GTTGTGAGAGGAGAGGCTCAAGCAGAGAACCGGGGCTGGCAGCGGGCTTGGCGGCGAC	4931
OY	2107	GAGTTCGGGGTGGGCGTGGGCGTGGGCGGCCCGCCACTCGGAGCAGCGGCGCACCTGC	2166
Db	4932	GAGTTCGGGGTGGGCGTGGGCGTGGGCGGCCCGCCACTCGGAGCAGCGGCGCACCTGC	4991
OY	2167	CAGGCCCCGGGCAATGAGAGGCTTAGACACCCGGGCGCAGCGGCTCGGAGAGGTGATCGG	2226
Db	4992	C-GGCCCCGGGCAATGAGAGGCTTAGACACCCGGGCGCAGCGGCTCGGAGAGGTGATCGG	5050

[illegible]

QY	1933	UCCTGGGCTCCCACTTGGGTGGACCTTTGAAGAGCCCTTCAAGCCACCGCTGACCTGTGG	1992
Db	26888	GCCTGGGCTCCCACTTGGGTGGACCTTTGAAGAGCCCTTCAAGCCACCGCTGACCTGTGG	26822
QY	1993	AGCCCTTTCTGGGCTGGCCAAAGGACCGAGCCGGGCTCCCTCACCTTGCAGGAGGTGG	2052
Db	26828	AGCCCTTTCTGGGCTGGCCAAAGGACCGAGCCGGGCTCCCTCACCTTGCAGGAGGTGG	26766
QY	2053	AGGAGAGGCTCAAGACAGAAACGGGGCTGCGACGGCGCTTGGGGCCAGCTGAGTTG	2112
Db	26768	AGGAGAGGCTCAAGACAGAAACGGGGCTGCGAGCTGGGCTGCTGGGGCCAGCTGAGTTG	26709
QY	2113	CGGGTGGGCTGGGCTTGGGGGGCCCGGCACTGGAGAGACGGGGCCAGCCCTCCAGGGC	2172
Db	26708	CGGGTGGGCTGGGCTTGGGGGGCCCGGCACTGGAGAGACGGGGCCAGCCCTCCAGGGC	26656
QY	2173	CCGGGCAATGAGAGGCTTACACACCCGGGGCCAGCGGCTGCGAGAGGTACTGGGTCCCC	2232
Db	26649	CCGGGCAATGAGAGGCTTACAGACCCGGGGCCAGCGGCTGCGAGAGGGTACTGGGTCCCC	26596
QY	2233	AGCAGTCCGACCCGGCGCGCTGTGCTGCTGATTTCTACATGGGCTTACAGACTTT	2292
Db	26589	AGCAGTCCGACCCCGCGCGCTGTGCTGCTGATTTCTACATGGGCTTACAGACTTT	26554
QY	2293	CCCCGGGGGCGAGGGCTGGGACCTGCAGCCCGCATGCTGAGCTGCC-----CTGCAT	2347
Db	26553	CCCCGGGGGCGAGGGCTGGGACCTGCAGCCCGCATGCTGAGCTGCC-----CTGCAT	26496
QY	2348	GGGCTCCTGTGCGGGCCCGAGACCTCCCGACGAGCACCCCTGCTCCACAGCGCCAG	2407
Db	26493	GGGCTCCTGTGCGGGCCCGAGACCTCCCGAGAGAGCGGGGCGCCCTGCTCCACGCGCCAG	26433
QY	2408	TCCCATGACACGACGAGGGGCTGAGAGTCCGGGGCCAGCGGCACTGGGACTGGCAGCG	2467
Db	26433	TCCCATGACACGACGAGGGGCTGAGAGTCCGGGGCCAGCGGCACTGGGACTGGCAGCG	26375
QY	2468	CTACCCCTGCAGCCCTGGTGGGATCCGGAATCCACTGGGTGTAAGCCAGCTGGGCTCTGACTTG	2527
Db	26374	CTACCCCTGCAGCCCTGGTGGGATCCGGAATCCACTGGGTGTAAGCCAGCTGGGCTCTGACTTG	26315
QY	2528	GTGAGAGCTTGGGAGACCTTATCTGTAGCTCAGGGATCTGTAAT-----	2572
Db	26314	GTGAGAGCTTGGGAGACCTTATCTGTAGCTCAGGGATCTGTAATACCCAACTGGGACT	26255
QY	2573	-----ACACAACTCAGCACCCCTGTGTAGCTCAGGGTCTG	2608
Db	26254	CTATCTAGCTCGAGGTTTGTAAACACACAACTCAGCACCCCTGTGTAGCTCAGGGTCTG	26199
QY	2609	TGATGACCAACATCCACACACTCTGTATCTACTACTCTGATGGGGCTTGGAGAACCTTTA	2668
Db	26194	TGATGACCAACATCCACACACTCTGTATCTACTACTCTGATGGGGCTTGGAGAACCTTTA	26135
QY	2669	TGTTAGCTCAGGGATTGTAAATACACACATCGGACACTGTGTATCTAGCTCAAGTTTGT	2728
Db	26134	TGTTAGCTCAGGGATTGTAAATACACAAATCGGACACTGTGTATCTAGCTCAAGTTTGT	26075
QY	2729	AAACACACCAATCAGCACCCCTGTGTAGCTCAGGGATGTGTGANTSCAACCAATCGACACT	2788
Db	26074	AAACACACCAATCAGCACCCCTGTGTGTAGCTCAGGGATGTGTGANTSCAACCAATCGACACT	26015
QY	2789	CTGTATCGGGCTACTTTCATAGGGGCACTCCGTGAAGAGACCAACCAAGCTTTGTGTG	2848
Db	26014	CTGTATCT-----	26007
QY	2849	AGCAATTAAGCTTCTATACACTGGGTGTCAGGTGGGCTGAGTCCGAAAAAGATCAGCA	2908
Db	26006	-----	26007
QY	2909	AGGAGATTAAGGGTGGGGCCGTTTATATAGGATTTGGGTAGTAAGAAAAATTACAGTCA	2968
Db	26006	-----	26007

Db 8648 CGGAGGTGGAGGTGGAGTGAACCGAGATGGCCCACTGCACTCCAGCCTGAGCGACAG 8589
QY 5173 GCCTTGTGGCTGTAGAAAACGTTCAAGCCTAGGCCGGGACGGTGGCTCAAGCCTGTAA 5232
Db 8588 AGTGAAGCTCTATCTCAAAAAAAGCAAGGCGGTGGTGGCTCAAGCCTGTAA 8529
QY 5233 TCCAGGACCTTGGAGGCGGAGGCGGTGGATCAGAGGTCAAGAGATCGTGAACATCC 5232
Db 8528 TCCAGGACCTTGGAGGCGGAGATGGGCGGATACGAGGTGAGAGATCGAAGATCC 8469
QY 5293 TGGCTAACAGGCTGAAACCCCGCTCTACTATAAAATAC---AAAAATTTGGCCGGGATG 5349
Db 8468 TGGCTAACAGGCTGAAACCCCGCTCTACTATAAAATACAAAAAATTTAGCCGGGATG 8409
QY 5350 GTGGCGGGACCTGTAGTTCCAGCTACTCGGAGGCTGAGGACAGAGATGGCGTGAAC 5409
Db 8408 GTGGCGGGACCTGTAGTTCCAGCTACTCGGAGGCTGAGGACAGAGATGGCGTGAAC 8349
QY 5410 CGAGAGCGAGGTTGGAGTGAAGCCGAGATCCGCCCACTGCACTCCAGCCTGGCGACAG 5469
Db 8348 CGGAGGTGGAGCTTGCAGTGAAGAGATCGCCCACTGCATCCAGCCTGGCGACAA 8289
QY 5470 AGCAAGACTCCATCTGGAAAAAGAAAAAGAAAA 5501
Db 8288 AGCGAGACTCGGTCTCAAAAAAATATAATA 8257

RESULT 12
US-60-485-450-11934/c
: Sequence 11934, Application US/60485450
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: CHANG, Sheng-yung
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
: TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
: FILE REFERENCE: CL001470
: CURRENT APPLICATION NUMBER: US/60/485,450
: CURRENT FILING DATE: 2003-07-09
: NUMBER OF SEQ ID NOS: 47859
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11934
: LENGTH: 48853
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(48853)
: OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-485-450-11934

Query Match 11.4%; Score 710.4; DB 7; Length 48853;
Best Local Similarity 63.3%; Pred. No. 2.2e-106;
Matches 1425; Conservative 0; Mismatches 606; Indels 221; Gaps 13;

QY 3253 AGCTACTGTGTGGGCGCTTGGAGATGTTGTGTGACACTGTGTATCTAGTTAATCTA 3312
Db 3260 AGCTACTGTGTGGGCGCTTGGAGATGTTGTGTGACACTGTGTATCTAGTTAATCTG 3201
QY 3313 GTGGGAGCGTGAAGACCTTGTGTAGTCAAGGGATTGTAAACCAACCAACGCGC 3372
Db 3200 GTGGGAGCGTGAAGACCTTGTGTAGTCAAGGGATTGTAAATGCAACCAATCAGCGC 3141
QY 3373 CTGTCAAAACAGACACTGGCTCTACATACAGAGATGTGGTGGGCGCAGATAGA 3432
Db 3140 CTGTCAAAACAGACACTAGGCTCTACATACAGAGATGTGGTGGGCGCAGATAGA 3081
QY 3433 GATATAAAGCAGGCTCCGAGCAGACAGTGGCAAGCGCACAGGTCCCTATCCACAATA 3492
Db 3080 GATATAAAGCAGGCTCCGAGCAGACAGTGGCAAGCGCACAGGTCCCTATCCACAAG 3021

QY 3493 TGGCAGCTTGTGTCTTTTGTCTTGTGGCATTAATCTTGCTACTGCTGCTTTTGGGCTC 3552
Db 3020 TGGAGGCTTGTGTCTTGTGGCATTAATCTTGCTACTGCTGCTTTTGGGCTC 2961
QY 3553 ACAGTCTTGTATGAGCTGTAACTCACTCCAGAGGCTGACCTTCACTCCGAAAGCC 3612
Db 2960 ACAGTCTTGTATGAGCTGTAACTCACTCCAGAGGCTGACCTTCACTCCGAAAGCC 2901
QY 3613 ACTAAGACACAGAGCCCAAGCGGAGATGAATGAACAATCCGCGCGCTGCTTAAAGCT 3672
Db 2900 AGCGAGACACAGAGCCCAAGCGGAGAA -CAAAAAATCCAGACCGCTTAAAGCT 2842
QY 3673 ATTAACACTACCGGAGAGTGTGACGCTTCACTCTCAAGCAGGAGACAGAACCCAC 3732
Db 2841 GTAACTACCGCGCAAGGTGTGAGCTTCACTCTCAAGCAGGAGACAGAACCCAC 2782
QY 3733 CAGAAGGAAGAACTGGGAACACTGTGAAATATGAAGAAACAACTCCAGATGACCA 3792
Db 2781 CAGAAGGAAGAACTGGGAACACTGTGAAATATGAAGAAACAACTCCAGATGACCA 2722
QY 3793 CCTTAAGAGCTGTAACTCACTGAGAGGTCGCGGCTTCTTGAAGTCAAGTGA 3852
Db 2721 ACTTAAGAGCTGTAACTCACTGAGAGGTCGCGGCTTCTTGAAGTCAAGTGA 2662
QY 3853 CCAAGCACTACCACTTTGCGACCAAGCCAGAGATTGAGATCAGCTGGGCAACATG 3912
Db 2661 CCAAGCACTACCACTTTGCGACCAAGCCAGAGATTGAGATCAGCTGGGCAACATG 2606
QY 3913 ATGAATATGCCCTCTCTCAAAAAAATTAACAAAAATTTGGCGGACATGTGTGTC 3972
Db 2605 GCGAGA-----CTTTTCANAAAAAATTAAGTTCGACGGGCGGCGGTGTGCT 2554
QY 3973 CGTGCTGTGTGCTCCAGCTACGCGGAGGCTTAAAGTGGAGATCGCTGAGCTGGAG 4032
Db 2553 CAGGCTGTATCCACACTTTGGAGGCGGAGGTGGGAGATCACTTGAAGTCAAGTAG 2494
QY 4033 GTGAAGACTCAGTGAAGTGTGATTTACCAAGCCCTTGAAGTGGGAGACAGTAG 4092
Db 2493 TTGAGA-----CCAGCTGTGCCAACAATGTGTGA 2465
QY 4093 ACCCTGTTCCTCCCGCCCAAAAAAATTAACAAAAATTTGAAGTGTGATGATGATG 4152
Db 2464 ACTGTGTCTACTATATAATTA-----GAC 2439
QY 4153 TAGCGGAGTGTGCTCATGCTGTAAATCCAGCACTTTGGAGCCGAGCGGCGGTCA 4212
Db 2438 AGGCAAGGTAACTCACTGAGGCTGTGATCCAGCACTTTGGGACAGCAAGGGGAGGTGAT 2379
QY 4213 CTTAAGTCAAGAGTGTGAACCAAGCTGGCCAAATGAGAAAGCCCATCTCTTAA 4272
Db 2378 CACAAGGTCAAGAGTGTGAGCAAGCTGACCAACATGTGAAACTGCTCT----- 2327
QY 4273 AATACAAATTTAGCCGCGCTGTGGGGAGTGGAGCAATGCCGTAAATCCAGTATCTC 4332
Db 2326 ACTTAATAATTTAGCC-----GATGACACGCACTGTATCTCCAGCAATC 2281
QY 4333 AGGAGGCTGAAGAGAGATCACTTGAACCCAGAGAGCGCGGCTTGTGATGAGCGAGA 4392
Db 2280 AGGAGGCTGAAGAGAGATTCGCTTGAATCAAGAGGTGAGACTTGTGATGAGCGAGA 2221
QY 4393 TCGTGCATTTGCACTCAAGCACTTCAAGCTGGGCAACAAGAGCCAACTCTCTTAA 4452
Db 2220 TCACACCACACTCCAGCC-----TGGGAGAGAGAGCCGAATCCATTCCTCAA 2171
QY 4453 AAAAAAAGTGAAGTCTGACATATTAAGAGTGTGCAATGCAATAGTTGCCAGGCAAC 4512
Db 2170 GAAACACAAAACA----- 2158
QY 4513 ATGTTTAAGATGTGAGCTCTGCTTCATGCTGTGTAAACCAACCTCAAGGC 4572
Db 2157 -----AAACAATTAACCAAAATTAAC 2139
QY 4573 CAGGTCAAGTGGCTCATGCTTAATTCAGACACTTTGGAGGCGGAGGCGGTGATCA 4632

Db 2960 CTAGACAGCAAAATACACTATTTTAATGAGCAGAAATGCTCCGAACCCCTGAGAGAC 3019
Qy 1685 GATCTAAATCTGAATCTACTGCTGCTCAGCCACACAGTAGTTCTGTGATCTTGACAGAT 1744
Db 3020 TTGGAGAGGCTTTTGAAGTTTAAAGAAAGATAGTAAGAGAGATTCCATTGAAAGG 3079
Qy 1745 TTTTTCACCTCT- -CTGAGGCCATCCCTTGCTTACACACACCAGCTTGACAGAGATG 1802
Db 3080 AATAGAAATGTAGTTGAAGCACTTCTCAGAGATGAGTCCAAAGCTTTCTGTAGAGAG 3139
Qy 1803 AATAGCAAGTCCCTTACACCTGTAACTCCAGCACTTTGGAGGCCAGGGGGGGAGT 1862
Db 3140 GTGAGCCACAGAGACAGACATATGACCTACTCTGTATAGTTGTGTAGCTCTGTGTA- 3198
Qy 1863 GGCCTGAGCCTGAGAGAGTGAACAGCATGCCGAGTCCCTCACAAGCCCTCTGCTCTCGG 1922
Db 3199 - - -GTACAAATGAGAGATGACAGCCGTGCTGAGAGTCTCACAAGCCCTGCTGCTCTCGG 3255
Qy 1923 GGCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1982
Db 3256 GGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3315
Qy 1983 GGCATCTGAGAGCCCTTTCTGAGGCTGAGCAGAGCCGAGCCGCTGCTGCTGCTGCTG 2042
Db 3316 GCACTGTGAGAGCCCTTTCTGAGGCTGAGCAGAGCCGAGCCGCTGCTGCTGCTGCTG 3375
Qy 2043 GAGAGTGTGAGAGAGAGAGCTCAAGCAGAGACCGGGGCTGCGCAGCGCTTGTGCGGCG 2102
Db 3376 GAGAGGGGTGAGAGAGAGAGAGCGGAGGAGACCGGGGCTGCGCAGCGCTTGTGCGGCG 3435
Qy 2103 GCTGAGTTCGGGGTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGT 2162
Db 3436 GCTGAGTTCGGGGTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGT 3495
Qy 2163 CTGACAGAGCCCGGAG 2222
Db 3496 CTG-CTGAGCCCTTGTGAG 3554
Qy 2223 TGGGTGAGCCAG 2282
Db 3555 TGGGTGAGCCAG 3610
Qy 2283 TGGAGAGCTTCCCGGGGAG 2338
Db 3611 TGGAGAGCTTCCCGGGGAG 3670
Qy 2339 -CCCTTCATGAGAGCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2396
Db 3671 GCGCCCTCATGAGAGCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3730
Qy 2397 ACAGGAGCCAGTCCATGAG 2456
Db 3731 ACAGGAGCCAGTCCATGAG 3789
Qy 2457 CTGGAGAGAGAGTACCCCTGAG 2516
Db 3790 CTGGAGAGAGAGTACCCCTGAG 3849
Qy 2517 TCTGAGTCTGTGAG 2576
Db 3850 TCTGAGTCTGTGAG 3906
Qy 2577 CAATCAGACACCTGTGTCTAGTCAAGAGTCTGTGAATGCACCAATCCACTCTGTATCT 2636
Db 3907 - - - - -CAACAATGACACTCTGTATCT 3928
Qy 2637 ACCTACTGATGAGGAG 2696
Db 3929 ACCTACTGATGAGGAG 3988
Qy 2697 AATCGGAGAGTCTGTATCTAGTCAAGAGTGTGTAAACACACCAATCAGACAGAGAGAGAG 2756
Db 3989 AATCAGAGAGTCTGTATCTAGTCAAGAGTGTGTAAACACACCAATCAGACAGAGAGAGAG 4048

Qy 2757 GCTCAGGAGTGTGAATGACCAATGACAGAGTCTGTATCTGCTACTTTCATGAGG 2811
Db 4049 GCTCAGGAGTGTGAATGACCAATGACAGAGTCTGTATCTGCTACTTGTGTGAGG 4103
RESULT 14
US-60-487-610-19299
; Sequence 19299, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487, 610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19299
; LENGTH: 70556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(70556)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
US-60-487-610-19299
Query Match 10.9%; Score 677.2; DB 7; Length 70556;
Best Local Similarity 67.1%; Pred. No. 5.4e-101;
Matches 1366; Conservative 6; Mismatches 254; Indels 410; Gaps 13;
Qy 1862 TGGCTGAGCAG 1921
Db 31200 TGGAAATCAATCTGAG 31255
Qy 1922 GCGCCTCTCTGAG 1981
Db 31256 GCAACCTCTCTGAG 31315
Qy 1982 TGCATGTGTGAG 2041
Db 31316 TGCATGTGTGAG 31375
Qy 2042 GGGAGAGTGTGAG 2101
Db 31376 GGGAGAGTGTGAG 31429
Qy 2102 AGCTGAGAGTTCGGGAG 2161
Db 31430 AGCTGAGAGTTCGGGAG 31489
Qy 2162 CCGTGCAG 2221
Db 31490 CCGTGCAG 31548
Qy 2222 CTGGAG 2281
Db 31549 GTGAGAGTCTCAG 31604
Qy 2282 TTAGCAGAGTTCGGGAG 2338
Db 31605 TTAGCAGAGTTCGGGAG 31664
Qy 2339 - - -CCCTTCATGAG 2396
Db 31665 ACCCCCTCATGAG 31724
Qy 2397 ACAGGAGCCAGTCCATGAG 2456
Db 31725 ACCGAGCCAGTCCATGAG 31783

Result No.	Score	Query Match	Length	DB	ID	Description
1	711.8	11.4	3669	11	BC033022	BC033022 Homo sapi
2	710.4	11.4	1066	13	BX423847	BX423847 Homo sapi
3	707.8	11.4	1201	9	AL332400	AL332400 AL332400
4	707.2	11.3	2067	11	AF318322	AF318322 Homo sapi

C	5	697.8	11.2	1201	13	BX358085	BX358085	BX358085
C	6	692.8	11.1	1201	13	BX402423	BX402423	BX402423
C	7	690	11.1	955	13	BX407975	BX407975	BX407975
C	8	687.8	11.0	1201	13	BX402424	BX402424	BX402424
C	9	670.4	10.8	1201	13	BX358084	BX358084	BX358084
C	10	600	9.6	879	13	BX446821	BX446821	BX446821
C	11	593.6	9.5	1914	11	APF89565	Homo sapi	APF89565
C	12	486.8	7.8	1060	29	BZ598327	WMHC17TF	BZ598327
C	13	479.6	7.7	816	10	BF344606	BF344606	BF344606
C	14	478	7.7	631	10	AM859880	QVA-CT036	AM859880
C	15	461.2	7.4	723	13	BX095550	BX095550	BX095550
C	16	460.8	7.4	806	29	BZ600533	WMACQ31TR	BZ600533
C	17	458.6	7.3	1201	13	BX343659	BX343659	BX343659
C	18	457.2	7.3	943	13	BX349993	BX349993	BX349993
C	19	456	7.3	629	28	AQ041508	CIT-HSP-2	AQ041508
C	20	452	7.2	604	12	BM008701	BM008701	BM008701
C	21	443	7.1	909	10	BG675935	BG675935	BG675935
C	22	439.4	7.0	567	12	BM706647	U-E-CQ0-	BM706647
C	23	436.4	7.0	846	14	CD171692	CD171692	CD171692
C	24	433	6.9	763	28	AO371176	PC11-15	AO371176
C	25	429	6.9	977	14	CD051193	AGENCOURT	CD051193
C	26	428.6	6.9	948	10	BF795432	BF795432	BF795432
C	27	423	6.8	989	13	B0619187	B0619187	B0619187
C	28	421.6	6.8	678	29	AG064422	AG064422	AG064422
C	29	420.4	6.7	674	29	AG097408	AG097408	AG097408
C	30	417.6	6.7	743	29	AG088193	Pan trogl	AG088193
C	31	414.2	6.6	711	14	CB962291	CB962291	CB962291
C	32	411	6.6	900	13	B0166056	B0166056	B0166056
C	33	408.6	6.6	549	28	AQ411493	AL513354	AQ411493
C	34	405	6.5	1201	9	AL513354	AL513354	AL513354
C	35	403	6.5	681	29	AG103225	Pan trogl	AG103225
C	36	402.6	6.5	647	29	AG177729	Pan trogl	AG177729
C	37	402.6	6.5	920	13	B0552848	B0552848	B0552848
C	38	401.4	6.5	955	10	BF795502	BF795502	BF795502
C	39	400	6.4	635	12	B1830860	B1830860	B1830860
C	40	398.4	6.4	816	28	AQ746239	AQ746239	AQ746239
C	41	396.4	6.4	519	10	BF813114	OVA-C1015	BF813114
C	42	396.2	6.4	907	13	B0890552	B0890552	B0890552
C	43	396.2	6.4	949	13	B0716016	B0716016	B0716016
C	44	396	6.4	507	28	AQ415290	RPCT-11-1	AQ415290
C	45	396	6.4	932	13	BX348654	BX348654	BX348654

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	
Email: cgabs-remail.nih.gov	
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.	
CDNA Library Preparation: Michael J. Brownstein (MHGRI) & Shirakawa	
Toshiyuki and Piero Carninci (RIKEN)	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUM)	
DNA Sequencing by: Institute for Systems Biology	
http://www.systemsbiology.org	

contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRK Plate: 34 Row: c Column: 24
This clone has the following problem: retained intron.

FEATURES

source
1.3969
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4828044"
/issue_type="Testis"
/clone_lib="NH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

BASE COUNT 1047 a 928 c 902 g 1092 t
ORIGIN

Query Match 11.4%; Score 711.8; DB 11; Length 3969;
Best Local Similarity 87.9%; Pred. No. 8.2e-07;
Matches 824; Conservative 0; Mismatches 102; Indels 11; Gaps 4;

QY 1869 AGCTGAGAGGTGACAGCATGCCGCGACGCTCTACAGCCCTGCTGCTGCGCGCTC 1928
DB 411 AGACCCAGAGGTGACAGCATGCTGCGACGCTCTACAGCCCTGCTGCTGCGCGACCTC 470
QY 1929 CTCTGCTGCGCTCCACACTTGGTGGACATTGAGAGCCCTTACAGCCGCTGAGACTG 1988
DB 471 CCTGCTGCTGCGCTCCACACTTGGTGGACATTGAGAGCCCTTACAGCCGCTGAGACTG 530
QY 1989 TGGGAGCCCTTCTGCTGCTGCGCGACAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2048
DB 531 TGGGAGCCCTTCTGCTGCTGCGCGACAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
QY 2049 GTGAGAGGAGAGGCTCAAGCAGAACCGGGGCTGCGCAGCGCCCTTGGGGCCAGCTGCA 2108
DB 591 GTGAGAGGAGAGGCTCAAGCAGAACCGGGGCTGCGCAGCGCCCTTGGGGCCAGCTGCA 650
QY 2109 GTTCCGGGTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTT 2168
DB 651 GTTCCGGGTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTT 709
QY 2169 GGGCCCCGAGATGAGAGGCTTACAGCCGCGCCAGCGGCTGCGAGGGGTACTGAGTGT 2228
DB 710 GGGCCCCGAGATGAGAGGCTTACAGCCGCGCCAGCGGCTGCGAGGGGTACTGAGTGT 769
QY 2229 CCGCAGCAGTGGCAGCCCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2288
DB 770 CCGCAGCAGTGGCAGCCCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 825
QY 2289 CCTTCCCGGGGCGAGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCT 2343
DB 826 CCTTCCCGGGGCGAGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCT 885
QY 2344 CCATGGGCTCTGTGTGGGGCCGAGCTCCCGCAGCAGCAGCAGCCCTGCTCCACAGCGC 2403
DB 886 CCATGGGCTCTGTGTGGGGCCGAGCTCCCGCAGCAGCAGCAGCCCTGCTCCACAGCGC 945
QY 2404 CCACTGCTCATGACACGCAAGGGGCTGAGAAAGTGGGGGCGACGAGCCGGGACTGGCAG 2463
DB 946 CCACTGCTCATGACACGCAAGGGGCTGAGAAAGTGGGGGCGACGAGCCGGGACTGGCAG 1004
QY 2464 GGAAGTACCCCTTGTGCTGCGGAGTCCACTGGGTGAGAGCAGCTGGGCTCTGTGAG 2523
DB 1005 GGAAGTACCCCTTGTGCTGCGGAGTCCACTGGGTGAGAGCAGCTGGGCTCTGTGAG 1064
QY 2524 TGTGTGAGAGACTTGTGAGAAAGCTTGTGTGTAGCTAGAGGATGTAAATACCAATTCAG 2583
DB 1065 TGTGTGAGAGACTTGTGAGAAAGCTTGTGTGTAGCTAGAGGATGTAAATACCAATTCAG 1124

QY 2584 CACCGTGTCTAGCTCAGGCTCTGGAATGACACCAATCCACACTGTATCTAGTACT 2643
DB 1125 CACCGTGTCTAGCTCAGGCTCTGGAATGACACCAATCCACACTGTATCTAGTACT 1184
QY 2644 CTGATGGGCGCTTGGAGAACCTTATGTCTAGCTCAGGAGTATTAATACCAATTCAGC 2703
DB 1185 CTGATGGGCGCTTGGAGAACCTTATGTCTAGCTCAGGAGTATTAATACCAATTCAGC 1244
QY 2704 ACTGTCTATCTAGCTCAGGCTTGTAAACACCAATTCAGCAGCTGTGTCTAGCTCAGG 2763
DB 1245 ACTGTCTATCTAGCTCAGGCTTGTAAACACCAATTCAGCAGCTGTGTCTAGCTCAGG 1304
QY 2764 GTATGTGAATGACACCAATTCAGCAGCTGTGTCTAGCTCAGG 2800
DB 1305 GTTGTGAATGACACCAATTCAGCAGCTGTGTCTAGCTCAGG 1341

RESULT 2

LOCUS BX423847 1066 bp mRNA linear EST 13-MAY-2003
DEFINITION BX423847 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
ACCESSION CS0DM014YB01 5-PRIME, mRNA sequence.
VERSION BX423847
KEYWORDS BX423847.1 GI:30659589
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1066)
AUTHORS L.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France

EMAIL: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. Contact : Feng liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AM0042D010P1.

FEATURES

source
1.1066
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM014YB01"
/issue_type="FETAL LIVER"
/dev_stage="Fetal"
/note="Organ: Fetal"
/note="Organ: Liver; Vector: PCWSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the PCWSPORT 6
vector. Library was not normalized."

BASE COUNT 200 a 320 c 314 g 223 t 9 others
ORIGIN

Query Match 11.4%; Score 710.4; DB 13; Length 1066;
Best Local Similarity 85.3%; Pred. No. 2.4e-06;
Matches 834; Conservative 6; Mismatches 127; Indels 11; Gaps 4;

QY 1859 GATAGCTTGAAGCTGAGAGGTGACAGCATGCGCGAGAGCTTCACAGCCCTGCTGCTC 1918
DB 50 GATATTCGCGGAGTACAGAGGTGACAGCATGCTGCGAGAGCTTCACAGCCCTGCTGCTC 109
QY 1919 TCGGCGCTCTCTGCTGCTGCTCCACTTGGTGGCACTTGTGAGAGAGCCCTTCAGCCAC 1978
DB 110 TCGGCGCTCTCTGCTGCTGCTCCACTTGGTGGCACTTGTGAGAGAGCCCTTCAGTCCCC 169
QY 1979 CGGTGACAGTGTGGAGACCCCTTCTGCGCTGGCGAAGCCAGCCGCGCTCCCTCAGCTT 2038
DB 170 CACTGACAGTGTGGAGACCCCTTCTGCGCTGGCGAAGCCAGCCGCGCTCCCTCAGCTT 229

Db 642 GGACTGGCAGGAGCTCCACCTGACAGCCCAAGTGCAGATCCAGTACGTAGGTGAAGCCAGCTG 701

QY 2514 GGCTCTGAGTGTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTAGGAGATGTAATA 2573

Db 702 GGCTCTGAGTGTGGTGGAGAGTCTTTATCTAGCTAGGAGATGTAATA 761

QY 2574 CACCAATCAGCACCCTGTGTCTAGCTAGGAGTCTGGAATGCACCAATCCACCTGTGA 2633

Db 762 CACCAATCAGCACCCTGTGTCTAGCTAGGAGTCTGGAATGCACCAATCCACCTGTGA 821

QY 2634 TCTAGCTACTGTGATGGGCTTGGAGAACCTTTATGTCTAGCTAGGAGTGTGAATAAC 2693

Db 822 TCTAGCTACTGTGATGGGCTTGGAGAGTCTTTATGTCTAGCTAGGAGTGTGAATAAC 881

QY 2694 ACCAATCGGCACTGTCTATCTAGCTAGGAGTGTGAATAACACCAATCCACCTGTGT 2753

Db 882 ACCAATCGGCACTGTCTATCTAGCTAGGAGTGTGAATAACACCAATCCACCTGTGTAT 941

QY 2754 CTAGCTCAGGATATGTGATGCACCAATGCAGAGTCTGTATCTGGCT 2800

Db 942 CTAGCTCAGGATTTGTAAACACCAATGCAGCCTGTGTATCTGGCT 988

RESULT 4
AF318322 2067 bp mRNA linear HTC 01-JAN-2002

LOCUS AF318322
DEFINITION Homo sapiens PPI1662 mRNA, complete cds.
ACCESSION AF318322
VERSION AF318322.1 GI:18027735
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2067)
Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T.,
Man,D.F. and Gu,J.R.
TITLE Novel human cDNA clones with function of inhibiting cancer cell growth

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2067)
AUTHORS Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T.,
Man,D.F. and Gu,J.R.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China

FEATURES
source location/Qualifiers
1..2067
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..2067
/gene="PPI1662"
1093..1701
/gene="PPI1662"
/codon_start=1
/product="unknown"
/protein_id="AAL55829.1"
/db_xref="GI:18027735"
/translation="MGIGPALGAAGRPRAVRADLIARPGACRGCTSPSSAGPA
LCILSRMALAAPPRGRARDLPQPAVEPPTRSGSCGARSPTSTPCSRASPDIHPR
AECEERTARDQAPPAAPPAVRDPLGEASVAPSDVESPVLLRDCKHTNOHPVFS
REVSAVPDLYLAALVGPRTFISSGIVNPIGIVYLAQGL"

BASE COUNT 406 a 603 c 590 g 468 t

ORIGIN

Query Match 11.3%; Score 707.2; DB 11; Length 2067;
Best Local Similarity 89.1%; Pred.No.1.7e-06;
Matches 845; Conservative 0; Mismatches 88; Indels 15; Gaps 7;

QY 1873 TGAGAGGTGACAGCATCCGCGAGTCTCAGAGCCCTGCTGGCTGGCGCTCTCT 1932

||||| ||||||| || ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 841 TGAGGGGTGACAGAGCTGTGGCAGTCTCAGACAGCCCTCGCTGCTCGGGCGCTCTCT 900

QY 1933 GGCTGGGCTCCACTTCGCTGGACATTGAGAGACCTTTACGCCACCGCTGCACGTG-GG 1991

Db 901 GGCTGGGCTCCACTTCGCTGGGACATTGAGAGACCTTTACGCCACCGCTGCACGTGAG 960

QY 1992 GAGCCCTTTCTGAGGCTGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2051

Db 961 GAGCCCTTTCTGAGGCTGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020

QY 2052 GAGGAGG--AGGCTCAGAGAGAGACCGGGAGCTGGCAGACGAGCGCTTGCAGGAGGAG 2109

Db 1021 GATCGAGAGAGAGCGGAGAGGAGGAGACCGGGAGCTGGCAGAGCGCTTGCAGGAGGAG 1080

QY 2110 TTCCGGGCTGGGCTGGGCTTTGGCGGAGCCGCACTGGAGACGAGGAGGAGGAGGAG 2169

Db 1081 TTCCGGGCTGGGCTGGGCTTTGGCGGAGCCCTGCACTGGAGACGAGGAGGAGGAGGAG 1139

QY 2170 GCGCGGGGCAATGAGAGGCTTACACCGGAGGAGG-AGGCTGGAGGAGGAGGAGGAGG 2228

Db 1140 GCGCGGGGCAATGAGAGGCTTACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1199

QY 2229 CCCAGCAGTGCAGAGCCGCGCGGCTGTGCTGATGATTTCTACTAGGAGGAGGAGGAG 2288

Db 1200 CCCAGCAGTGCAGAGCCGCGCGGCTGTGCTGATGATTTCTACTAGGAGGAGGAGGAG 1255

QY 2289 CTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2343

Db 1256 CTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1315

QY 2344 CCATGGGCTGCTGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2403

Db 1316 CCATGGGCTGCTGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1375

QY 2404 CCAGTCCCATTCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2463

Db 1376 CCAGTCCCATTCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1434

QY 2464 GCAGTACCCCTGACAGCCCTGTGGGAGATCCACTGGGTGAGAGCAGGAGGAGGAGGAG 2523

Db 1435 GCAGTACCCCTGACAGCCCTGTGGGAGATCCACTGGGTGAGAGCAGGAGGAGGAGGAG 1494

QY 2524 TCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTAGGAGTGTGAATAACCAATCAG 2583

Db 1495 TCTGGTGGAGACTTGGAGAACCTTTATGTCTAGCTAGGAGTGTGAATAACCAATCAG 1554

QY 2584 CACCCCTGTGTAGCTCAGGAGTCTGGAATGCACCAATCCACCTCTGTATCTAGCTACT 2643

Db 1555 CACCCCTGTGTAGCTCAGGAGTCTGGAATGCACCAATCCACCTCTGTATCTAGCTACT 1614

QY 2644 CTGATGGGAGCTTGGAGAACCTTTATGTCTAGCTAGGAGTGTGAATAACCAATCAGG 2703

Db 1615 CTGATGGGAGCTTGGAGAACCTTTATGTCTAGCTAGGAGTGTGAATAACCAATCAGG 1674

QY 2704 ACTCTGTATCTAGCTCAAGGTTTGAACACCAATCAGACCCCTGTGTCTAGCTCAGG 2763

Db 1675 ACTGTGTATCTAGCTCAAGGTTTGAACACCAATCAGACCCCTGTGTCTAGCTCAGG 1734

QY 2764 GATGTGTAATGCACCAATGCAGACTGTGTATCTAGCTAGGAGTGTGAATAACCAATCAG 2811

Db 1735 GATGTGTAATGCACCAATGCAGACTGTGTATCTAGCTAGGAGTGTGAATAACCAATCAG 1782

RESULT 5
BX358085/c 1201 bp mRNA linear EST 05-MAY-2003

LOCUS BX358085
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION BX358085
VERSION BX358085.1 GI:30370184
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Dp		121	GGCTCTCTGGCTTGGGCTCTTA	CTTACTTTGGCGGCACTTGGAGACCCTT	CAGCCACCGCTG	180
Qy		1984	CACCTTGGAGAGCCCTTCTTG	GGCTGGCCAAAGCCAGACCGGCTC	CCCTCAGTTTCAGG	2043
Dp		181	CACCTTGGGAGAGCCCTTCTTG	GGCTGGCCAAAGCCAGGACCGCTC	CTTCAAGCTTGGGG	240
Qy		2044	GAGGTGTGGAGGAGAGGCTCA	AGAGAGAACCGGGGCTGGCCAGCGGCTT	GGCGGCGAG	2103
Dp		241	GAGGTGTGGAGGAGAGGCGC	GAGGGGAGACCGGGGCTGTGTGCGCGCTT	GGCGGCGAG	300
Qy		2104	CTGAGATTCCGGGTGGGGCTG	GGGAGCTTGGCGGGCCCGGCACTTCGAG	ACGAGCGGCGACGCC	2163
Dp		301	CTGAGAGTCCCGGGTGGGCT	GGGCTTGGCGGGCCCGGCACTTCGAG	ACGAGCGGCGACGCC	360
Qy		2184	TGCGAGGCCCGGGGCAATG	AGAGGCTTAGCACCCCGGGCAGCGGCT	GGGAGGGTGTACT	2223
Dp		361	TGCTGTGGCGCGCTGGCAAT	GAGGAGACTTAGCACCGGGCAGACAGCT	GTGGAGGGGTGTCT	420
Qy		2224	GGGTGGCCCGCAGAGATG	AGCAGCGCGCGGCGGCTGTCTGGCTCG	ATTTTCACCTGGGCTT	2283
Dp		421	GGGTGGCCCGCAGAGATG	AGCAGCGCGCGGCGGCTGTCTGGCTCG	ATTTTCACCTGGGCTT	476
Qy		2284	AGCAGCCCTTCCCGCGGGG	CAGGGGCTCGGGACCTGAGCGCCGCA	TGCTTGAAGCGCTCC	- 2341
Dp		477	AGCTGCTCTTCCCGGGGGC	AGGGGCTGTGAGCGCCGCACTGTA	AGCTTCCAC	536
Qy		2342	---CTCCATGGGCTCTCTG	CGGGCCGAGCCTCCCGCAGACACACACCC	CCCTGCTCCAC	2398
Dp		537	CCACTGCCAAGGGCTCTCTG	CGGGCCGAGCCTCCCGCAGACACACACCC	CCCTGCTCCAC	596
Qy		2399	AGCGGCCAGTCCCATCGAC	CAACGGAGGGCTGAGAGTGGGGGCGAC	AGCGACCGGAGCT	2458
Dp		597	GGCGCCAGTCCCATCGAC	CAACGGAGGGCTGAGAGTGGGGGCGAC	AGCGACCGGAGCT	655
Qy		2459	GGCAGGCACTACCCCTTG	CAGCCCTGTGTGGCGGAATCCACTGGGT	TGAAGCCAGCTGGGCT	2518
Dp		656	GGTAGGCACTACCCCTTG	CAGCCCTGTGTGGCGGAATCCACTGGGT	TGAAGCCAGCGGCT	715
Qy		2519	CTGAGTCTGTGTGAGACT	TGGAGAACCTTTATGTCTAGCTC	AGGATCGTAAATACACA	2578
Dp		716	CTGAGTCTGTGTGAGACT	TGGAGAACCTTTATGTCTAGCTC	AGGATCGTAAATACACA	775
Qy		2579	ATTCAGACACCGTGTCTA	GGCTCAGGGTCTGTGAATGCACCAAT	CACACTGTATCTAG	2638
Dp		776	ATTCAGACACCGTGTCTA	GGCTCAGGGTGTGTGAATGCACCAAT	CACACTGTATCTAG	833
Qy		2639	CTACTCTGATGGGCGCTTG	AGAACCTTTATGTCTAGCTCAGGGAT	TGTAATACACAA	2698
Dp		834	CTGCTCTGTGTGGGCGCTTG	AGAACCTTTATGTCTAGCTCAGGGAT	TGTAATACACAA	893
Qy		2699	TCGGCACTCTGTATCTA	GGCTCAAGGTTTGTAAACACACCAAT	CAGACCGCTGTAGC	2758
Dp		894	TYGCACACTCTGTATCTA	GGCTCAAGGTTTGTAAACACACCAAT	CAGACCGCTGTGTAGC	953
Qy		2759	TCAGGGTATGTGAATGC	ACCAATGCACACTGTCTAT	2794	
Dp		954	TCAGGGTATGTGAATGC	ACCAATGCACACTGTCTAT	2794	
RESULT 7						
LOCUS	BK407975	955 bp	linear	EST 15-MAY-2003		
DEFINITION	BK407975 Homo sapiens FETAL LIVER Homo sapiens cDNA clone					
ACCESSION	CSDD0M14YB01	5-PRIME, mRNA sequence.				
VERSION	BK407975					
KEYWORDS	BK407975.1	GI:30768714				
SOURCE	EST.					
ORGANISM	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 955)					

AUTHORS	Ll.M.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Peng ; filiang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0A5015E02QPL.
FEATURES	
source	Location/Qualifiers 1..955 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODM014YB01" /tissue_type="FETAL LIVER" /dev_stage="fetal" /clone_1lib="Homo sapiens FETAL LIVER" /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT	176 a 293 c 291 g 191 t 4 others
ORIGIN	
Query Match	11.1%; Score 690; DB 13; Length 955;
Best Local Similarity	87.7%; Pred. No. 6, 4e-06;
Matches 798;	Conservative 3; Mismatches 98; Indels 11; Gaps 4
Dp	1859 GGATGGCTTGAGCCTGAGAGGTGACAGCATGCGGCAGTCCTCACAGCCCTGTTGCTC 1911
Dp	52 GGAATTCCCCGGGATGAGAGGTGACAGCATGCTGCGAGTCTCAGAGCCCTGCTTGCTC 111
Dp	1919 TCGGGGCCCTCTCTCCCTGCGGCTCCCACCCTCTGCTGGTGACTTTAGAAGCCCTTAGCCCA 1977
Dp	112 TCGGACCTCCCTCTCTGCTGGCTCCCGCTTTTGTGTGACATTGAGAGCCCTTCAGTCCC 171
Dp	1979 CGCTCAGCTGTGGAGAGCCCTTTCTTGGGCTGGCCAAGGCGAGAGCGGCTCCCTCAGCTT 2031
Dp	1172 CACTGCACTGTGGAGAGCCCTTTCTTGGGCTGGCCAAGGCGGAGCCCACTCCCTTAAGCTT 231
Dp	2039 GCAGGGAGGTGTGAGAGAGAGGCTCAAGCAGAGAAACGGGGCTGGCAGAGCGGCTTGGCG 2091
Dp	232 GCAGGGAGGTGTGAGAGAGAGAGAACAGAGAGCGGGAACCGGGGCTGTGTGCTGCATTTGGCG 291
Dp	2099 GCCAGCTGGAGTTCGGGGGTGGGCTTGGGCTTGGCGGCGCCGCACTCGAGAGCAGGGGCC 2155
Dp	292 GCCATCTGTGAGTMCGGGGGTGGGCTTGGGCTTGGTGGGCGCCGCACTCAGAGCAGCAGCG 351
Dp	2159 AGCCCTGCGAGAGCCCGGGGCAATGAGAGGCTTAGACACCGGGGCGAGCGGCTGGGAGGGT 2211
Dp	352 AGCCCTG-CTGGCCCCGGGCAATGGGGACTTAGCACTGGGCCAGTGGCTGGGAGGGT 410
Dp	2219 GTACTGGGTGCCAGAGTGCACAGCCCGCGGCGCTGTGCTGCCTCATTTCTACTGG 2278
Dp	411 GTACTGAGTCCCGGAGCAGTGTGGCCACCGGGCGCTG-----CGTGCATTTCTGCTGG 466
Dp	2279 GCCTTAGCAGCCTTCCCGCGGGGAGGGCTCTGGGACCTGACAGCCCGGCATGCTGAGCCT 2338
Dp	467 GCCTTGGCTGCTTCCACGGGGGAGGGCTCGGGACCTGAGCCCGGCATGCTGARCCT 526
Dp	2339 -----CCGCTTCATATGGGCTCTCTGTGGGGCCGAGAGCTCCCGAGAGAGACACCCCTGCG 2393
Dp	527 CCTACCCCAATCAATGGGCTCTCTGTGGCGCTGARGCTTCCCGAGAGAGACACACCCCTGCG 586
Dp	2394 TCACAGAGGCGCCATGCCATGCATGACACAGCAAGGGGTGAGAGTGGGGCGAGAGGACCGG 2453
Dp	587 TTCACAGGCGCCATGCCATGCATGACACAGCAAGGGGTGAGAGTGGGGCGAGAGGCGCCGCA-CA 645
Dp	2454 GGACTGGCAGGACGCTACCCCTGACGCCCTGTGGCGGATTCACACTGGGTGAAGCAGCTG 2513

|||||
Db 646 GGAATGAGCAGACGCTCCACCTGAGCCAGTCAGATCCAGATAGTAGTGAAGCAGCTG 705
OY 2514 GGCTCCGAGTCTGGTGGAGACTTGGAACTTTATGCTAGCTCAGGAGTCTTAATA 2573
Db 706 GGCTCCGAGTCTGGTGGAGACTTGGAACTTTATGCTAGCTCAGGAGTCTTAATA 765
OY 2574 CACCAATCAGACCCCTGATGCTAGTGAAGGCTGTGAATGACCAATTCACACTGTGA 2633
Db 766 CACCAATCAGACCCCTGATGCTAGTGAAGGCTGTGAATGACCAATTCACACTGTGA 825
OY 2634 TCTAGTACTCTGATGAGGCTGGAGAACCTTTATGCTAGCTCAGGAGTCTTAATA 2693
Db 826 TCTAGTACTCTGATGAGGCTGGAGAACCTTTATGCTAGCTCAGGAGTCTTAATA 885
OY 2694 ACCAATCGACACTCTGTATCTAGCTCAGGAGTCTTAATAACACCAATCAGACCCCTGT 2753
Db 886 ACCAATCGACACTCTGTATCTAGCTCAGGAGTCTTAATAACACCAATCAGACCCCTGT 945
OY 2754 CTAGCTCAGG 2763
Db 946 CTAGCTCAGG 955

RESULT 8
BX402424/c 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX402424 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
ACCESSION BX402424
VERSION CS0D1033YB14 5-PRIME, mRNA sequence.
KEYWORDS BX402424.1 GI:30618809
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A10092B080P1.
FEATURES
SOURCE location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1033YB14"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 268 a 303 c 332 g 234 t 64 others
ORIGIN

Query Match 11.0%; Score 687.8; DB 13; Length 1201;
Best Local Similarity 89.2%; Pred. No. 5.9e-06;
Matches 805; Conservative 4; Mismatches 78; Indels 15; Gaps 6;

OY 1915 GCTCTCGGCGCTCTGCTGGCTGGCCCACTTCGGTGGAGCTGAGAGCCCTTACG 1974
Db 975 GCTCTCGGCGCTCTGCTGGCTGGCCCACTTCGGTGGAGCTGAGAGCCCTTACG 916
OY 1975 CCAACCGCTGACATGTGGAGCCCTTCTGTGGCTGGCCCAAGGAGCCGCGCTCCCTCA 2034
|||||

Db 915 CCACCGCTGACATGTGGAGCCCTTCTGTGGCTGGCCCAAGGAGCCGACCTCTCTCA 856
OY 2035 GCTTGCAGAGAGTGTGGAGGAGAGCTCAAGCAGAACCGGGGCTTCCGACCGCTT 2094
Db 855 GCTTGCAGAGAGTGTGGAGGAGAGCTCAAGCAGAACCGGGGCTTCTGTGGCTT 796
OY 2095 GCGGGCAGCTGAGATTCGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 2154
Db 795 GCGGGCAGCTGAGATTCGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 736
OY 2155 GCGGGCAGCTGAGATTCGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 2214
Db 735 GCGGGCAGCTGAGATTCGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 677
OY 2215 GGGTGTACTGGGTGCGGAGAGTGGCCAGCCCGGCGGCTGTGCTGTGATTTCTCA 2274
Db 676 GGGTGTACTG-GTCCCCAGCAGTGGCCAGCCAC-NCAGSTGGGCTGTGATTTCTCA 623
OY 2275 CTGGGCTTACGACCTTCCCGGGGAGGGGCTGGGAGCTGAGCCCGGCTGAGTCA 2334
Db 622 CCGAGCTTACGCTGCTCCCGGGGAGGGGCTGGGAGCTGAGCCCGGCTGAGTCA 563
OY 2335 GCTTCCC-----CTCCATGGGCTCTGCTGCGGCGGAGCCCTCCCGAGCAGCACC 2389
Db 562 GCTTCCCAGCCAGCTCCAGAGGCTCTGCTGCGGCGGAGCCCTCCCGAGCAGCACC 503
OY 2390 CTGCTCCAGAGCGCCAGTCCCATGACGACGAGGCTGAGAGTGGGCGGCGGCGG 2449
Db 502 CTGCTCCAGAGCGCGGCGGAGTCCCATGACGACGAGGCTGAGAGTGGGCGGCGG 444
OY 2450 ACCGGGAGCTGGGAGGCTACCGCTGAGCGGCTGGGAGGAGTCCACTGGGAGGCA 2509
Db 443 TCGGGAGCTGTAGGAGCTTCCAGCTGAGCGGCTGGGAGGAGTCCACTGGGAGGCA 384
OY 2510 GCTGGGCTCTGAGTCTGTGGAGACTTGGAGAACTTTATGCTAGCTCAGGAGTGA 2569
Db 383 GCTGGGCTCTGAGTCTGTGGAGACTTGGAGAACTTTATGCTAGCTCAGGAGTGA 324
OY 2570 AATACCAATCAGACCCCTGTGCTAGCTAGGCTGTGTATATGACCAATCCACACT 2629
Db 323 AATACCAATCAGACCCCTGTGCTAGCTAGGCTGTGTATATGACCAATCCACACT 264
OY 2630 TGTATCTAGCTACCTGATGAGGCGCTTGGAGAACTTTATGCTAGCTCAGGAGTGA 2689
Db 263 --TATCTAGCTGCTGTGGGCTTGGAGAACTTTATGCTAGCTCAGGAGTGA 206
OY 2690 AATACCAATCAGGACTGTATCTAGCTCAGGAGTGTGTAACACCAATCAGCACCCT 2749
Db 205 AATACCAATCAGGACTGTATCTAGCTCAGGAGTGTGTAACACCAATCAGCACCCT 146
OY 2750 GTGCTGAGCTCAGGCTATGATGACCAATCAGCAGCTGTATGCTACTTTCATG 2809
Db 145 GTGCTGAGCTCAGGCTATGATGACCAATCAGCAGCTGTATGCTACTTTCATG 86
OY 2810 GG 2811
Db 85 GG 84

RESULT 9
BX358084 1201 bp mRNA linear EST 05-MAY-2003
LOCUS BX358084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
DEFINITION clone CS0D1033YB14 3-PRIME, mRNA sequence.
ACCESSION BX358084
VERSION BX358084.1 GI:30368189
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.

Oy	2648	TGGGGCCCTTGGAGAACCTTTATGTGTAGCTCAGGAGATGTGTAATACACCATCGGCACCTC	2707
Db	809	TGTGAATGACCAATATAGACACTCTGTATCTTACGTTACTGTAGGGAGCTTGAGAACCTT	750
Oy	2708	TGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCCCTGT	2751
Db	749	TGTATCTGCGCTCAGTATGATTGTAACGCAACCAATCAGCCCTGT	706
RESULT 12			
BZ598357/c			
LOCUS	BZ598357	1060 bp	DNA
DEFINITION	WHA01717F Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-15K1, genomic survey sequence.		
ACCESSION	BZ598357		
VERSION	BZ598357.1	GI:31506819	
KEYWORDS	GSS.		
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1060)		
AUTHORS	Volik,S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q., Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P., Gray,J.W. and Collins,C.		
	ESP: a sequence-based approach to the structural genomics of tumours		
TITLE	Unpublished (2002)		
JOURNAL	Contact: Volik SY		
COMMENT	Colln Collins' lab		
	UCSF Comprehensive Cancer Center		
	UCSF Box 0808, San Francisco, CA 94143-0808, USA		
	Tel: 415 502 7066		
	Fax: 415 502 5665		
	Email: svolik@cc.ucsf.edu		
	This clone is available from Amplicon Express		
	http://www.genomex.com		
	Class: BAC ends.		
FEATURES			
source	Location/Qualifiers		
	1..1060		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
	/clone="MCF7_1-15K21"		
	/sex="female"		
	/clone_idb="Human MCF7 breast cancer cell line library (MCF7_1)"		
	/note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."		
BASE COUNT	219 a 321 c 317 g 203 t		
ORIGIN			
Query Match	7.8%; Score 486.8; DB 29; Length 1060;		
Best Local Similarity	79.2%; Pred. No. 0.038;		
Matches 740; Conservative	0; Mismatches 127; Indels 67; Gaps 11;		
Oy	1873	TGAGAGGTGAGACATGCGCGGACAGTCCACACAGCCCTGTCGCTCTGGGGCCCTCTCT	1933
Db	1046	TGAGAGGTGAGAGTGTG-CTGAGAGCTTTCACAGCCTTGTCCCTTGCGGGCTCCCTTT	988
Oy	1933	GCTGTGAGCTCCACACTTGTGCTGGACATTGAGAGAGCCCTCAGAGCCACGCTGACATGTGGG	1992
Db	987	GCTGTGAGCTCCACACTTGTG-GCACATTGAGAGACCTTTCACGCCACCTGCTGCACTGT-GG	930
Oy	1993	AGCCCTTTCGTGGCGTGGCACAAGGCGCAGAGCGGCTCCCTCAGCTTCAGAGGAGGTGTGG	2052
Db	929	AGCGCCTTTCGTGGGT-GCCAAGGCGCAAGCGCGGTCCCTCAGCT--CAGAAGGTGTG	873
Oy	2053	AGGAGAGAGCTCAAGCAGGAACCGGGCTGCGCACAGCGGCTTGGGGGCGACCTGGAGTTC	2112
Db	872	AGGAGAGAGCGCCGACACAGGAGCAAGGGCTGCGCGGGGCTGTGTGGAGACACTGGAGTTC	813

OY		2113	CGGGTGGGCGCGGGCTTTGGCGGGGCCCGGCACATCGAGCAGAGGGCCAGCCCTTCAGACC	2172
Db		812	CAGGTGGGTGTGGGCTTGGCGGGGCCCTGCACACTCGAGACAGCCAGCCGGCCCTGCC -GGCC	754
OY		2173	CCGGGCAATGAGAGGGCTTAGCACCCCGGGCCAGCGGCTGCGGAGGGTGTACTGGGTGCC	2232
Db		753	CCAGGCAATGAGGGGCTTAGCACCCCGGGCCAGTGCTGACAGAGGGTGTACTGGGTCCCC	694
OY		2233	AGCAGTGCACCCCGCGCGGCTGTGCTCGCTCGATTCTTCACHTGGGCTTTAGCAGCCTT	2292
Db		693	AGCAGTGCAGCGGCCACCATGGCGCTG---CGCTCATTTCTACATGCGGCTTACCTGCCTT	638
OY		2293	CCCGCGGGGGCGGGGCTGGGGGACATGCAAGCCCGCATGCTGAGGCTC-----CCCTCAT	2347
Db		637	CTGGCGGGGGCGGGGCTGGGAGCTGCAGCTTCAGCTGCCATGCTGAGGCTCCACAGCCCTCGT	578
OY		577	GGGCTCTCTGCACGGGCCCGAGGCTCCCTCGATGATGATGCTGCGCCCTGCTCCACGGGCCAG	518
Db		2408	TCCCATGAGCACCGCAAGGGCTGAGAAGTGGGGGCGCACGGCACCGGACTGCGCAGGCGAG	2467
OY		517	TCCCATGAGAGACCCCAAGGGCTGAGAGATGGGGCACACAAGC -GTGGAGACTGGCAGGCGAG	459
Db		2468	CTACCCCCTGCAGGCGCTGGTGGGAATCCACTGGGGTAAGACCAAGCTGGGCTCCTGAGTCTG	2527
OY		458	TTCCAACTGCGACGCCCCAGTGGAGATCCACTGGGTGAAGCCAGCTGGGCTCTGATGCTA	399
Db		2528	GTGAGAGACTTGGAGAACCTTTATGTCTAGCTCAGGGATCGTMAAT-----	2572
OY		398	GTGGGAACCTTGGAGAACCTTATGTCTAGCTAAAGACTGTAAATACACCAATGGCAGCT	339
Db		2573	-----ACACCAATCAGCAGCCTGTGTCTACTCAGGGTC	2606
OY		338	CTGATCTAGCTCAGGCTTAAATGTTTAAACACACCAATCAGCAGCCTGTGTCTACTCAGGGCT	279
Db		2607	TGTAATATSCAACCAATCCACACTCTGTATCTAGTACTGTATGGGGGCTTGGAGAACCTT	2666
OY		278	TGTGAATGACCAATTCAGACACTCTGTATCTAGTACTGTGTGGGACTTGGAGAACCTT	219
Db		2667	TATG-----TCTAGCTCAGGGATGTAAATACACCAATCGGCACTCTGTATAGC	2717
OY		218	TGTGTGACACTCTGTATCTAGTAAATCTGTGTGGAGCTGGAGAACCTTGTGTCTAGC	159
Db		2718	TCAAAGTTTGTAAACACCAATCAGCAGCCTGT	2751
OY		158	TCAGGGATGTAAATGACACCAATCAGGGCCCTGT	125
RESULT_13				
LOCUS	BF344606/c			
DEFINITION	602015227/F1 NCI_CGAP_Brn64 Homo sapiens cDNA IMAGE:4151022			
ACCESSION	BF344606			
VERSION	BF344606.1 GI:11291975			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
	1 (bases 1 to 816)			
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)			
TITLE	Unpublished			
JOURNAL	Contact: Robert Strausberg, Ph.D.			
COMMENT	Email: csapbs-remail.nih.gov			
	Tissue Procurement: David N. Louis, M.D.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	Data sequencing by: Incyte Genomics, Inc.			
	Gene distribution: MGC clone distribution information can be			

